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Study of gene expression patterns in Eurasian perch (*Perca fluviatilis* Linnaeus, 1758) eggs related to their quality and to the domestication process

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Abstract

In the aquaculture context, increase on production are expected for the next years and yet, many reproductive issues are reported, including high mortality during early life stages. It concerns mostly species for which the domestication process is at the very beginning. My PhD work aimed at better understanding and potentially helping improving reproductive performance by investigating the transcriptomic content of the Eurasian perch (*Perca fluviatilis*) eggs in association with their quality which may constitute one of the sources for embryonic mortality. Eurasian perch is a species, in process of domestication, with strong importance for aquaculture diversification in inland Europe.

We employed microarray and RT-qPCR analyses to characterize gene expression patterns of Eurasian perch eggs presenting different potential to develop properly after fertilization. The experiments were conducted in two scientific contexts. In the first one, different methods to access egg quality were employed and their potential impacts on the transcriptomic results were evaluated. Therefore, when eggs were classified into the respective quality groups (high or low) using early embryonic survival as criteria, we were always able to identify distinct patterns of gene expression between quality groups. However, the number and nature of the differentially expressed genes (DEG) were variable and only one gene was commonly differentially expressed no matter the methods employed. This shows how transcriptomic results are sensitive to methods and should be deeply considered for intra- and inter-species comparisons. The second context consisted of investigating whether females presenting different histories of domestication would differ in their eggs mRNA content, and how it affects egg quality. In this study, females closest to wild populations presented better egg quality. In addition, two distinct patterns of gene expression were observed and more than 300 DEG were identified between populations. Because not much is known about the causes of high variability in reproductive performance in species in process of domestication, these findings could open new hypothesis of investigation. Finally, it became important to determine the moment until which the gene identified in the previous approaches were exclusively supporting embryonic early development. With this purpose, a preliminary study allowed making a first evaluation of the zygotic genome activation (ZGA) in this species.

As a whole, this study identified numerous maternal-effect genes which implication in embryos early development should be further investigated. In addition, these results suggest that more comparable methods to investigate egg quality in Eurasian perch could be established. These methods will make possible more precise studies in the variation of the development success under the influence of distinct factors, such the domestication process.

Similar methods could also be established in other species considering their own common or divergent characters. It would help understanding molecular mechanisms species specific or widely found in finfish species.

Keywords: microarray, egg content, gene ontology, mRNA, fish populations, reproductive cycle, oogenesis

Résumé

Avec le déclin grandissant des prises de pêches, une augmentation de la production piscicole est attendue pour les prochaines années. Cependant, de nombreux problèmes de reproduction sont observés dans les élevages, principalement une mortalité élevée au début de la vie. Cela concerne principalement des espèces piscicoles pour lesquelles le processus de domestication commence. Mon travail de thèse a visé à mieux comprendre et potentiellement aider à améliorer les performances de reproduction en étudiant le contenu transcriptomique des œufs de perche commune (*Perca fluviatilis*) en lien avec leur qualité. Ces résultats participent à la compréhension des mécanismes moléculaires impliqués dans la mortalité embryonnaire précoce. Cette espèce, en cours de domestication, revêt une grande importance dans le contexte de la diversification des espèces d'intérêt aquacole en Europe continentale.

J'ai utilisé des analyses par puce à ADN et RT-qPCR pour caractériser les profils d'expression génique dans les œufs de perche de qualité variables. Les expériences ont été menées dans deux contextes scientifiques. Dans un premier temps, j'ai comparé l'effet des méthodes d'évaluation de la qualité des œufs sur les résultats transcriptomiques obtenus. Ainsi, les œufs ont été classés dans des groupes de qualité (bonne ou mauvaise) en utilisant divers critères liés au développement embryonnaire (taux de survie, taux de malformation) et divers seuils limites pour borner ces groupes. L'utilisation de critères de survie embryonnaire précoces a permis d'identifier des profils d'expression génique distincts entre les groupes de qualité. Cependant, le nombre et la nature des gènes exprimés de manière différentielle (DEG) étaient variables. Un seul gène était exprimé de manière différentielle dans toutes les analyses, quelles que soient les conditions. Cela montre à quel point les résultats transcriptomiques sont sensibles aux méthodes d'évaluation qui doivent être sérieusement pris en compte en amont de comparaisons intra et inter-espèces. Dans un deuxième temps, j'ai comparé le contenu transcriptomique d'œufs de femelles avec des histoires de domestication différentes. Dans cette étude, les femelles les plus proches des populations sauvages présentaient une meilleure qualité d'œufs. En outre, deux modèles distincts d'expression génique ont été observés et plus de 300 DEG ont été identifiés entre les populations. Étant donné que les causes de la variabilité élevée des performances de reproduction des espèces en cours de domestication sont mal connues, cette découverte pourrait ouvrir de nouvelles hypothèses d'investigation. Enfin, il devenait important de déterminer le moment où le gène identifié dans les approches précédentes soutiendrait exclusivement le développement embryonnaire précoce. Dans ce but, une étude préliminaire a permis de faire une première évaluation de l’activation du génome zygotique (ZGA) chez cette espèce.

L’ensemble de ces résultats ouvre la voie vers l’établissement de nouvelles méthodes d’investigation de la qualité des gamètes chez la perche commune. Ces méthodes permettront de faire des études précises de l’évolution du succès de développement à chaque génération au cours d’un processus de domestication. Des méthodes similaires pourraient être établies chez d’autres espèces en prenant en compte leurs particularités. Il serait alors intéressant de tenter d’étudier des espèces présentant des caractères communs ou divergents. Nous pourrons alors tenter de comprendre les régulations propres à chaque espèce ou au contraire largement retrouvés chez plusieurs espèces de poisson.

Mots-clés : *puce à ADN*, *contenu de l’ovocyte*, *ontologie des gènes*, *ARNm*, *populations de poissons*, *cycle de reproduction*, *oogenèse*

Résumé élargi en français

Avec le déclin grandissant des prises de pêche, une augmentation de la production piscicole est attendue pour les prochaines années. Cependant, de nombreux problèmes de reproduction sont observés dans les élevages, principalement une mortalité élevée au début de la vie. Cela concerne principalement des espèces piscicoles pour lesquelles le processus de domestication commence et parmi ceux-ci se trouve la perche commune (*Perca fluviatilis*). Cette espèce revêt une grande importance dans le contexte de la diversification des espèces d’intérêt aquacole en Europe continentale. Bien que le contrôle du cycle de vie soit maîtrisé dans les environnements captifs, cette espèce présente toujours une grande variabilité dans les performances de reproduction. Une des principales causes signalées pour ce problème est la variation de la qualité des ovocytes produit. La littérature consacrée à la qualité des ovocytes de poisson est abondante. Cependant, le contexte scientifique variable rend la compilation et l'analyse des données plus complexes. Ainsi, la comparaison des données de différentes études peut conduire à une mauvaise interprétation car le contexte peut ne pas être correctement pris en compte. D'autre part, la qualité des œufs est déterminée par leurs propriétés intrinsèques, y compris leur contenu moléculaire, et un défaut d'accumulation et / ou de synthèse pourrait entraîner des troubles du développement.

L’objectif de ce travail de thèse est de mieux comprendre et potentiellement aider à améliorer les performances de reproduction en étudiant le contenu transcriptomique des ovocytes de perche commune en lien avec leur qualité. Plus précisément j’ai caractérisé le profil d'expression des transcrits dans les ovocytes II de perche commune, nécessaire au contrôle de leur développement embryonnaire précoce. J'ai réalisé mes expériences dans deux contextes scientifiques : (i) pour faire un lien entre le succès de l'embryogenèse de la progéniture et la qualité des ovocytes de type II en utilisant différentes méthodes de classement et (ii) selon le niveau de domestication des génitrices. Dans les deux cas, les questions ont été principalement analysées au niveau transcriptomique par microarray (technique large échelle) qui a été fait à partir d’une base de données préalablement obtenue en séquençant les trancrits de différents tissus (Phylofish database). Puis, les gènes identifiés comme intéressants ont été confirmés par des techniques plus spécifiques comme le RT-qPCR.

Dans le premier contexte, j'ai cherché une relation entre le contenu en ARNm dans les ovocytes et leur capacité à soutenir un développement embryonnaire normal après la fécondation. Entre-temps, j'ai également testé l'effet des méthodes employées pour évaluer la qualité des ovocytes sur les résultats transcriptomiques obtenus. Ainsi, j'ai utilisé soit chaque critère caractérisant la qualité des ovocytes individuellement, soit une analyse multicritères pour définir les différents groupes de qualité. Pour la première méthode, les ovocytes ont été classés dans des groupes de qualité (bonne ou mauvaise), en utilisant divers critères liés au développement embryonnaire (survie, éclosion et l'apparition de malformations) et divers seuils limites (taux) pour borner ces groupes. L'utilisation de critères de survie embryonnaire précoces a permis d'identifier des profils d'expression génique distincts entre les groupes de qualité. Ainsi, ces travaux ont montré une relation entre le contenu transcriptomique des ovocytes et le développement précoce des embryons. Cependant en fonction du stade ou la survie a été évalué ou selon les taux limites utilisés, j'ai pu montrer que le nombre et la nature des gènes différemment exprimés (GDE) sont différents entre les groupes de pontes de qualités variables. Ceci suggère que la méthode utilisée pour identifier ces groupes de qualité a un effet sur le résultat transcriptomique. Un seul gène était exprimé de manière différentielle dans toutes les analyses, quelles que soient les conditions. Ce gène, *CD68*, codant pour la protéine Macrosialine, a été plus exprimé dans tous les groupes de mauvaise qualité (Log2 Fold-change 1.5 – 2.2). Cette protéine est souvent utilisée comme marqueur macrophage et est associée aux endosomes / lysosomes. Cela permet de faire l'hypothèse que, dans les ovocytes, elles peuvent participer à l'incorporation et à l'accumulation de lipides, car ceux-ci sont importants pour le métabolisme des lipides pendant l'ovogenèse. De plus, des analyses de *Gene Ontology* ont permis d'identifier des gènes liés au système immunitaire et a la traduction était surreprésentée dans certaines listes de GDE. Ces gènes étaient pour la plupart plus exprimés dans des groupes de mauvaise qualité. En opposition, tout en utilisant des critères tardifs pour évaluer la qualité des ovocytes, tels que le taux d'éclosion et le taux de malformations, aucun GDE n'a pu être identifié. Ces résultats suggèrent que les problèmes à des stades de développement embryonnaire tardifs pourraient être liés à d'autres molécules que les ARNms maternels.

Concernant l'analyse multicritères, une étude précédente au laboratoire a analysé plusieurs pontes de qualités variables à l'aide d'une analyse en composantes principales (ACP) suivie d'une analyse d'agrégation hiérarchique (HCA) sur 12 critères décrivant la survie à divers stades, l'apparition de malformations à l'éclosion et la période d'éclosion. Ils ont pu définir trois groupes de qualité, un de bonne qualité (taux de survie et d'éclosion plus élevés et taux de malformations plus faible) et deux de qualité intermédiaire (taux de survie et d'éclosion intermédiaires pour les deux et le groupe deux présentant un taux de malformations plus élevé alors qu'il était inférieur pour le troisième). Un quatrième groupe était composé pour les pontes ayant échoué à la fécondation ou au développement dans les 24 premières heures après la fécondation. Cela correspond au groupe de mauvaise qualité. L'intérêt de cette approche permet non seulement de comparer des groupes de pontes de mauvaise et bonne qualité mais permet d’identifier un continuum de qualités depuis la pire qualité jusqu’à la meilleure. J’ai donc comparé le contenu transcriptomique des ovocytes associés à chacun de ces 4 groupes de qualité. Ce travail m’a permis de mettre au point une technique d’analyse permettant la comparaison simultanée des résultats obtenus pour les 4 groupes. J’ai ainsi pu identifier des gènes dont l’expression est spécifiquement différente dans un groupe par rapport aux trois autres et cela démontre que les groupes 1 à 3 n'ont que de petites différences entre eux tandis que le quatrième a un profil transcriptomique très différencié par rapport aux autres groupes confirmant le lien entre développement précoce et contenu transcriptomiques des ovocytes. Ainsi, par une analyse de *Gene Ontology* sur les GDE du groupe quatre, j’ai pu identifier que des termes liés à la transcription étaient surreprésentés. La plupart des gènes présents dans ces termes étaient moins exprimés dans le groupe quatre (mauvaise qualité).

Cette approche a permis de démontrer qu'il existe une relation claire entre la teneur en ARNm des œufs et leur qualité. Et cette connexion est plus forte avec les premiers stades de développement embryonnaire. Il a également été possible de donner une vue d'ensemble de transcrits cruciaux pour un développement embryonnaire correct. A l’avenir, il sera possible d’étudier plus précisément les conséquences d’une dérégulation de ces gènes par des études fonctionnelles utilisant la technique knock-out, par exemple. De plus, ces constats ont montré à quel point les résultats transcriptomiques sont sensibles aux méthodes d’évaluation de la qualité des ovocytes qui doivent être sérieusement pris en compte en amont de comparaisons intra et inter-espèces.

Dans le deuxième contexte, les relations entre le contenu transcriptomique des ovocytes selon l’histoire de domestication, j’ai comparé deux populations aux histoires différentes. La première était une F1, dont les individus sont nés en captivité mais issus de parents sauvages prélevés dans la nature alors qu'ils étaient encore au stade embryonnaire. Et la seconde population est composée de poissons captifs depuis au moins sept générations dans des bassins en circuit fermé, ici appelé de population F7+, la plus avancée dans le processus de domestication. Cette analyse m’a permis d’identifier 358 transcrits avec des profils d’expression différents entre les deux populations. De plus, les pontes issues de poissons F7+ ont un taux de survie inférieur à celles issues des individus F1, indiquant également une qualité d'ovocytes inferieure dans cette population plus domestiquée.

Une analyse de *Gene Ontology* sur les GDE a révélé que des gènes présentant fonctions liées au système immunitaire étaient surreprésentés parmi eux. Cette constatation est conforme à d'autres études dans la littérature qui ont montré que le processus de domestication a un impact sur les fonctions du système immunitaire. Fait intéressant, dans d'autres études, cette fonction a été identifiée dans des embryons à des stades de développement tardifs ou chez des poissons adultes, ce qui peut indiquer que, chez la perche commune, puisque les gènes du système immunitaire ont été identifiés dans les ovocytes, ils peuvent avoir des fonctions au-delà du système immunitaire.

De plus, afin de mettre en évidence les différences d'expression d'ARNm des ovocytes entre les populations, nous avons sélectionné les gènes les plus différentiellement exprimés (Log2 Fold-change > 4) pour confirmer cette différence par RT-qPCR. Parmi les sept gènes testés, quatre ont vu leur expression différentielle confirmée. Le géne *period 2 (per2)* est connu pour avoir son expression contrôlée au cours des rythmes circadiens dans de nombreuses espèces. Il était plus exprimé dans les ovocytes des populations F1 et peut présenter des fonctions pendant le stade de clivage embryonnaire indépendamment du rythme circadien pour la perche commune. Les trois autres GDE étaient plus fortement exprimés dans la population F7+. Le premier, *HECT domain and Ankyrin repeated Containing E3 ubiquitin-protein ligase 1* (*hace1*), est lié à l'homéostasie redox chez les vertébrés et comme permettrait d'éviter la polyspermie chez les invertébrés marins. Ces deux fonctions pouvant avoir un impact sur le développement embryonnaire suggérant qu'il serait intéressant d'approfondir les recherches sur l'implication de ce gène dans le développement embryonnaire normal. L'autre gène est *muscle excess 3 (mex3b)*, qui s'est avéré essentiel pour le développement embryonnaire, plus spécifiquement pour la structuration et la dégradation de l'ARNm chez le xénope (*Xenopus laevis*). Ces résultats indiquent une conservation potentielle de ce mécanisme entre les amphibiens et les poissons. De plus, une protéine non caractérisée, présentant une homologie avec d'autres protéines, chez d'autres espèces animales (également non caractérisée chez ces espèces), était également plus exprimée dans la population F7+.

Ces résultats renseignent sur l'effet qu'un processus de domestication peut avoir sur la reproduction des poissons. En effet, Les différences d'accumulation et de synthèse des ARNm au cours de l'ovogenèse ont abouti aux différences trouvées par microarray dans les ovocytes des deux populations. Cela montre que la domestication, ou le niveau d'adaptation des génitrices à l'environnement captif, a un impact potentiel sur la teneur en trancrits dans les ovocytes et donc potentiellement sur leur qualité.

Le contenu en ARNm des ovocytes est l'unique source de transcrits permettant le développement embryonnaire normal jusqu'à l'activation du génome zygotique (ZGA). Il m'a semblé important d'identifier cette étape chez la perche commune. Donc, la dernière partie qui compléte ma thèse est l'identification précise de la période où l'embryon commence à exprimer son propre génome et n'est plus uniquement sous le contrôle maternel. De cette façon, il sera possible de dire jusqu'à quel moment les gènes identifiés dans les 2 contextes précédemment décrits, ont un impact direct sur le succès du développement des embryons.

Pour cela, j'ai quantifié l'expression de gènes connus comme étant maternels ou zygotiques chez le poisson zèbre (*Danio rerio*) dans des embryons de la perche commune aux différents stades du développement embryonnaire (entre 5 et 33 heures après la fécondation). Quatre gènes ont montré des profils d'expression en accord avec les profils maternels (eml2 et tbp) et zygotiques (foxa3 et id1) du poisson-zèbre alors que d’autres (*ccnb1*, *plk1* et *klf4*) avaient des profils différents entre les espèces. Ces résultats suggèrent que certains mécanismes conduisant à la ZGA peuvent être conservés entre la perche commune et le poisson zèbre mais qu’il existe néanmoins des différences. De plus, une augmentation significative de l'expression des gènes zygotiques a été observée 23h après la fécondation. Ce stade précède directement la gastrulation (environ 24 heures après la fécondation pour la perche commune). Il est donc possible de faire l'hypothèse d'un lien potentiel entre une mortalité précoce élevée et les défauts de ZGA. Ainsi, les différences d’expression des gènes identifiés dans les approches précédentes pourraient avoir leurs principales conséquences avant la gastrulation.

Dans cette thèse, l'association entre les phénotypes observés au cours du développement embryonnaire et les différents profils transcriptomiques des ovocytes a fourni de nouvelles informations sur la biologie de la reproduction chez la perche commune. Nous avons fait un pas en avant dans le déchiffrement des mécanismes moléculaires impliqués dans le développement précoce des embryons et l’effet de leur dérégulation. Nous avons également montré qu’un facteur intrinsèque, l'histoire de la domestication des génitrices, peut avoir un impact sur le transcriptome des ovocytes et sur leur qualité. De plus, nous avons fourni des premiers résultats sur le début de la transcription zygotique chez l'embryon de perche commune. Ces travaux devraient être poursuivis afin d'améliorer l'information dans les repères de développement embryonnaire et dans les mécanismes moléculaires qui peuvent être partagés entre les espèces. Les mécanismes partagés sont particulièrement importants pour comprendre la conservation ou la perte de certaines caractéristiques à travers l'évolution des espèces.

Ce travail aide à comprendre la grande variation observée dans la reproduction des poissons en élevage en se concentrant sur les espèces pour lesquelles le processus de domestication est actuellement en cours. Habituellement, ces espèces présentent une grande variation de la qualité des ovocytes II au sein d’un même stock de géniteurs. Comprendre les mécanismes moléculaires altérés dans les ovocytes II et le moment où ces perturbations ont un impact sur la génération suivante est fondamental pour comprendre les échecs de la reproduction.

L’ensemble de ces résultats ouvre la voie vers l’établissement de nouvelles méthodes d’investigation de la qualité des gamètes chez la perche commune. Ces méthodes permettront de faire des études précises de l’évolution du succès de développement à chaque génération au cours d’un processus de domestication. Des méthodes similaires pourraient être établies chez d’autres espèces en prenant en compte leurs particularités. Il serait alors intéressant de tenter d’étudier des espèces présentant des caractères communs ou divergents. Nous pourrons alors tenter de comprendre les régulations propres à chaque espèce ou au contraire largement partagés par plusieurs espèces de poisson.

Mots clés : puces à ADN, contenu de l’ovocyte, ontologie des gènes, ARNm, populations de poissons, cycle de reproduction, oogenèse

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I. General context

1. Aquaculture and fish production

According to Food and Agriculture Organization (FAO), in its last report “State of World Fisheries and Aquaculture” (SOFIA, 2018), projections showed that fish production, consumption and trade are expected to continue to increase up to 2030 and aquaculture will contribute the most for this trend (Figure 1). It started from the 80’, in response to a global increase of demand for aquatic products associated to a stabilization or reduction on the amount of captured fish. Aquaculture, thus, became an alternative to maintain the market supply.

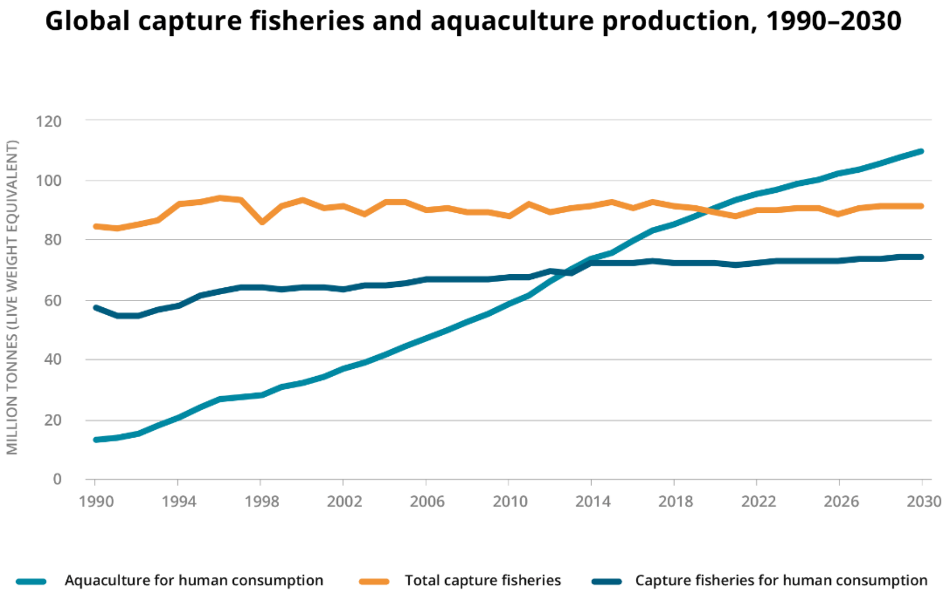


Figure 1. FAO projections for fish production from capture and aquaculture for human consumption or other uses. Note: Excludes aquatic mammals, crocodiles, alligators and caimans, seaweeds and other aquatic plants. From FAO/SOFIA, 2018.

In comparison to the other sectors of food production, aquaculture is the one that grow the most. In 2016, Asia remained the biggest producer in the world, mostly due to the Chinese contribution, and, since 2002, it is the first exporter of fish with a production that continues to grow. Production increase is also seen for other continents including Europe, Americas, and Africa (FAO, 2018).

Among the more than 33.000 cataloged finfish species (Froese and Pauly, 2000), 369 (including 5 hybrids) have already been produced and this number increases each year (FAO, 2018). In Europe, Norway is responsible for most of production of this continent, being the Atlantic salmon (*Salmo salar*) the main species produced. Thus, there is still plenty of opportunity for growth and for diversification on the supply of finfish for consumers. It would be interesting to better develop the chains on inland finfish species, once it exists a marketing demand for local species.

In addition to socio-economic features, fish production increase depends on properly control of several aspects of fish' life in captivity, being properly management of nutrition, health and reproduction, the main ones. Technical packages are still in process of development for many species and many blockage points remain to be solved. Those are mainly identified when new species start to be domesticated. There are some initiatives aiming at studying and developing the productive chain of finfish species presenting economical potential. An example is the recently finished Diversify project (2013-2018). It consisted of an European project which was focused on six species presenting some characteristics needed for aquaculture such as fast growth and good acceptance for the market and thus, a good potential for their productive expansion in Europe. The studied species were: meagre (*Argyrosomus regius*), greater amberjack (*Seriola dumerili*), wreckfish (*Polyprion americanus*), Atlantic halibut (*Hippoglossus hippoglossus*), grey mullet (*Mugil cephalus*) and pikeperch (*Sander lucioperca*). Among many tasks, they were interested in solving bottlenecks during the fish management in captivity, including high mortalities rates during the fish' early developmental stages.

2. Embryos early mortality and fish eggs

High early mortality of embryos is a huge concern in aquaculture since it leads to considerable economical loses. The causes for so are hardly explained because many factors are implicated in the process. Variations are seen between spawning seasons, between fish populations and even within a population, making difficult to properly track and make reliable patterns to study reproductive impairments. On the other hand, it is broadly known that proper embryos development relies on eggs' properties and as so, the production of good quality egg will give the proper conditions for early development success. Thus, researches on egg quality are a promising path to help in aquaculture improvement.

Finfishes present diverse reproductive strategies that in many cases can be observed at the eggs' level (Table 1). For some species, morphological features, which may constitute some advantage in nature, make, from a researcher and/or producer point of view, more challenging working with such material. A good example is the presence of stickiness substance in the outer layer of the eggs of many cyprinids and other species such as pikeperch (*Sander lucioperca*). Because their presence may cause a general attachment of the eggs, making difficult an equal oxygenation, it needs to be removed to ensure embryonic development after artificial fertilization (Kucharczyk et al., 2007). Thus, depending on the species, technical adaptations should be made in order to obtain reproduction in captivity. Because evaluating egg quality itself is already very time consuming, studies on this topic that could allow some level of comparison between species could be useful to gain time in experimentations.

Table 1. Diversity of fecundity, egg size and egg features in fish.*

Species	Fecundity (#eggs/kg)	Egg diameter (mm)	Spawning	Egg features
Eel (*Anguilla anguilla*)	2 650 000	2	Sea water	Floating, pelagic
Turbot (*Scophthalmus maximus*)	1 000 000	1	Sea water	Floating, pelagic
Cod (*Gadus morhua*)	500 000	1.5	Sea water	Floating, pelagic
Seabass (*Dicentrarchus labrax*)	200 000	1.1-1.3	Sea water	Floating, pelagic
Common carp (*Cyprinus carpio*)	175 000	1.35	Freshwater	Adhesive
Eurasian perch (*Perca fluviatilis*)	145 000	1.5-2	Freshwater	Egg ribbons
Zebrafish (*Danio rerio*)	120 000	0.8-1	Freshwater	Demersal
Trout (*Oncorhynchus mykiss*)	3 000	4-5	Freshwater	Demersal
Tilapias (*Oreochromis sp.*)	50-200	2-4	Freshwater	Mouth breeding

*Adapted from: (Bobe, 2015; Jalabert, 2005)

3. Researches on egg quality

In the last years, many research projects intend to investigate egg quality using different gene expression tools. As many molecular mechanisms are commonly shared between phylogenetically close species, investigations on these mechanisms in relation to the embryos early development are of great interest. In this path, the Maternal Legacy Project (2014-2018), which was the starting point for this PhD, had the goal of not only making a molecular portrait of developmentally competent (high quality) zebrafish (*Danio rerio*) eggs, but also to make comparisons between species, including rainbow trout (*Oncorhynchus mykiss*), sea bass (*Dicentrarchus labrax*) and perch (*Perca fluviatilis*). It corresponds to a project supported by the French National Agency of Research (ANR, *in French*).

In this context, the present PhD work has the aquaculture as a background, in a moment when producing eggs of high quality is essential for its development. As a consequence, we sought a better understanding of the molecular mechanism implicated during Eurasian perch (*Perca fluviatilis*) early embryonic development, which is a species with potential for aquaculture diversification in Europe. We employed different approaches to deeply investigate the gene expression profiles while using different ways to evaluate egg quality and also in association with the domestication process. Thus, this work may constitute a pathway of how starting thinking egg quality in a fish species one sees potential for domestication.

II. Scientific context

1. Oogenesis in Teleosts

Gonochoristic species have separate individuals that produce their gametes independently through gametogenesis. This process is called spermatogenesis in males and oogenesis in females. This last one allows the production of mature and ready to be fertilized eggs. After fertilization a certain number of primordial germ cells (PGCs) are produced. During early embryonic development, they will migrate and reach the place where the gonads will develop. In Teleosts, these cells can be recognized by the identification of some cytoplasmic determinants such as Vasa and Nanos, which correspond to localized RNA important during blastomeres cleavage (Abrams and Mullins, 2009; Houston, 2013). The PGCs will suffer structural changings, being converted into oogonia, in females. These ones will divide by mitosis and form nests of oogonia in the ovarian tissue (Lubzens et al., 2010, 2017). In Teleosts, in opposition to many others vertebrates, oogonias continue to divide by mitosis through females' life, thus there is no limit for the number of oocytes that an ovary can produce (Tyler and Sumpter, 1996).

Oogenesis will be the process of production of haploid cells through meiosis (which consists of a synthesis phase followed by two rounds of cell division). In a first moment, the undifferentiated cells, oogonias, will be recruited to enter in meiosis. In the following, meiosis will arrest to allow oocyte growth and it will be resumed only during oocyte maturation. At the end of oocyte maturation, the second meiosis will be arrested and kept this way, through ovulation, until fertilization. These steps are quite conserved among Teleosts species and will be further developed in the following sub-sections.

1.1. *From meiosis I arrest to its resumption*

Called growth phase, the period between the meiosis I arrest and resumption is marked by the folliculogenesis, the synthesis and/or incorporation of most of the content present in the mature egg and the Balbiani's body formation and disappearance. Authors used to sub-divide this phase in different ways. As the incorporation of Vitellogenins provokes the major increase in size, here we will use the terms previtellogenic and vitellogenic phases, as previously used by Patiño and Sullivan, (2002) to describe two of the main oogenesis phases.

1.1.1. Pre-vitellogenic phase

First meiosis will be arrested in *prophase* (in late pachytene or early diplotene stages) and the follicle layers will develop all around each of the oocytes. A follicle comprises the oocyte, granulosa and theca cells, plus a surface epithelium. This structure will remain identical during all the period of oocyte development (Patiño and Sullivan, 2002; Tyler and Sumpter, 1996).

An intense accumulation of RNA is seen right after meiosis arrest. A gradual formation of loops in some regions of DNA in the chromosomes, the “lampbrush chromosomes”, is observed and it allows oocyte transcription. In addition to many mRNA, ribosomal RNAs are commonly amplified and packed into nucleoli. At this stage, a variate number of nucleoli can be observed mostly at the periphery of the nucleus (Wallace and Selman, 1990). The nucleus moves gradually to the cortex of the oocyte and an important cytoplasmic event takes place: the formation of the Balbiani body (Bb). It is one of the earliest asymmetry markers in the oocyte, being constituted of many organelles (mitochondria, endoplasmic reticulum, RNAs…) and not delimited by any membrane. Later on, this body will be disassembled and most of its RNAs will localize at the vegetal pole of the oocyte (see below) (Lubzens et al., 2017). The accumulation of newly formed organelles, mRNA and proteins contributes for a starting decrease in the nucleo-cytoplasmic ratio (Wallace and Selman, 1990).

The next event in the oocyte growth is the appearance of cortical alveoli at the periphery of the oocytes. These alveoli are vesicles that dyes for proteins and carbohydrates in histology. With the increased accumulation, they start moving to the center of the cell and eventually will return to the periphery when the centripetal accumulation of vitellogenin starts (Lubzens et al., 2010). Cortical vesicles will be released in the perivitelline space during the cortical reaction right after eggs’ fertilization (Żarski et al., 2012a). Their content will participate in the vitelline envelope hardening and help preventing polyspermy (Tyler and Sumpter, 1996).

1.2. *Vitellogenic phase*

In this phase a major intake of vitellogenins (Vtgs) takes place, contributing for a huge increase in size and weight of the oocytes. For example, the gonado-somatic index (GSI), which estimates the gonads development by measuring the relationship between its weight in comparison to the body weight, may increase 50- to 100-fold during this phase (Tyler and Sumpter, 1996). At the end of this phase, all maternal molecular material necessary for embryonic development such as mRNA, carbohydrates, proteins, lipids and vitamins should be present into each oocyte. However, some of them still need to be processed.

Vtgs are large molecular weight (300-640 kDa) phospholipoglycoproteins, found in the blood of all oviparous vertebrates females species during vitellogenic phase (Lubzens et al., 2010; Tyler and Sumpter, 1996). Under hormonal control (see section Hormonal control of oogenesis), they will be produced mostly in the liver. However, in zebrafish (*Danio rerio*) expression of *vtg* has been characterized in adipocytes associated with other organs including intestine and ovaries (Wang et al., 2005), implying that other organs may contribute for the plasmatic Vtgs abundance (Lubzens et al., 2010). Three Vtgs (A, B and C) have been characterized, and all of them are sequestered by the oocytes. Vtgs arrive first through the blood stream at the follicle passing from the theca capillaries to the granulosa layer and then using pore canals through the *zona radiata* to reach the oocytes. These ones will express Vtgs surface receptors (VtgR), allowing Vtgs sequestration through receptor mediated endocytosis. They are internalized within coated pits and vesicles that will move to the oocytes periphery, fuse with lysosomes and form multivesicular bodies (MVB) (Lubzens et al., 2010; Wallace and Selman, 1990). At this stage, partial Vtgs processing takes place and the yolk proteins resulting are stored into yolk globules (Carnevali et al., 1999). Lysosomal endopeptidase, e.g. cathepsins, are responsible for the Vtgs proteolysis (Lubzens et al., 2010), giving raise to two major yolk proteins: lipovitellin and phosvitin. The first one is an important nutritional source of amino acids and lipids and the second one is responsible for delivering the minerals required for embryos skeletal development and metabolic functions. Lipids correspond to up to 20% of the oocytes wet weight (Johnson, 2009), 60-80% of them are phospholipids, that are usually rich in polyunsaturated fatty acids. Those represent important membrane components in all organisms (Patiño and Sullivan, 2002). High amount of yolk globules will accumulate in the oocytes until the end of the Vtgs uptake at meiosis resumption.

1.3. *From meiosis I resumption to meiosis II arrest*

This period comprises the oocyte maturation. During maturation, oocytes will resume meiosis (nuclear maturation) and the first polar body will be released. The cytoplasmic maturation will also take place and it will be characterized by the synthesis of proteins from Vitellogenin and oocytes hydration.

At this stage, germinal vesicle (nucleus) migrate toward the periphery and the envelope of the germinal vesicle breaks down (GVBD) (Selman et al., 1993). The first meiotic division takes place, with the expulsion of the polar body I, containing the homologous chromosomes. The remaining chromosomes will then progress in the cell cycle until the metaphase of the second meiotic division when the meiosis will arrest again.

Following the initial processing of the Vtgs, a secondary yolk proteolysis occurs during meiotic resumption. Among the yolk proteins Vtgs-derived, free amino acids and small peptides will also be generated (Carnevali et al., 1992) that, along with the accumulation of ions such as K^+, Cl^- Pi and NH_4^+ (Roderick Nigel Finn et al., 2002) will contribute for the production of osmotic gradients resulting in water influx into the fish oocytes. Additionally, aquaporins translocation to the oocyte plasma membrane, shortly after GVBD (Fabra et al., 2006), facilitates this process. Hydration during oocytes maturation can contribute for up to 88% of their final size, in some Teleosts, for others, however, this process is negligible. It will be especially important for marine species producing pelagic (buoyant) eggs (Tyler and Sumpter, 1996).

1.4. *Ovulation*

Last stage of oogenesis, ovulation corresponds to the process by which *metaphase II* oocytes will be released from their follicles. Depending on the species, the eggs will require some maturation time in the ovarian cavity before leaving the ovary and complete the ovulatory process (Lubzens et al., 2010; Patiño and Sullivan, 2002; Tyler and Sumpter, 1996; Wallace and Selman, 1990). After that, the mature eggs should be ready to be fertilized and able to carry on the early embryonic development.

This process requires the separation of the oocyte from the granulosa layer and rupture of the follicle layers. In most Teleosts, eggs are completely deprived of somatic cells and the mature oocyte will be exposed to ovarian or coelomic fluid or directly to ambient water (Lubzens et al., 2010; Patiño and Sullivan, 2002). After ovulation, the remaining post-ovulatory follicles enter in regression and should be progressively reabsorbed by the ovarian tissue.

1.5. *Oogonia recruitment and hormonal control of oogenesis*

The entry in meiosis marks the oogonia recruitment and the beginning of the oogenesis (Figure 2). Once entering meiosis, the oogonia, now called oocytes, will leave the oogonia nest and will be surrounded by pre-follicle cells (Selman et al., 1993). Oogonial proliferation happens usually in short periods during or after ovulation and their recruitment can occur any time up to mid vitellogenic phase (Tyler and Sumpter, 1996).

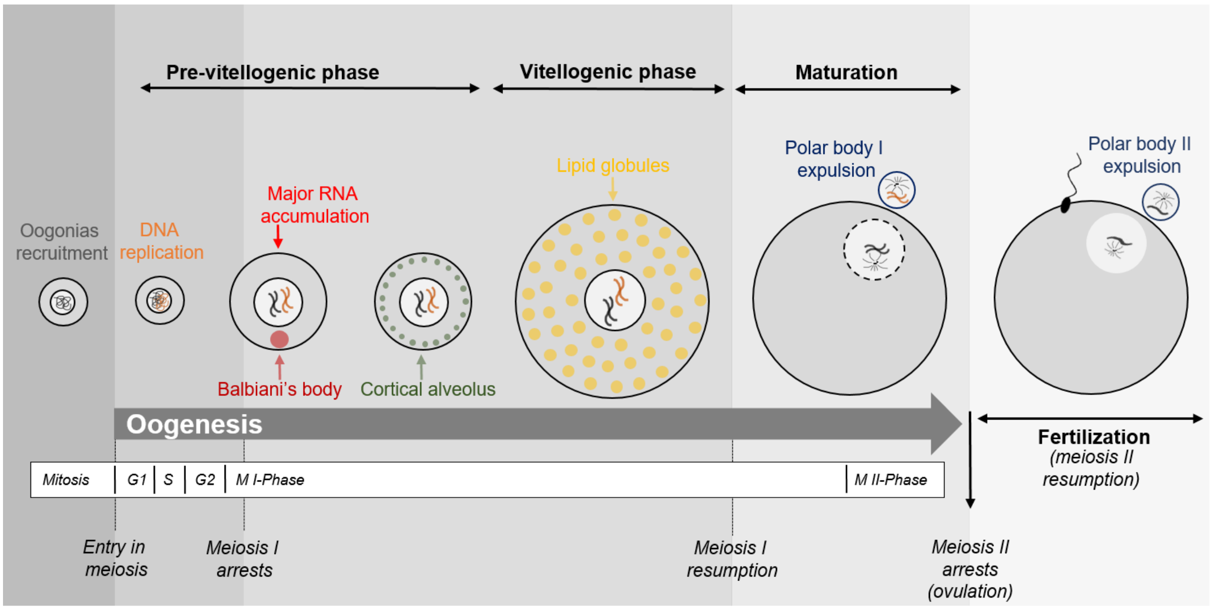


Figure 2. Scheme presenting the oogenesis process in Teleosts. Gray shaded backgrounds mark the important steps of the cellular cycle during oogenesis. Adapted from: (Lubzens et al., 2010, 2017; Marlow, 2010).

The reproduction cycle in teleost fish, will be controlled through hormonal variations: the hypothalamus-pituitary-gonads axis (Zohar et al., 2010). External signs (mainly environmental cues) will be interpreted by the hypothalamus that will release stimulants (Gonadotropin Releasing Hormone - GnRH) to the pituitary. This last one, through one of these two reproductive hormones (Folicule Stimulating Hormone - FSH and Luteinizing Hormone - LH), will stimulate the gonads and control many aspects of their development. The pattern suggested for several fishes is that FSH will regulate vitellogenic phase by stimulating the production of estradiol-17β (E2) in the ovarian follicles and that LH will regulate the oocytes maturation, through the stimulation of the production of the maturation-inducting hormone (MIH) (Nagahama and Yamashita, 2008).

In the ovarian follicle, the theca layer will produce the testosterone (T) that will be converted in E2 in the granulosa layer. This last one will regulate the ovarian growth by stimulating the hepatic vitellogenin production (Lubzens et al., 2010; Nagahama and Yamashita, 2008). Thus, T and E2 will be essential during the vitellogenic phase. Once this phase is complete, T and E2 synthesis decrease and hormones acting on the oocytes maturation as, for example, the maturation-inducting hormone (MIH) and the maturation-promoting factor (MPF), are produced. MIH acts activating MPF which will release the oocyte from meiotic arrest (Nagahama and Yamashita, 2008). MIH will also be required for the last stage of oogenesis, ovulation (Patiño and Sullivan, 2002).

Oogenesis is a hormonally regulated process and in the absence of the proper stimuli the follicles may proceed to atresia which is marked by the reabsorption of the follicles. It can be seen in histological preparation by the disintegration of the oocyte with the hypertrophy of the follicle cells that become phagocytic with presence of many vacuoles to incorporate and digest the oocytes components (Lubzens et al., 2010).

1.6. *mRNA dynamic during oogenesis and its importance for embryonic development*

Most of transcription in the oocytes takes place during pre-vitellogenic stage, even if some transcription occurs during vitellogenesis, as suggested by Kleppe et al., (2014) that found different transcriptomic profiles in Atlantic cod (*Gadus morhua)* oocytes at different developmental stages (from pre-vitelogenic oocytes to ovulated eggs). Most of mRNAs needed during vitellogenesis are usually transcribed during pre-vitellogenic phase. For example, Vtg receptor (VtgR) transcription predominates during pre-vitellogenic, which suggests that they will be recycled by the oocyte surface during vitellogenic phase (Perazzolo et al., 1999). At the end of the vitellogenesis, no more transcription is seen, once germinal vesicle will break down, which is incompatible with transcription. Also sets of mRNA start being degraded, mostly those ones required during vitellogenesis (Svoboda et al., 2017). In other words, at the end of vitellogenic phase, possible changes in the oocyte transcripts profile should be due to mRNA degradation instead of transcription.

In zebrafish, studies of the mRNA dispersion in oocytes showed dynamic patterns, with important change of localization during oogenesis. They indicate the first appearance of the animal-vegetal poles which determines the antero-posterior axis. Thus, embryonic patterning is established into the oocytes long before ovulation (Abrams and Mullins, 2009). As mentioned, RNAs will mark the vegetal pole. The transcripts *buc*, *nanos*, *vasa* and *dazl*, for example, are located in the Bb during early pre-vitellogenesis phase. After the body disassemble, *buc*, *vasa* and *dazl* localize at the vegetal pole, while *nanos* diffuses in the cytoplasm. At the end of the pre-vitellogenic phase, two of these mRNAs will change their distribution, *vasa* will localize at the periphery and *buc* concentrates in the animal pole (Figure 3) (Abrams and Mullins, 2009). It is certain that the distribution of these transcripts are important for the establishment of this first embryonic axis. However, it is still unknown if these modifications are due to degradation in the previous location, to the movement of the transcripts into the oocyte or to increase of transcription activity in the new locations.

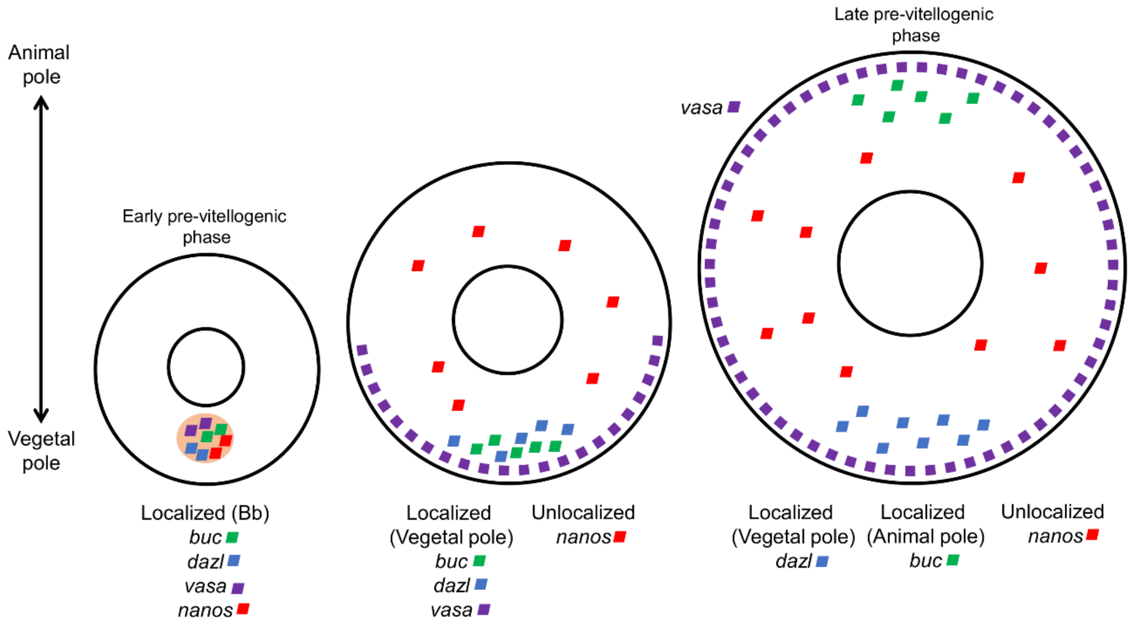


Figure 3. mRNAs localization during oocyte development. During early pre-vitellogenic phase of oogenesis buc, nanos, vasa and dazl transcripts localize to the Balbiani body (Bb, orange). Onde Bb disassembles, buc, vasa and dazl mRNAs stay at the vegetal cortex, while nanos becomes unlocalized. Note vasa has a broad vegetal cortical domain at this moment. During late pre-vitellogenic phase, dazl and nanos keep their distribution, buc, localizes in the animal pole and vasa is localized radially at the oocyte cortex. Adapted from: (Abrams and Mullins, 2009).

Later events during embryonic development are also under control of maternal factors such as dorsoventral axis patterning and tissues morphogenesis. The knowledge in the establishment of the dorsoventral axis is the most advanced and has shown to involve genes belonging to three signaling pathways: Wnt/β-catenin, Wnt/Ca^{2+} and TGF-β (Lyman-Gingerich and Pelegri, 2007). For example, *hecate* and *tokkaebe* that participate in the Wnt signaling pathway, are important to induce dorsal organization. It was proved by the observation of radially ventralized zebrafish embryos that were mutants for these two genes (Abrams and Mullins, 2009). As well as *hecate* and *tokkaebe*, many other maternal-effect mutants and transcripts have been identified as impacting not only axis establishment but also Bb formation, tissues morphogenesis and others aspects of zebrafish embryonic development (Table 2).

Table 2.Maternal regulators of zebrafish development. Adapted from: (Marlow, 2010).

Phase affected	Gene	Process affected	References
Egg activation	*Claustro*	egg activation/cytoplasmic segregation	(Pelegri et al., 1999, 2004)
	emulsion	egg activation/cytoplasmic segregation	(Dosch et al., 2004)
	*FatVg/a*dipophilin	cortical rotation, dorsal axis formation, and germ plasm segregation	(Chan et al., 2007)
	jumpstart	egg activation	(Dosch et al., 2004)
	under repair	egg activation/cytoplasmic segregation	(Pelegri et al., 1999, 2004)
Cleavage, mitosis	*acytokinesis*	cleavage	(Kishimoto et al., 2004)
	atomos	karyokinesis and cytokinesis	(Dosch et al., 2004)
	aura	cytokinesis/ membrane	(Pelegri et al., 2004)
	barrette	karyokinesis and cytokinesis/membrane deposition	(Pelegri et al., 2004)
	cellular atoll, Sas6	cytokinesis, centrosome assembly	(Dosch et al., 2004; Yabe et al., 2007)
	cellular island	cytokinesis	(Dosch et al., 2004)
	cobblestone	reduced cleavages/fewer cells	(Pelegri et al., 2004)
	futile cycle	pronuclear congression	(Dekens et al., 2003; Pelegri et al., 2004)
	indivisible	karyokinesis and cytokinesis	(Dosch et al., 2004)
	irreducible	karyokinesis and cytokinesis	(Dosch et al., 2004)
	nebel	cytokinesis/ furrow formation	(Pelegri et al., 1999, 2004)
	T cell leukemia/ lymphoma 1 gene, TCL 1	cleavage	(Narducci et al., 2002)

	weeble	partial cytokinesis	(Pelegri et al., 2004)
	bo peep	DNA loss/ fragmentation	(Pelegri et al., 2004)
	golden gate	defective chromatin segregation	(Pelegri et al., 2004)
	kwai	defective chromatin segregation	(Pelegri et al., 2004)
	screeching halt	chromatin bridges. Development stalls at MBT (MZT)	(Wagner et al., 2004)
	waldo	DNA loss/fragmentation	(Pelegri et al., 2004)
Epiboly, tissue cohesiveness, enveloping layer (EVL) differentiation	*bedazzled*	epiboly	(Wagner et al., 2004)
	betty boop/Map kap kinase2	epiboly	(Holloway et al., 2009; Wagner et al., 2004)
	EP-CAM, Tacstd	epiboly	(Amsterdam and Hopkins, 1999; Slanchev et al., 2009)
	Interferon Regulatory Factor 6, Irf6	epiboly	(Sabel et al., 2009)
	janus	blastoderm cohesiveness	(Abdelilah et al., 1994)
	mission impossible	gastrulation/ epiboly	(Pelegri et al., 2004)
	poky, IKK	epiboly, EVL differentiation	(Fukazawa et al., 2010; Wagner et al., 2004)
	slow	epiboly	(Wagner et al., 2004)
	yobo	epiboly	(Odenthal et al., 1996)
Patterning and morphogenesis	*activin-like receptor 8, alk8;lost a fin, laf*	maternal zygotic ventral specification	(Mintzer et al., 2001)
	blistered	ventral tail vein	(Wagner et al., 2004)

	brom bones/hnRNP1/PTB	egg activation; dorsal axis specification	(Mei et al., 2009; Wagner et al., 2004)
	eomesodermin	mesoderm patterning	(Bruce et al., 2003)
	hecate	dorsal axis specification	(Lyman Gingerich et al., 2005; Pelegri et al., 2004)
	Knypek, kny	gastrulation, neurulation, cilia polarity	(Borovina et al., 2010)
	lazarus, pbx4	maternal zygotic—hindbrain formation	(Waskiewicz et al., 2001)
	Ligand of Numb protein-X (Lnx-1)	dorsal-ventral axis formation	(Ro and Dawid, 2009)
	ogon, sizzled	maternal zygotic dorsal–vental patterning	(Miller et al., 1999; Wagner and Mullins, 2002; Yabe et al., 2003)
	one-eyed pinhead (oep)/ EGFCFC	maternal zygotic. Patterning mesendoderm along the animal-vegetal axis	(Gritsman et al., 1999)
	oval; intraflagellar transport protein 88, Ift88	cilia formation Hedgehog signaling	(Huang and Schier, 2009)
	pol delta 1, flathead, fla	replication, mitotic exit	(Plaster et al., 2006)
	pollywog	rostral andcaudal morphogenesis	(Wagner et al., 2004)
	POU domain, class 5, transcription factor 1 pou5f1/pou2; octamerbinding transcription factor 4oct4;speil ohne grenzen, spg	maternal zygotic regulation of epiboly endoderm formationMouse: development prior to blastocyst	(Foygel et al., 2008; Lunde et al., 2004; Reim and Brand, 2006; Reim et al., 2004)
	pug	posterior bodymorphogenesis	(Wagner et al., 2004)
	radar;gdf6	ventral axis specification	(Goutel et al., 2000; Sidi et al., 2003)

	runt-related transcription factor, runx2bt	ventral axisspecification	(Flores et al., 2008)
	scribble, landlocked	maternal zygotic gastrulation movements	(Wada et al., 2005)
	somitabun, piggy tail, Smad5	(*somitabun)*dominant maternal effect ventral fates. (*piggy tail*) maternal zygotic ventral specification	(Hild et al., 1999; Kramer et al., 2002; Mullins et al., 1996)
Zebrafish: limits expression of the Nodal related cyclops	*squint Nodal-related 2*	maternal zygotic. Patterning mesendoderm along the animal–vegetal axis	(Bennett et al., 2007; Dougan et al., 2003; Feldman et al., 2000; Gore et al., 2005; Pei et al., 2007)
	Tokkaebi, tkk; Syntabulin	dorsal axis specification	(Nojima et al., 2004, 2010)
	Trilobite, tri; van gogh	gastrulation, neurulation, cilia polarity	(Borovina et al., 2010; Jessen et al., 2002)

2. Early embryonic development and the maternal-to-zygotic transition

Following ovulation, the eggs will be fertilized, allowing the second meiotic division and the second polar body expulsion. Next, male and female pronuclei will fuse and embryonic development will start with the first cell division. Early embryonic development of animals will rely on maternal factors, meaning that an ovulated egg should carry all necessary content to support this process. Maternal investment in oogenesis corresponds to a maternal effect, which is all non-genetic contribution of the female to the phenotype of her offspring (Green, 2008). One of the earliest studies giving evidences of this phenomenon was performed on fertilized eggs of purple sea urchin (*Arbacia punctulata*). After having their nucleus removed, they continue to develop showing the ability of the maternal factors to carry on embryonic development, independently of the zygotic genome until a certain stage (Harvey, 1936). Nowadays it is possible to infer that development was arrested when the “embryo” reached the maternal-to-zygotic transition (MZT) (Blaxter, 2014). This became possible due to the fast increase of omics technologies allowing us to have new information on the changes happening during early development. It also allowed to demonstrate comparable phenomena in many animals, such as echinoderms, nematodes, insects, fish, amphibian and mammals (Figure 4) (Tadros and Lipshitz, 2009).

Following the exclusive maternal control, in proper conditions, embryos will be asked to start handling their own development, by transcribing their genome and translating their own proteins. The period between the exchange from maternal to embryonic control is known as the MZT (Tadros and Lipshitz, 2009). Embryonic development involves a variate number of complex events including patterning, morphogenesis, cell differentiation and growth. For many organisms, the task of controlling the first cell divisions relies on maternal factors with a gradual transfer of responsibilities to the developing embryo. The timing and dynamic of this transition still lack complete understanding. Overall, the MZT encompasses two main steps, maternal mRNA decay and zygotic genome activation (ZGA).

In addition to the MZT, another important transition takes place during embryonic development in fish and other non-mammalian vertebrates, the midi-blastula transition (MBT). The MBT is characterized by the beginning of the asynchronous cell division period, lengthens of the cell cycle, introduction of gap phases and cell cycle checkpoints (Zhang et al., 2017). The MBT coincides with the major ZGA in many species, such as zebrafish (Cheung et al., 2018c). In medaka (*Oryzias latipes*), both transitions seem to happens in distinct moments. In this species, RNA polymerase II activity was detected before MBT, right after 64-cells stage (Kraeussling et al., 2011).

2.1. *Maternal mRNA decay*

After fertilization, a variable number of maternal loaded transcripts starts to be degraded and will progressively be replaced by zygotic transcripts. As said, the timing and duration of these events are variable according to the species (Figure 4). Taking as example two nematode species *Ascaris suum* and *Caenorhabditis elegans*, in the first one the maternal loaded transcripts will be less implicated during early embryonic development once almost all of them are completely degraded after fertilization and the embryonic major transcription occurs right after fertilization (Wang et al., 2014). In opposition, for *C. elegans*, the embryos will develop under maternal transcripts influence up to 4-cell stage, after what the zygotic genome will begin to be transcribed and the maternal transcripts will be degraded (Baugh et al., 2003). In addition, most of the *A. suum* orthologs for the maternal genes identified in *C. elegans* are, in fact, zygotic transcribed genes, showing that the repression of the zygotic transcription is not required for *A. suum* early embryonic development (Blaxter, 2014). This example shows that even species that share morphological aspects during development, present completely different molecular patterns for MZT. Among the studied species, *A. suum* constitutes an exception once for most of the studied species, their embryos pass from a zygotic quiescent transcription stage, and are thus under an exclusive maternal influence, until the onset of the embryonic transcription (Figure 4). In fish, due to the diversity of species, differences, as shown in the nematodes example, can also be present. Concerning species from different taxa, many time the MZT pattern is conserved, but presenting temporal distinction. In mouse, for example, the ZGA occurs before the first cell division (Li et al., 2013), while in frog several rounds of blastomeres cleavages take place before the ZGA (Yang et al., 2015) (Figure 4).

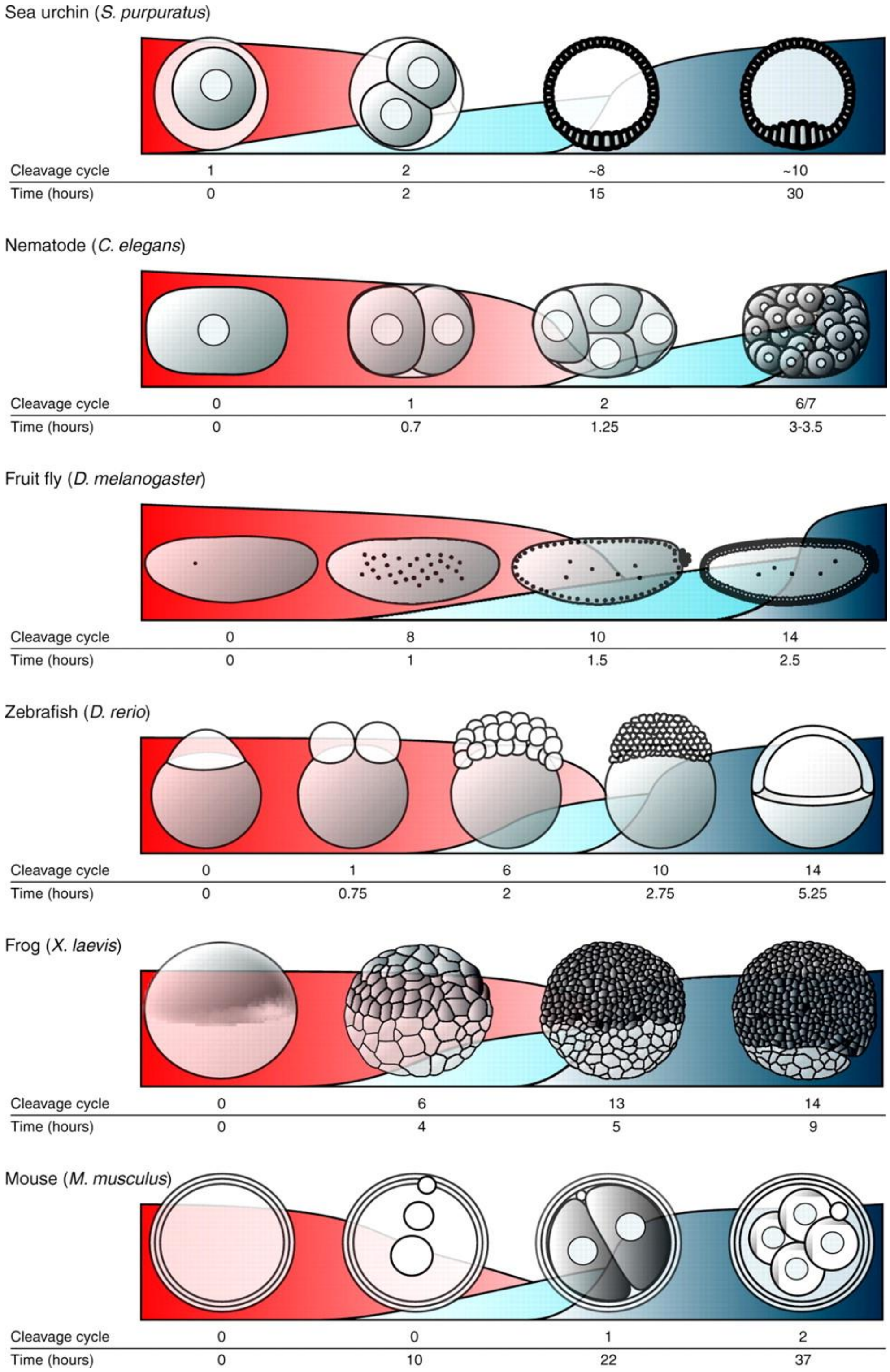


Figure 4. A comparative overview of the maternal-to-zygotic transition (MZT) in several model organisms. Key embryonic stages for each model organism are depicted schematically above the corresponding cellular cleavage cycle and time after fertilization. The red curves represent the degradation profiles of destabilized maternal transcripts in each species. The light and dark blue curves illustrate the minor and major waves, respectively, of zygotic genome activation. The last embryonic

stage presented for each organism is the developmental point at which there is a major requirement for zygotic transcripts (From (Tadros and Lipshitz, 2009)).

Maternal RNAs seem to decay in response to developmental events as fertilization and embryonic genome activation. In mammals there is a reduction of about 50% of the amount of transcripts in the eggs from fertilization until ZGA (Svoboda et al., 2017). In zebrafish (*Danio rerio*), which is one of the Teleosts species most studied, the different events of the ZGA have been characterized. Considering mature eggs, their transcripts will start to be degraded after fertilization and follow different kinetics per group of transcripts, being they before, during or after ZGA (Figure 5) (Aanes et al., 2014; Mathavan et al., 2005).

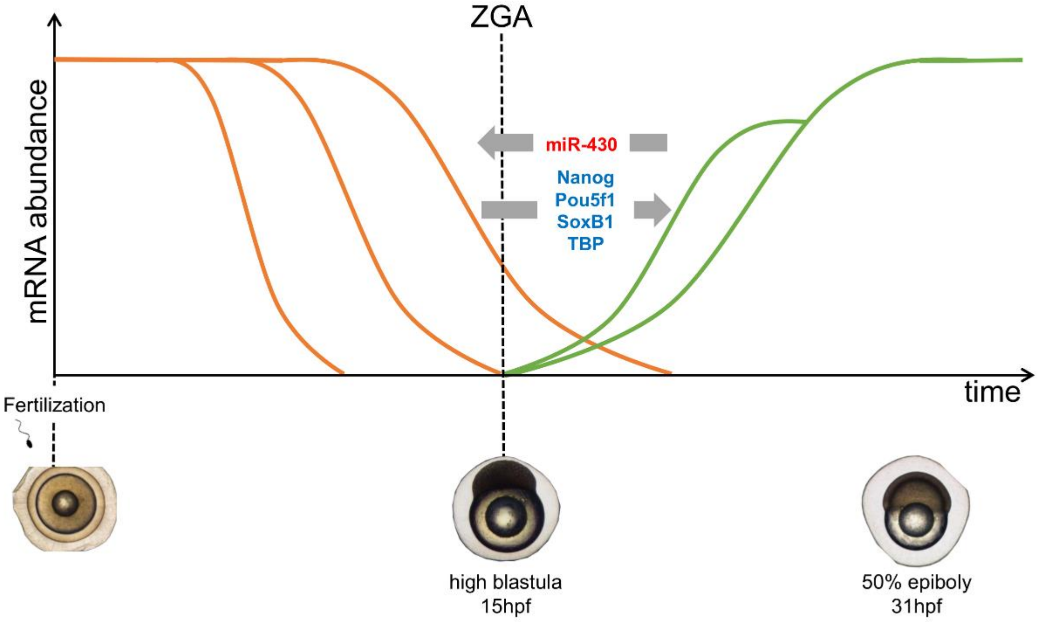


Figure 5. Scheme representing mRNAs dynamic proposed for zebrafish during maternal-to-zygotic transition. Orange lines represent the three patterns of maternal mRNA degradation. Green lines represent the zygotic genome activation. Nanog, Pou5f1, SoxB1 and TBP are necessary to activate a large number of zygotic genes, including miR-430 that is responsible for the clearance of many maternal mRNAs. Below the graph, pictures represent embryos of Eurasian perch (*Perca fluviatilis*) representing the stages of the events in zebrafish (Adapted from: (Cheung et al., 2018c; Lee et al., 2013; Svoboda et al., 2017)).

Functional analyses of maternal loaded transcripts commonly reveal more basic cellular functions, the so-called “housekeeping” functions, such as cell cycle, DNA replication and intracellular protein trafficking (Aanes et al., 2011). They are expected to be more abundant in a period of the development on which embryos accumulate a large number of cells before gastrulation (Zhang et al., 2017). They will mostly be degraded independently or during

ZGA (Aanes et al., 2011) through maternal programed mechanism for transcripts destabilization (Bazzini et al., 2016; Mishima and Tomari, 2016). The last portion of maternal transcripts has a role in later stages of the development, being also implicated in the ZGA. They will depend on the zygotic transcription to be cleared. The best known mechanism for so is through zygotically transcribed miRNAs (Despic and Neugebauer, 2018). They have been studied in some organisms, such as frog (*Xenopus laevis - miR-427*) (Lund et al., 2009), fruit fly (*Drosophila melanogaster - miR-309*) (Benoit et al., 2009) and zebrafish (*miR-430*) (Giraldez et al., 2006). For the last one, maternal Nanog together with Pou5f1 and SoxB1 directly regulate the expression of *miR-430* that is responsible for clearance of many maternal transcripts (Lee et al., 2013). Similar mechanisms to degrade maternal mRNA using *miR-430* were also proposed in medaka (*Oryzias latipes*), for which the expression of this *miR-430* also increased from MBT (Tani et al., 2010).

2.2. *Zygotic genome activation (ZGA)*

Zygotic transcription switch on is usually described to happen in two stages: a minor followed by a major transcription activation. Minor transcription produces factors that will, among other functions, be responsible for the final maternal mRNA clearance, as described above. Major transcription will begin between the high and oblong stages at the blastula period in zebrafish (Aanes et al., 2014; Harvey et al., 2013) and will produce factors needed in later stages of embryonic development. Thus their functional analysis revealed that they are mostly transcription regulators, which will allow cells differentiation and specialization (Aanes et al., 2014; Zhang et al., 2017).

Some mechanisms for transcription onset have been studied. Among the most described there are the nucleocytoplasmic ratio (N/C), maternal clock and chromatin regulation. The first one implies the presence of maternal factors repressing embryonic transcription that will be “diluted”, due to the increase of the nuclear material in comparison to the cytoplasmic in result of the cell divisions. The maternal clock mechanism postulates that the onset of zygotic transcription relies more on the developmental stage rather than on the cell cycle. For example, the polyadenylation of the maternal mRNAs and the increase on their translation may act as activators of the transcription. Some transcriptional repressors and activators have been identified: TKK as a repressor in Drosophila (Benoit et al., 2009) and TBP as an activator in zebrafish (Ferg et al., 2007; Veenstra et al., 1999) (Figure 5). Concerning the chromatin regulation, it has been hypothesized that its organization should be more permissive to local changes once they will allow transcription and thus, ZGA. These changes are usually preprogrammed by histone marks and/or other epigenetic patterns [reviewed in (Lee et al., 2014; Tadros and Lipshitz, 2009; Yartseva and Giraldez, 2015; Zhang et al., 2017)].

Many aspects of the MZT are still to be elucidated and the use of methodologies allowing making a distinction between maternal and zygotic transcripts (for example: (Harvey et al., 2013; Lee et al., 2013)) are precious to better explain this phenomenon. For example, a study aiming at characterizing the transcription dynamic during zebrafish early development, used total RNA for microarray analysis and identified changes in the mRNA levels before MBT. They suggested that zygotic transcription starts before this period (Mathavan et al., 2005). Another study characterized the transcriptome dynamic during MZT in the same species, using poly(A) selected RNA-seq as the screening method and also found increase of many transcripts before the MBT. They suggested that it was in association with cytoplasmic maternal mRNA polyadenylation (Aanes et al., 2014). Finally, a last study, aiming at identifying the maternal and zygotic transcriptomes in the same species, tracked RNAs containing paternal single nucleotide polymorphisms (SNPs). They found that most of genes described as being transcribed before the MBT by the first above mentioned study (Mathavan et al., 2005), corresponded in fact to maternal mRNA polyadenylation, rather than only zygotic transcription (Harvey et al., 2013). They were able to highlight some aspects of post-transcriptional processing happening before ZGA and only detected zygotic transcripts before MBT. Thus, methods that consider the different sources of variation affecting the transcriptome will be valuable to bring lights to existing disagreements.

Which remains clear in the MZT is that it corresponds to a period tightly regulated and as so, small impairments may lead to an inability of the embryos to control their development, and consequently it may lead to their death. Thus, issues during the MZT may be connected with early mortalities during the first steps of embryonic development. For example, simultaneous removal of maternal Nanog with SoxB1 and/or Pou5f1, which are factors acting on the onset of zygotic transcription in zebrafish, completely block gastrulation resulting in developmental arrest (Lee et al., 2013).

3. Egg quality

At the beginning of the 20th century, the embryologist E. B. Wilson formulated the increasingly emerging biological principle that embryonic development is largely dependent on the process by which the oocyte is generated (*“embryogenesis begins during oogenesis”)* (Coticchio et al., 2004). From there, many of scientists have tried to find a good way to predict the ability of an egg to develop properly into a healthy embryo. However, very limited success has been achieved.

In fishes, there are three main definitions of egg quality. For Kjorsvik et al. (1990), the egg quality can be defined as “the egg’s potential to produce a viable fry”. For Bromage et al. (1992), good egg quality is usually defined as those which “exhibit low levels of mortality at fertilization, eying, hatching, and first feeding and those which produce the fastest-growing and healthiest fry and older fish”. The last definition that was found and the most used nowadays comes from Bobe and Labbé (2010), to whom the egg quality or oocyte developmental competence is “the ability of the egg to be fertilized and subsequently develop into a normal embryo”. In common, all these authors preconize the production of individuals in good health and lacking deformities.

The quality of an egg is determined, aside of the environmental aspects, by its intrinsic properties: its genes, maternal transcripts, nutrients contained within the yolk and many organelles, all of which are provided by the mother (Brooks et al., 1997). Defects of accumulation would lead to developmental impairments and thus lack of developmental success.

3.1. *Using survival to assess fish egg quality*

Fish populations are dependent upon the production of good quality eggs. Poor egg quality is one of the major constraints in the expansion of aquaculture of both marine and freshwater fish species (Brooks et al., 1997; Kjorsvik et al., 1990). A better understanding of the mechanisms of the egg production during oogenesis will be an important step to better control the quality of the eggs produced (Migaud et al., 2013).

The compilation and analysis of the literature devoted to fish egg quality is complex due to the use of heterogeneous criteria based on the developmental performance (evaluation of the embryonic and larval development completion, including the occurrence of malformations), which is the classical and reliable way to assess egg quality. Survival is usually estimated at the 2-cell stage (fertilization rate), eyed stage (or until some other stage as, for example, swimming bladder inflation) and at hatching (hatching rate). The choice of the stage evaluated is usually species-specific, and may depend on the rearing practices or yet on the project’s goal, in case of research studies. A standardized methodology that would take into account classic criteria but also survival at later stages and the occurrence of embryonic malformations would be of great interest (Bonnet et al., 2007a).

The use of these criteria to evaluate early developmental success is efficient, but it can be long and costly for fish farmers, once they do not predict the egg quality. It becomes necessary to identify predictors before fertilization, in order to avoid time and money spending.

3.2. *Criteria used to predict fish egg quality*

Coticchio et al. (2004), affirmed that, in mammals, the assessment of oocyte quality is probably the most important and difficult task for in vitro fertilization. For them, a mature and good quality oocyte is identified by a perfectly spherical shape, a regular pellucid coat surrounding the oocyte, an intact polar body I, and a translucent, homogeneously colored cytoplasm without inclusions. In addition, they also attempt to the meiotic spindle position that may be a valuable criterion for assessing oocyte quality. Indeed, once it marks the oocyte animal pole, it establishes the proper orientation of the first cleavage plane. In humans, morphological aspects allowing identifying oocytes of better quality are of major importance once molecular tools imply the loss of material already scarce. It thus justifies the use of model species to employ more invasive methods to evaluate egg quality.

Researches for indicators allowing to predict egg quality before fertilization kept their focus on morphological parameters such as egg size (Nguyen et al., 2012), egg transparency and chromosomal aberrations (delayed anaphases, chromosomes fragments remaining in the equatorial plane, anaphases bridges) (Kjorsvik et al., 1990), blastomere morphology (Bromage et al., 1994; Kjørsvik et al., 2003; Shields et al., 1997; Vallin and Nissling, 1998), fragmentation of the oil droplet (Żarski et al., 2011a) and the duration and intensity of the cortical reaction (Kjørsvik and Lønning, 1983; Żarski et al., 2012a). However, most of them are species specific, can be highly affected by rearing practices, such as the use of hormonal treatments for reproductive management and are usually indicators of bad instead of good quality.

Eggs biochemical parameters have also been investigated, such as fructose, galactose and glucose contents (Lahnsteiner et al., 2001), proteins level (Nguyen et al., 2012), fatty acid composition (Henrotte et al., 2010; Lanes et al., 2012; Luo et al., 2015) and cortisol content (Skaalsvik et al., 2015). In species for which it is possible, the biochemical analysis of the ovarian fluid was also performed: pH (Fauvel et al., 1993), osmolality, conductivity and volume (Skaalsvik et al., 2015) and aspartate aminotransferase activities (Lahnsteiner et al., 1999, 2001)). Most of them are still primary studies and were performed in few species. Their continuity could allow some future applicability.

Functional genomic studies became also an affordable approach to investigate fish egg quality due to the increase of the number of new techniques making many of them cheaper. Proteomic and transcriptomic analysis and their relationship with egg quality are available for some fish species, such as zebrafish (Cheung et al., 2019; Yilmaz et al., 2017), Eurasian perch (Castets et al., 2012), rainbow trout (Aegerter et al., 2005; Bonnet et al., 2007b; Rime et al., 2004), sea bass (Żarski et al., 2017a), Atlantic cod (Lanes et al., 2013; Rise et al., 2014), Atlantic halibut (Mommens et al., 2014) and striped bass (Chapman et al., 2014), only three of them correspond to proteomic analysis while the majority are transcriptomic studies. This may be partly explained by the huge amount of Vtgs in the eggs, which constitutes one of the major obstacles to perform protein profiling and also reduces the capacity of identify stage specific proteins (Lubzens et al., 2010). A possible obstacle for the omics approaches in general is still the lack of data for some species (e.g.: species for which annotated genome and proteome are not available) (Rodrigues et al., 2012). In some cases, it may be worth to use *de novo* sequencing techniques to overcome this issue.

Despite of the central dogma of biology that links DNA, RNA and proteins, only the quantitative analysis of mRNAs or proteins is not sufficient to predict each other (Gygi et al., 1999). Even taking into account some translational variations, the levels of protein were weakly correlated with the mRNA abundance (Nie et al., 2006). It is due mostly to technical limitations we have so far to properly measure the many sources of variation existing during this process. For example proteins presenting a high translational rate will not need high level of the correspondent mRNAs (Nie et al., 2006). These variations will be especially important during dynamic transitions, as during embryonic development (Peshkin et al., 2015). Figure 6 illustrates the relationship between mRNAs and proteins, as well as some methods available to detect their abundance, synthesis and decay.

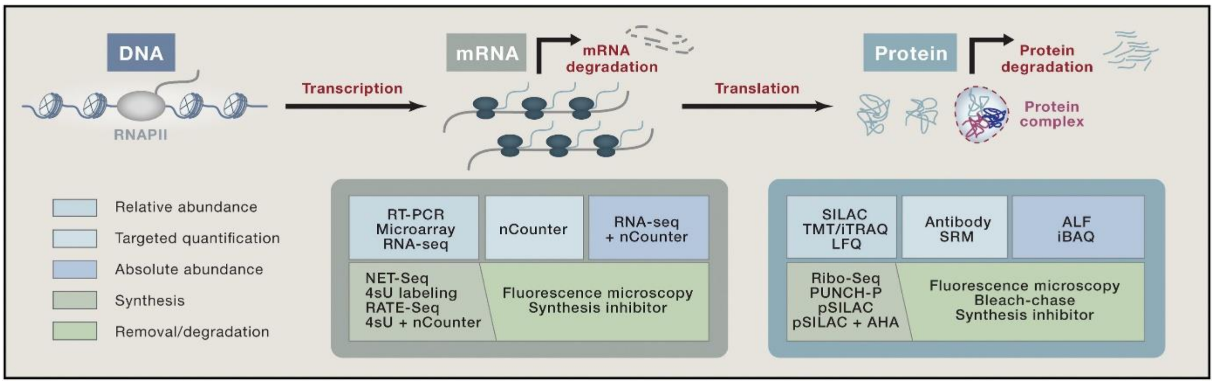


Figure 6. Sequential mechanisms controlling gene expression and thus the relationship between mRNAs and proteins mechanisms, types of molecules, methods for their respective quantitative

measurement, and the properties measured by the respective methods are indicated (From (Liu et al., 2016)).

In addition to the improvement of the techniques allowing quantifying the different levels of transcripts and proteins, the design of general mathematical models to explain the relationship between mRNAs and proteins level is of great interest. Despite of no direct relationship between proteins and mRNA levels, many maternal mRNAs have already been directly associated with embryonic proper development, confirming that they provide a meaningful information regarding egg quality evaluation.

3.3. *Maternal mRNAs and egg quality*

It has been reported that human spermatozoa provide about 2700 unique mRNAs that may play a role during fertilization and embryonic development (Ostermeier et al., 2002). The same trend was found in zebrafish for which more than 1700 unique transcripts, mostly coding for ribosome and cytoskeleton proteins were identified in their sperm (Wu et al., 2011). However, more studies on the function of these spermatozoa mRNAs for embryonic development remain to be done (Herráez et al., 2017). In spite of this, good quality mature eggs are the major and most variate source of mRNAs for the developing embryos, being responsible to support the earliest events during development.

Many maternal mRNAs have direct roles during early and later stages of the embryonic development. In early stages they are essential for patterning, as seen in the oogenesis section, but they will also support basic cellular functions as intercellular adhesion and the increase of embryonic metabolism (Pelegri, 2003).

Maternal-effect mutants and transcripts identified so far demonstrate the impact of the maternal factors in the development [reviewed in (Bobe, 2015; Cheung et al., 2018c; Lyman-Gingerich and Pelegri, 2007)]. The phenotypes of the mutants presented deregulation affecting egg activation and fertilization (Dosch et al., 2004), gastrulation and later processes as tail formation, head morphogenesis and ventral tail fin morphology (Wagner et al., 2004). Transcripts usually identified in differential expression analysis between eggs of high and low quality are submitted to functional analyses in order to confirm their potential involvement in embryonic correct development. In zebrafish, for example, Rp2 translated from maternal *rp2* is essential for normal heart loop formation (Desvignes et al., 2015), absence of maternal *npm2* leads to developmental arrest before the onset of the epiboly (Bouleau et al., 2014), *nmp2a* is important at or right before fertilization while *nmp2b* is involved in processes leading up to or during ZGA (Cheung et al., 2018a) and *foxr1* may be required for proper cell division and survival (Cheung et al., 2018b). Other studies on maternal-effects mutants and transcripts affecting zebrafish development are shown in Table 1. [Reviewed in (Lubzens et al., 2010; Lyman-Gingerich and Pelegri, 2007; Marlow, 2010)].

The confirmed maternal genes highlight molecular pathways that are important for early development. They thus improve our knowledge on developmental mechanisms and open possibilities to solve issues related with this period.

As seen, egg content directly impacts embryogenesis, thus factors affecting oogenesis may also influence this process. The level of adaptation of the individuals to their environment, for example, is expected to be reflected in their ability to reproduce and thus in their capacity to produce high quality gametes.

4. Domestication process

The first movement toward domestication of an animal species consists in transferring them from their wild environment to captive conditions. Thus, they will have to gradually adapt to this new, artificial and anthropogenic environment. In this context, Edward O. Price, in 1984, defined domestication as the process of adaptation to a new environment, “achieved through genetic changes occurring over generations, and environmental stimulation and experiences during an animal’s lifetime” (Price, 1984). Domestication corresponds then, to an evolutionary and developmental process. As so, it will affect and change many life aspects including the reproductive biology.

In Teleosts fish, domestication started late if compared with mammals’ species (Teletchea and Fontaine, 2014). This is the reason why studying fish domestication usually does not give a clear answer of the domestication effect once many species did not achieve more advanced levels of domestication during the domestication process. To help interpreting results between fish populations concerning their adaptation to the captive environment, levels of domestication should be used instead of classical domesticated versus wild population comparisons in order to clarify the domestication status of the species or population studied. Table 3 presents an example of a classification according the domestication level of finfish species that assigns higher or lower levels for each of them considering animals’ capacity of feed, reproduce and participate in selective breeding programs in captivity (Table 3).

Table 3. Domestication levels of finfish used in aquaculture (Adapted from (Teletchea and Fontaine, 2014))*.

Domestication level	Description	n	Examples
0	Capture fisheries	4671	
1	First trials of acclimatization to the culture environment	39	White bream (*Blicca bjoerkna*, Cyprinidae)
2	Part of the life cycle is completed in captivity, but several bottlenecks still exist in others (e.g. reproduction, larval rearing…)	75	Pond loach (*Misgurnus anguillicaudatus*, Cobitidae), Japanese amberjack (*Seriola quinqueradiata*, Carangidae), Atlantic bluefin tuna (*Thunnus thynnus*, Scombridae), European eel (*Anguilla Anguilla*, Anguillidae)
3	The entire life cycle is closed in captivity, but with wild inputs	61	Pacific bluefin tuna (*Thunnus orientalis*, Scombridae), Senegalese sole (*Solea senegalensis*, Soleidae), roach (*Rutilus rutilus*, Cyprinidae)
4	The entire life cycle is closed in captivity without wild inputs, but no selective breeding program is used	45	Catla (*Catla catla*, Cyprinidae), snakehead (*Channa argus*, Channidae), mrigal carp (*Cirrhinus mrigala*, Cyprinidae), pikeperch (*Sander lucioperca*, Percidae), European perch (*Perca fluviatilis*, Percidae)
5	Selective breeding program is used focusing on specific goals (growth rate, fillet yield, flesh quality)	30	Common carp (*Cyprinus carpio*, Cyprinidae), rainbow trout (*Oncorhynchus mykiss*, Salmonidae), Atlantic salmon (*Salmo salar*, Salmonidae), sea bass (*Dicentrarchus labrax*, Moronidae)

* This study was published in 2014. It is possible that some species have changed their domestication level.

4.1. *Domestication and fish reproduction*

Many studies investigated the impact of domestication on the reproductive performance. However, they were mostly interested in the environmental impact of possible interbreeding in case of escapees and this makes that studies on the reproductive performance of wild and domesticated fish in captivity quite scarce. Recently, a meta-analysis investigated the influence of the birth-origin (wild or captive) on the reproductive performance in captivity. It was performed on 44 species belonging to invertebrates, fish, birds and mammals. It showed that captive-born animals present lower reproductive success in captivity compared to their wild-born counterparts. It was even more important in fish species reared in aquaculture systems for a commercial purpose and the offspring performance was the most sensitive trait (Farquharson et al., 2018). Additionally, studies comparing early embryonic developmental performance in wild and domesticated fish, in captivity, are available in other fish species, such as Atlantic cod (*Gadus morhua*) (Lanes et al., 2012), Atlantic Salmon (*Salmo salar*) (McGinnity et al., 2003), common sole (*Solea solea*) (Lund et al., 2008) and Eurasian perch (*Perca fluviatilis*) (Khendek et al., 2017; Křišťan et al., 2012). In all of them, early embryonic survival rates were lower in domesticated comparing to the wild counterparts. Interestingly, two other studies also aiming at comparing reproductive performance in captivity of wild vs. domesticated populations showed the absence of gametes releasing, despite of they presented gonads development, in pikeperch (*Sander lucioperca*) (Khendek et al., 2018) and regressed gonads during the spawning period in greater amberjack (*Seriola dumerili*) (Zupa et al., 2017) (Table 4).

Table 4. Studies evaluating the reproductive performance in “domesticated” and “wild” fish populations in captivity.

Species	“Domesticated” (D) features	“Wild” (W) features	Parameter evaluated	Results obtained		Reference
				W	*D*	
Atlantic cod (*Gadus morhua*)	4 year-old farmed fish	Caught ~1 month before spawning	Embryonic hatching rates	86 ± 3%	66 ± 3%	(Lanes et al., 2012, 2013)
Atlantic salmon (*Salmo salar*)	Norwegian Mowi origin two sea winter maturity	Burrishoole wild 1SW and 4SW	Embryonic survival until eyed stage	W > D at p < 0.001		(McGinnity et al., 2003)

	(2SW) and 3SW					
Eurasian perch (*Perca fluviatilis*)	Captive-reared for X generations 18-month-old fish First spawn	F1 stock 18-month-old fish First spawn	Embryonic hatching rates	37 ± 27%	2 ± 20%	(Khendek et al., 2017)
	3-years-old RAS-reared fish Spawned before	Wild captive-reared for 3 years	Embryonic hatching rates	62 ± 9%	27.9 ± 9.3%	(Křišťan et al., 2012)
Common sole (*Solea solea*)	F1 stock 3-years-old Second spawn	Wild caught Kept in captivity for less than 1 month before spawning	Embryonic hatching rates	72%	17%	(Lund et al., 2008)
Greater amberjack (*S. dumerili*)	Wild fish captive-reared for 2 years	Commercially caught at 3 distinct moments Sampled right after to be caught	Several parameter to estimates gonads development	Impaired gonadogenesis in D males and females		(Zupa et al., 2017)
Pikeperch (*Sander lucioperca*)	F1 of the W population 2-years-old	Captive-reared until 4-years-old	Several parameters to estimates gonads development Embryonic survival	Hatching rate of 47 ±1%	Delayed oogenesis No spawn	(Khendek et al., 2018)

As for egg quality analysis, the few number and the diversity of variables implicated in the studies on the domestication in one species, make difficult to draw proper conclusions about the consequences of the domestication process on fish reproductive performance as a whole. However, the available data shows that a general effect of domestication is to reduce the reproductive performance of fish in captivity and these results are in the opposite direction of aquaculture, which targets an increase of fish production. Thus, it points to an urgent need of improving breeding selective programs in order to overcome these issues. In this concern, females should be priority once they represent the major factor influencing early embryonic development, as showed in European eel (*Anguilla anguilla*). The authors of this study concluded that maternity explains 54.8% of the variation for fertilization success, 61.7% for embryonic survival, 88.1% for hatching success and 62.8% for larval deformities (Benini et al., 2018).

4.2. *Domestication and gene expression*

As an evolutionary process, domestication induces genetic and epigenetic changes resulting in gene expression modifications. At the molecular level, gene expression can be regulated at different stages including transcription, mRNAs stability and translation changes. (Takada et al., 2009). Usually, some generations are required to allow observing structural genomic modifications as a result of artificial selection, however differences in gene expression due to a rapid adaptation to new environments was already seen from the first generation of reproduction in captivity in steelhead trout (*Oncorhynchus mykiss*) (Christie et al., 2016). This fast changing on gene expression due to the new environment faced could be in result of epigenetic modification that may become permanent but still, genetic modifications should not be discarded.

Epigenetic changes correspond to genomic modifications that do not affect the nucleotides sequence. Once stabilized, these changes will lead to differential gene expression. It is referred as cellular memory, is susceptible to environmental variations and is passed to daughter cells by meiosis or mitosis even when the original stimuli are no longer present. In the case of gametes, the epigenetic patterns (epigenome) will pass from parents to offspring. Its main molecular basis are DNA methylation, post-translational modification of histone, chromatin organization and non-coding RNAs (Labbé et al., 2017). As a heritable feature, the epigenome will prepare the offspring to deal with the environment they will face. Due to the higher influence of temperature and water quality changes, fish are more prone to suffer epigenetic pattern alteration in order to better adapt (Labbé et al., 2017). Independent of the source (genetic or epigenetic), methods applied to measure global gene expression are able to identify possible changes.

Gene expression studies compared fish populations presenting variable levels of domestication and identified differentially expressed genes belonging to distinct pathways. In most of cases, they are implicated in the adaptation of fish to captive environments with potential roles in the early embryonic development (Bicskei et al., 2014, 2016; Chen et al., 2017; Christie et al., 2016; Lanes et al., 2012, 2013). These findings reinforce the impact of the parents' origin on the transcriptomic pool of their fry and on its early development. Interestingly, when evaluating the contribution of both parents in the mRNAs pool of eyed embryos, maternal contribution was dominant in comparison to the paternal in Atlantic salmon

(*Salmo salar*) (Bicskei et al., 2014, 2016). Domestication process can be seen, in this context, as an intrinsic factor that can affect oogenesis by modulating the synthesis and accumulation of transcripts into the oocytes. In turn, it may lead to variable reproductive performance, as seen in species in process of domestication.

5. Eurasian perch (*Perca fluviatilis* Linneaus 1758): a species in process of domestication

Eurasian perch is a freshwater fish that belongs to the Percidae family. As external morphological characters, it presents a laterally compressed body, dorsal rayed fin, divided into anterior and posterior parts, well developed anal spine and red/orange pelvic, anal and caudal fins. Dark vertical stripes can also be seen in the lateral part of the body (Figure 7) (Stepien and Haponski, 2015).

Figure 7. Eurasian perch (*Perca fluviatilis*). Photo: Yannick Ledoré.

It has a wide distribution across Eurasia (Figure 8) and is specially appreciated for recreation, commercial and aquaculture segments (Stepien and Haponski, 2015).

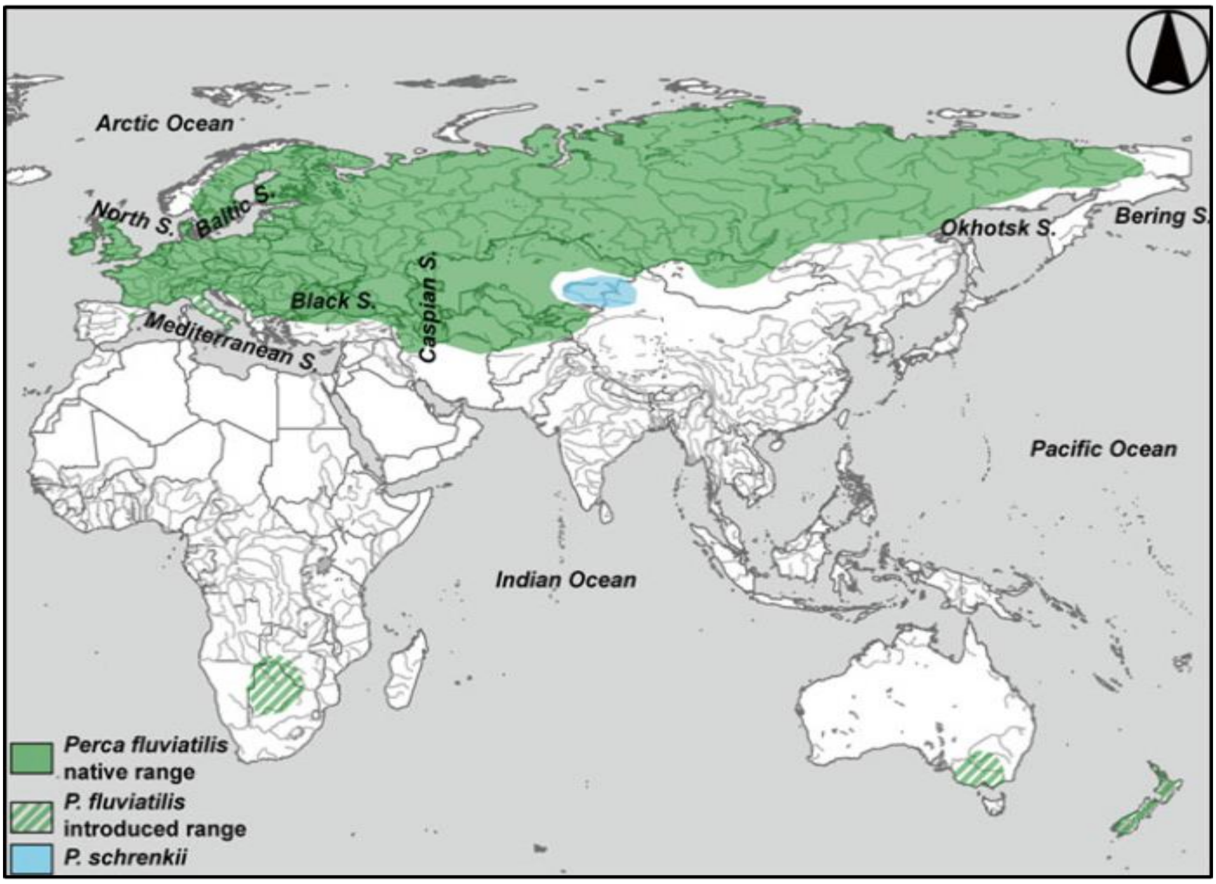


Figure 8. Global distribution of native and introduced populations of *Perca fluviatilis and P. schrenkii*. From (Stepien and Haponski, 2015).

5.1. *Reproductive biology and control*

Eurasian perch is an annual early spring spawner, with gonads developing synchronously (Teletchea et al., 2009). The first sexual maturation is sex dependent, with males maturing earlier (1-2 years old) and at smaller sizes (80-150 mm of total length) than females (3-4 years old and 150-200 mm of total length) in the wild (Feiner and Höök, 2015). In recirculating aquaculture system (RAS), while kept under controlled conditions, they can reach sexual maturity much earlier, between 11-14 months age for both sexes (Fontaine et al., 2015).

5.1.1. Eurasian perch eggs and spawning

As gonads will develop synchronously, it implies the existence of a major population of oocytes at the same developmental stage in the ovarian tissue, that will be ovulated together (Fontaine et al., 2015). Eurasian perch spawn is in ribbons/strands of variable extension (0.5 - 5.5 m). This ribbon structure is due the presence of a jelly coat surrounding each egg and connecting all of them (Figure 9). The jelly coat presents a microtubular network that externally ends in ring-like pores, that were proposed to be responsible for the stickiness observed in the egg ribbons. It may also have a protective function against slight mechanical impacts (Formicki et al., 2009). The exact moment of the ribbons formation has not been characterized. It should be in a short period of time between the release of the oocytes from their follicle and the moment when they leave the ovary.

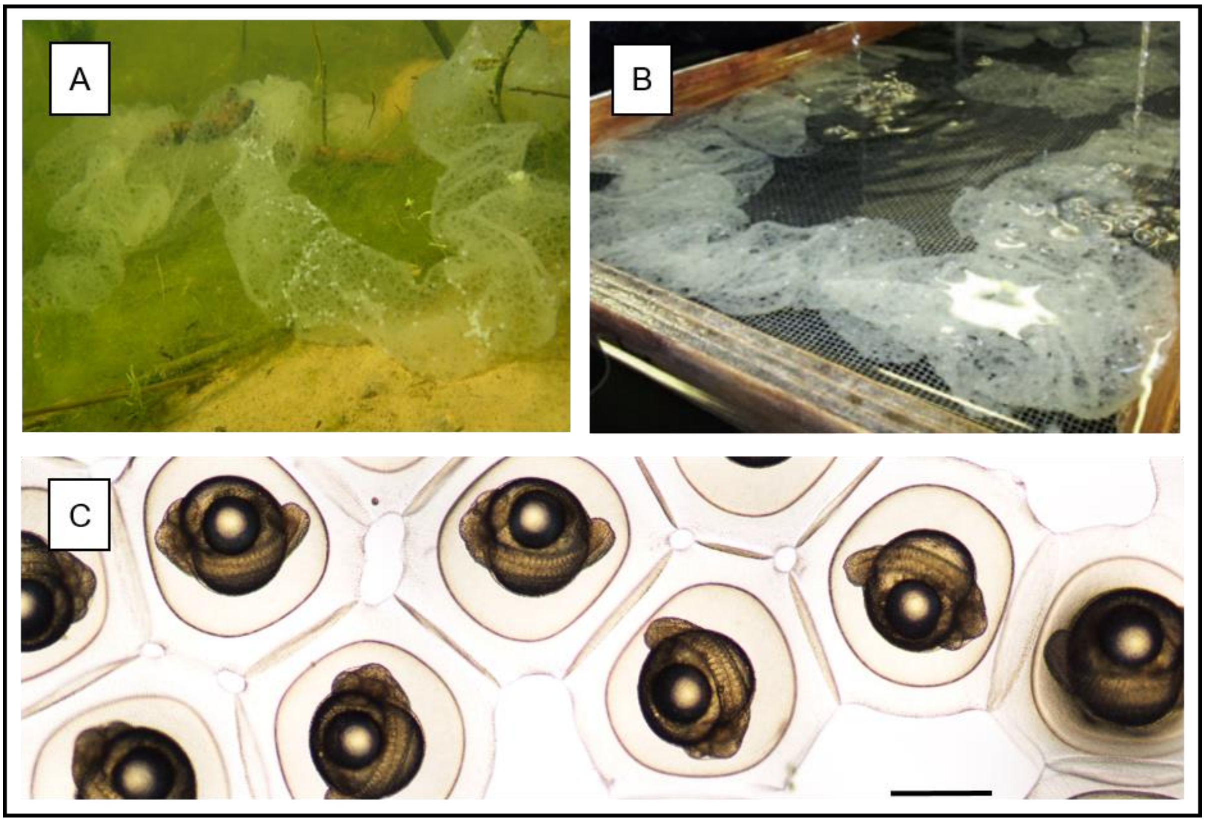


Figure 9. Eurasian perch spawn in (A) natural and (B) artificial environments. The spawn is structured in a ribbon. (C) View under microscope of embryos developing in the ribbon structure (72 hours post-fertilization). Photos: (A) Yannick Ledoré, (B) Daniel Żarski in (Żarski et al., 2017b) and (C) Personal archive. Scale bar corresponds to 1000 µm.

Another particularity of the Eurasian perch eggs is the presence of an oil droplet in the cytoplasm. During oocytes maturation, in addition to the GVBD, the formation of the oil droplet can be observed (Figure 10). This will be generated by the coalescence of smaller oil droplets that start to be seen in the oocyte cytoplasm at the beginning of the maturation stage (Żarski et al., 2012b). The presence of many oil droplets in the oocytes has been associated with the appearance of embryonic deformities (Żarski et al., 2011a). In opposition to the lipids associated to the Vtg, oil droplets are mostly composed by neutral lipids, including wax or steryl esters, that are preferentially used as energy source and are rich in monounsaturated fatty acids (Patiño and Sullivan, 2002; Wiegand, 1996). It still remains to be elucidated the source of these lipids and how they are incorporated into the oocytes (Johnson, 2009).

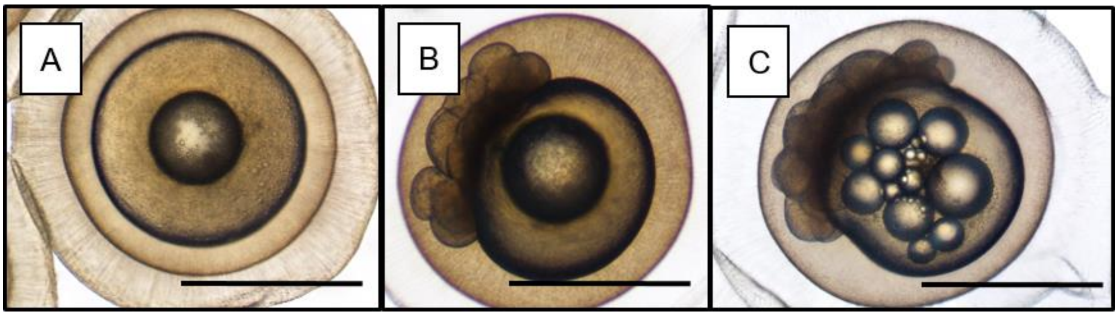


Figure 10. Mature and unfertilized Eurasian perch egg (A) and embryos at (B) 7 and (C) 9 hours post-fertilization observed under microscope. A unique oil droplet is present in (B) while many are seen in (C). Scale bars correspond to 1000 µm.

In Eurasian perch, a temperate fish, the gonads development is under clear environmental influence. Temperature and photoperiod variations will mark important phases of their oogenesis. A decrease on these parameters will induce ovarian development, then the wintering period, during which temperatures are low and days are short coincides with the vitellogenic phase, and allow the accumulation of the eggs content. At the end, an increase of temperature and of photophase duration will induce spawn. Thus, these factors will control the entry in pre-vitellogenesis, vitellogenesis, and the final stages – maturation and ovulation (Wang et al., 2010). In natural conditions, ovary development was evaluated and an increase in the GSI is seen from the beginning of fall until the spawning period, with the highest values being between 20-30% before spawning (Fontaine et al., 2015). The duration of each phase remains to be determined in this species and is important to allow reproductive manipulations and improvements.

5.1.2. Eurasian perch husbandry

Attempts of domestication have started in early 90' together with the increasing interest for this species primarily for restocking markets but also for human consumption (Fontaine and Teletchea, 2019). Eurasian perch has a traditional demand in several European countries and thus it has been seen as a promising candidate for the domestication and for the European continental aquaculture diversification (Fontaine, 2004; Gillet and Dubois, 1995). The production by capture considerably increased from the 80’ and since the years 2000 it is possible to observe an increase of production by aquaculture that continued in the following years (Figure 11).

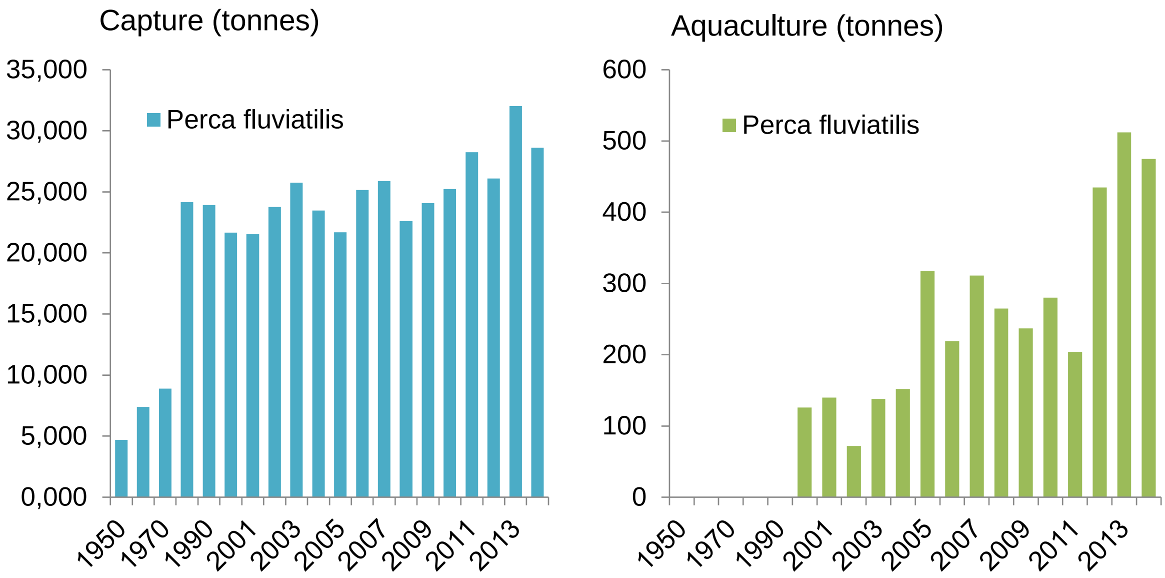


Figure 11. Global supply of Eurasian perch (Perca fluviatilis) from capture and aquaculture production. Source: FAO - Fish Stat.

During a process of domestication, the proper control of the reproductive cycle in captive environments is constantly challenging. The knowledge of the reproductive biology of this fish helped to improve methods for controlling it. Thus, in Eurasian perch it has been possible, due to the development of a photo-thermal program based on the simulation of natural variations of temperature and photoperiod, to induce gonads development, to maintain the progression of oogenesis and to induce spawning. This program consists of a decrease of photoperiod and temperature, as seen during fall in temperate regions, followed by a combination of chilling period and low photophase extent during a period of 4-5 months, at the end of which, both parameters will gradually be increased, stimulating the beginning of the spawning season (Figure 12) (Abdulfatah et al., 2011; Fontaine et al., 2015). In fish farms, out-of season spawning are successfully achieved by variating these two factors in indoor RAS.

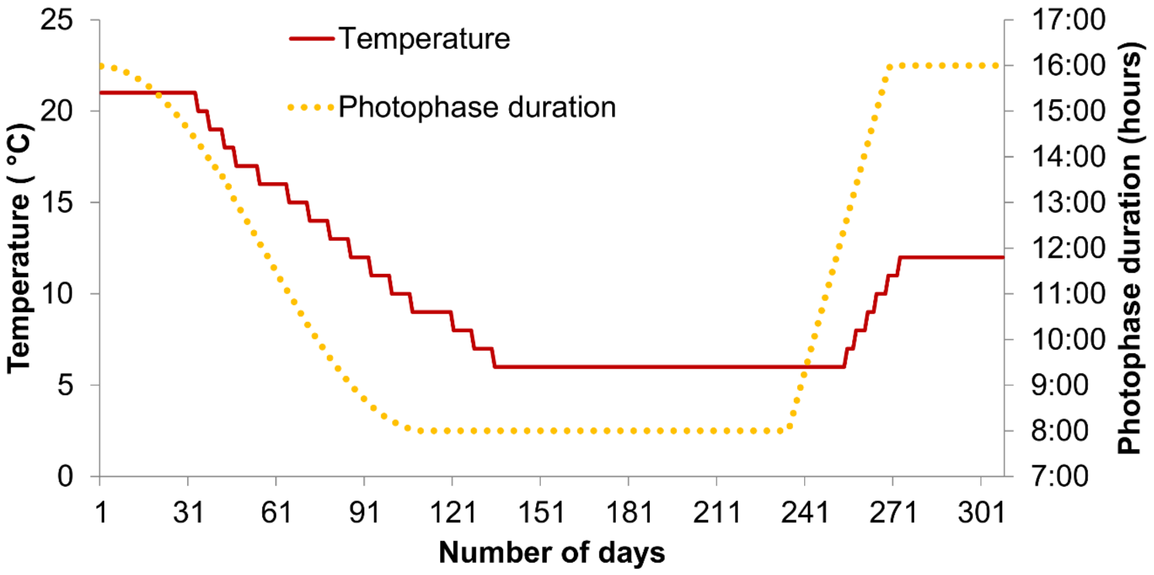


Figure 12. Photo-thermal program applied to induce gonads development and spawning in Eurasian perch (*Perca fluviatilis*). Adapted from: (Abdulfatah et al., 2011; Fontaine et al., 2015).

Temperature and photoperiod are considered as extrinsic factors determining the reproduction in this species, once their proper variation will trigger and allow it. On the other hand, other factors will modulate reproduction and direct influence its quality. Those can be species specific and intrinsic, or they can come from the environment. In Eurasian perch, intrinsic and extrinsic factors persist for being deeper investigated (Wang et al., 2010). However, some studies have already demonstrated that domestication may act as extrinsic factor influencing egg quality and early embryonic development (Khendek et al., 2017; Křišt'an et al., 2012).

A complementary method to obtain Eurasian perch spawn is to use hormonal treatments. GnRH or LH analogues can be employed at the beginning of the oocytes maturation phase to synchronize and induce spawn. This will facilitate the management organization during the spawning season. However, this practice has led to the production of eggs with variable quality (Żarski et al., 2011a). This may be due to the use of the hormones too early during oocytes maturation what may lead to impairments and thus reduce eggs quality. The recommendation is that hormonal induction should not be applied before the third stage of oocyte maturation, which can be identified by a migrating germinal vesicle (above half of the oocyte diameter), presenting clearly visible oil droplets (Żarski et al., 2012b).

5.2. *Egg quality*

Improving egg quality constitutes a way to increase fish production. However, few aspects affecting the egg quality or potential egg quality indicators have been investigated so far in Eurasian perch (Mélard et al., 1996) (later reviewed by (Schaerlinger and Żarski, 2015)). As advantage, the proper early development (Alix et al., 2015) and many deformities (Alix et al., 2017) have been studied and are of great value toward studying eggs quality in this species.

Concerning extrinsic factors that may modulate the egg quality in this species, the fatty acids composition of the broodstock diet (Henrotte et al., 2010), the use of different egg activation solutions (Żarski et al., 2012c), the use of hormonal stimulation of the reproduction (Żarski et al., 2012b), the comparison of the rearing systems (Alix et al., 2017) and the domestication process (Khendek et al., 2017; Křišťan et al., 2012) have been studied. These works represent a beginning of work on factors possibly affecting egg quality and many others have not been investigated yet (Schaerlinger and Żarski, 2015). With regard to molecular evaluations, variation of Cathepsin L, important for the use of the yolk reserves, on eggs and larvae (Kestemont et al., 1999), the composition of total lipids and fatty acids in embryos (Abi-Ayad et al., 2000), or some proteins the expression of which are potentially linked to the ability to properly develop after fertilization (Castets et al., 2012) have been investigated and give some clues in deciphering mechanisms implicated in Eurasian perch eggs quality. However, the most reliable work available so far is focused on an intrinsic morphological indicator: oil droplet fragmentation in non-activated eggs. The higher fragmented the droplet, the worst the quality of the egg. It could even be correlated to the occurrence of some severe deformities post-hatching (Żarski et al., 2011a). Thus, the level of oil droplet fragmentation could predict some late deformities in this species, when hormonal induction of reproduction is applied.

Molecular indicators may have advantages in comparison to morphological ones once they may be conserved among species, however, there is no clear molecular indicator of egg quality in Eurasian perch and considering the too few or ambiguous data obtained the research activities in this field are still to be done (Schaerlinger and Żarski, 2015). Thus, better characterization of the period between fertilization and 24 hpf, in association with deeper investigations on the egg mRNA profiles and its potential to properly develop after fertilization, would help brings light to early development issues and help improving the overall reproductive performance.

III. PhD work goals

My PhD mainly aimed at characterizing the gene expression pattern of eggs of Eurasian perch related to the early developmental performance. At the beginning, our research was part of a bigger project that aimed at comparing the expression of egg quality related genes in four distinct fish species in order to pinpoint potential shared molecular mechanism. Based on a previous analysis performed in zebrafish (*Danio rerio*) eggs depending on their quality, we checked whether the same genes were differently expressed in Eurasian perch in the same conditions. This part of the project helped me first to get familiar with molecular biology protocols and particularly to **improve the RNA extraction protocol** in Eurasian perch eggs. Then, data analysis about the **expression of quality-related genes in eggs of different fish species** allowed me to define several lines of research that were addressed in the next steps of my work. All aspects of this work are presented in **CHAPTER 1**.

In the following, two scientific contexts have been explored to characterize the Eurasian perch eggs' transcriptome variations depending on their *quality* or on the *domestication* level of the females. In **CHAPTER 2** I compared different methods to assess **egg quality** and their impact on the transcriptomic results obtained. First, I particularly focused on the impact of the type of criteria and methods to define high and low egg quality groups on the transcriptomic results. In a second moment, eggs were sorted, according to a previously reported multi-parametric statistical analysis, into four quality groups including not only high and low quality but also two groups of intermediate quality. Again, their transcriptomic profiles were compared.

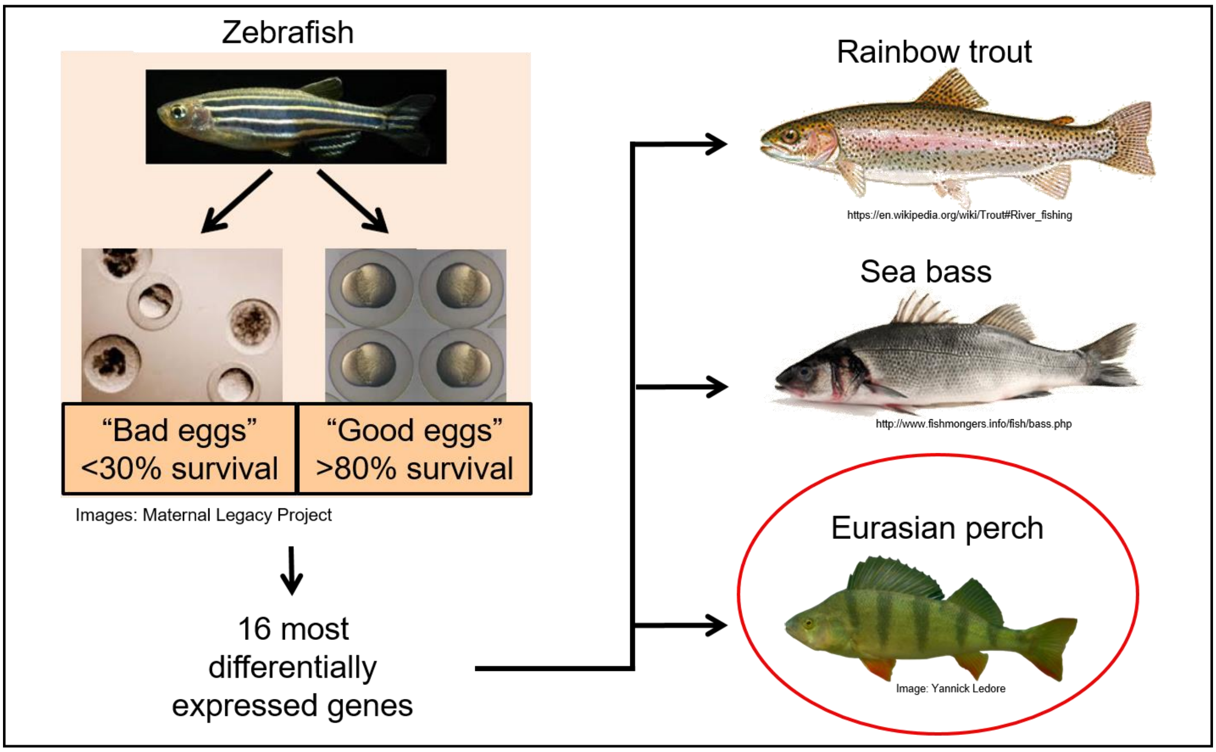
Finally, in **CHAPTER 3** I investigated whether the **domestication process** could act as an intrinsic factor, interfering on the synthesis of the mRNA during oogenesis, and potentially impact the reproduction success. It contains the results of gene expression comparison, morphological, endocrine, histological and genetic data of the broodstock, in addition to the characterization of the development of the embryos. Indeed, all these results will give an embracing view of the reproductive cycle and the developmental performance of the embryos belonging to the two populations analyzed.

IV. Chapter 1: Protocol adaptation to work with Eurasian perch eggs and compare the expression of egg quality-related genes between species

1. Context

1.1. *Finding shared molecular mechanisms between zebrafish and Eurasian perch: Maternal Legacy Project*

As mentioned, Maternal Legacy project was the starting point of this PhD. The major goal of the project was to investigate "what takes to make a developmentally competent egg". To explore this point, zebrafish (*Danio rerio*), a current model species for development in vertebrates, was used. In addition, researchers prospected that this species could be also used as a "model for understanding egg quality determinism" in aquaculture fish species. In a first moment, several quality-related genes were identified in zebrafish that were further investigated in this species and in aquaculture ones. Thus, another task of this project has as goal to analyze the expression of the genes, related with egg quality previously identified in zebrafish, and pinpoint a potential conservation of molecular mechanisms of developmentally competent eggs that would be shared by phylogenetically distant aquaculture species, including freshwater and marine species. These were rainbow trout (*Oncorhynchus mykiss*), sea bass (*Dicentrarchus labrax*) and Eurasian perch (*Perca fluviatilis*) (Figure 13). As project partner, we were in charge of conduct the investigations in Eurasian perch.



Images: Maternal Legacy Project

https://en.wikipedia.org/wiki/Trout#River_fishing

http://www.fishmongers.info/fish/bass.php

Image: Yannick Ledore

Figure 13. Summary of the task from Maternal Legacy project which our laboratory was implicated. The 16 most differentially expressed genes in zebrafish according to the egg quality were chosen to be evaluated in three species of interest for aquaculture.

To first identify the genes related with egg quality in zebrafish (*Danio rerio*), they sampled and evaluated zebrafish spawn of variable quality. High quality eggs presented survival rate >80% and the bad ones <30%, at 24 hours post-fertilization (hpf). In the following, they employed microarrays and RNA-sequencing to characterize the transcriptome of the eggs from these spawn, which correspond to the maternal transcriptome. While the results from RNA-seq were not associated with the difference in egg quality, the microarray results allowed to associate 66 genes that were differentially expressed depending on the egg quality (Cheung et al., 2019). Among those, they chose 16 mostly differentially expressed genes (DEG) to be further studied in others species. Additionally, their differential expression was confirmed by RT-qPCR and in the following they were used in other approaches, including knock-down (KD) studies to investigate the functional maternal contribution of some of these genes to zebrafish embryos developmental success (Cheung et al., 2019).

1.2. *Egg quality evaluation in zebrafish and in Eurasian perch*

In order to be able to compare results obtained in Eurasian perch with those from others species, we reasoned that the conditions of egg quality evaluation should be as closer as possible, once there exist already a diversity of intrinsic characters being different between species. Because different embryonic developmental stages has variable needs in terms of genes expression (Bozinovic et al., 2011; Mathavan et al., 2005), closer stages were chosen to allow making comparisons between species. Thus, the developmental stage used to assess zebrafish egg quality was considered to evaluate Eurasian perch eggs. In zebrafish, 24 hpf corresponds to the prim-5 developmental stage, within the pharyngula period (Kimmel et al., 1995). In Eurasian perch, this stage corresponds to the organogenesis 2 period (4-7 days post fertilization (dpf) (Alix et al., 2015) and thus we used the survival rate at 120 h, in order to have the closest stage used in zebrafish, to distinguish high or low quality eggs (Figure 14). In addition, the same thresholds were also employed, >80% for high and <30% for low quality. In total, six spawn were chosen to continue with the analysis.

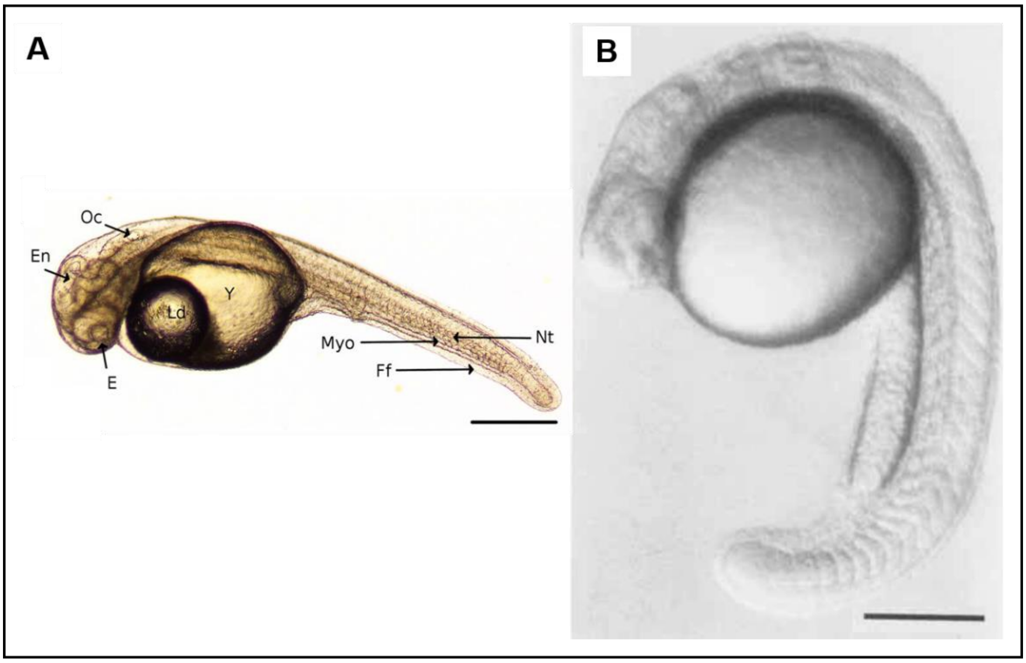


Figure 14. Developmental stages of (A) Eurasian perch and (B) Zebrafish chosen to evaluate the survival and estimate egg quality. (A): embryo at 120 hpf (Alix et al., 2015). Scale bar, 500 µm. (B): embryo at 21 hpf (Kimmel et al., 1995). Scale bar, 250 µm.

2. Part A – RNA extraction protocol adaptation and reference genes validation to perform gene expression in Eurasian perch eggs

2.1. *Obtaining good quality RNA from Eurasian perch eggs*

Due to the particularity of the Eurasian perch eggs, some improvements and adaptations had to be added to the RNA extraction protocol. These eggs have the property of form long ribbons that are kept attached by a jelly coat. This coat consists of a microtubular structure (Formicki et al., 2009) that, together with the chorion, protects the embryos/eggs from light mechanical impacts. In addition, the eggs contain high abundance of lipids in the yolk and also in the oil droplet, which also demanded some additional steps in the protocol. First, to ensure proper samples homogenization, a milling step was added in order to get rid more easily of the gelatinous envelope and the chorion surrounding the eggs. For so, a bullet blender (Next Advance) and zirconium oxide beads 1.0 mm were used. Two or three rounds of milling, with duration of two minutes, were performed always keeping the samples on ice at least for 5 minutes between them.

From homogenization, three different protocols, including the manufacture's, were tested. The first one corresponds to the manufacture's recommendation (TRIzol reagent, Life

Technologies), which produced for most samples, low concentrated, impure or degraded total RNA (Figure 15A). As the RNA originating using this protocol presented the purity indicator ratio of 260/230 under 1.0, we thought that it could come from phenol contamination during the aqueous phase pipetting, once it was very tiny. Thus, we employed a second separation phase using chloroform to be able to pipette again the aqueous phase and get rid of the phenol that could have lasted. The purity was barely increased with this protocol and the other two issues still remained. Then, we reasoned that the lipids excess could be a problem during the separation phase, once they have lower density in comparison to the proteins and thus delay the sedimentation of the eggs components, during centrifugation. By having a more efficient sedimentation, we expected an increase in the volume of the aqueous phase, allowing easier pipetting. For so, we still were adding a second separation step on the protocol, but using TRIzol instead of chloroform. Because TRIzol function also as a protector for RNAs, we also expected quality improvement. In addition, we increased the centrifugation time, so, after homogenizing, the samples were centrifuged for 30 min, instead of the 10 min recommended by manufacturer’s protocol. Then, after the first centrifugation, the top phase was removed and placed in a new tube, where chloroform was added to allow the second separation phase, for so, more 30 min of centrifugation was performed. It allowed an increase of about 50% of the volume of the aqueous phase. After that, the classical steps of precipitation, wash and resuspension were followed as manufacturer’s recommendation. As a whole, this last protocol was able to highly increase the integrity of total RNAs extracted. For example, with the protocol using chloroform twice, the proportion of samples presenting a RNA integrity number (RIN) higher that 8 represented 18% of the samples extracted, while for the last protocol, 83% of the samples presented a RIN higher then 8 (Figure 15B-C).

Total RNA was extracted from unfertilized frozen eggs from six spawn per group of quality. High and low quality groups contained spawn presenting survival rates higher than 80% and lower than 30% at 120 hpf, respectively. Extraction was performed using TRIzol reagent at a ratio of 100 mg of eggs (10-15 eggs) per mL of reagent and following the manufacturer's instructions with the above mentioned modifications. A NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies) was used to evaluate the quantity of total RNA and a 1% agarose gel or Bioanalyzer was used to evaluate the integrity of the RNA extracted. After RNA extraction, a DNase treatment (DNase I, RNase free - Thermo Scientific) was applied to 5 µg of all samples (n=12) following the manufacturer’s protocol.

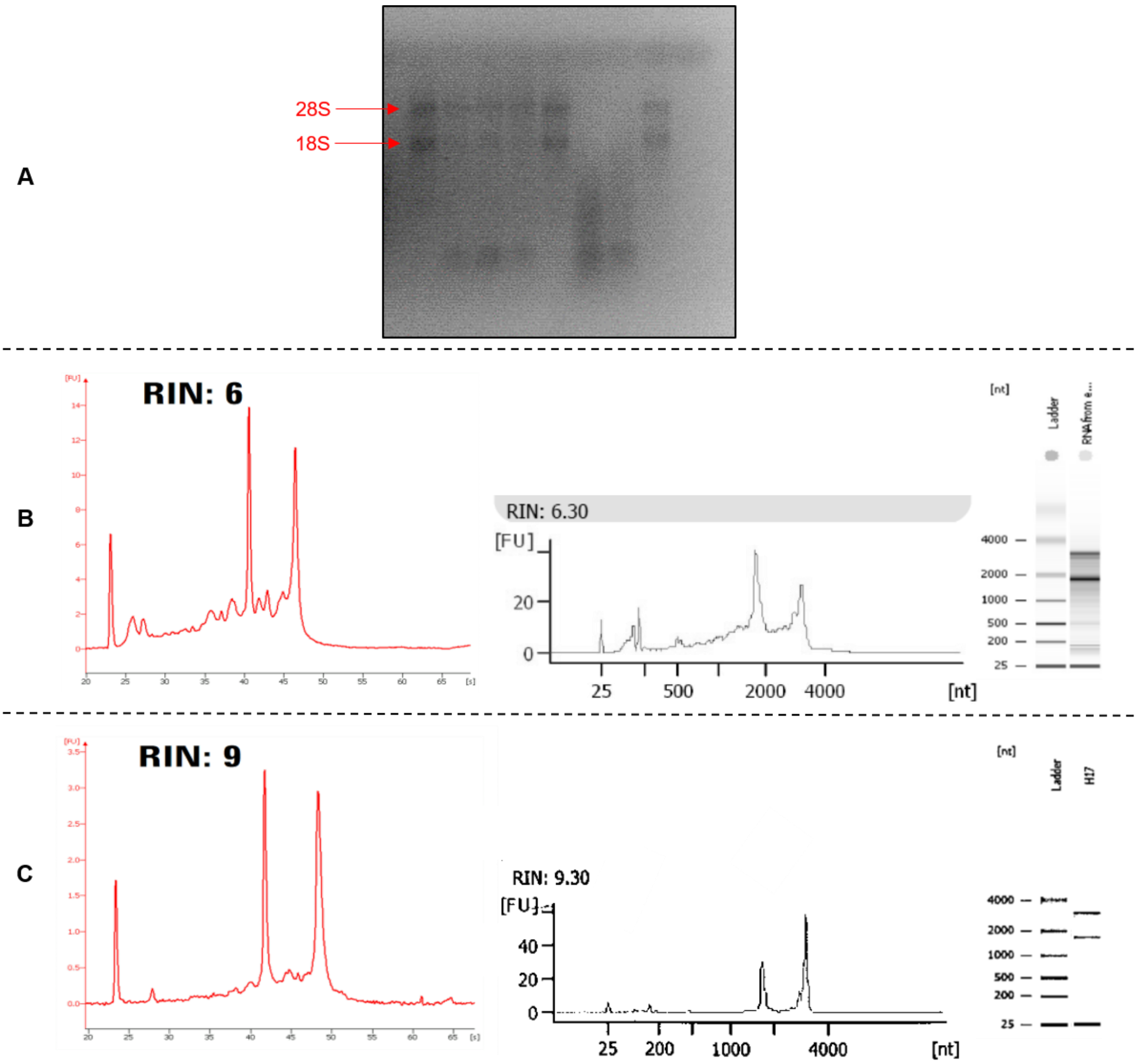


Figure 15. Improvement on RNA integrity number (RIN) after changes on the protocol of extraction. (A) 1% agarose gel image presenting the RNA bands after using the manufacture's protocol for extraction. Each row in (B) and (C) presents, from the left to the right, the expected Bioanalyzer electropherograms profiles (peaks) for RNA sample, the profiles we found when each of the 2 protocols was used, and the correspondent gel-like image (bands) generated for the same samples tested. Letters correspond to the protocol adaptation by the addition of a second separation phase with chloroform (B) and the last protocol with the second separation phase using TRIzol and additional centrifugation time (C).

2.2. *Eurasian perch orthologs for the zebrafish genes and primers design*

Due to the unavailability of the annotated perch genome in public databases at the beginning of my thesis, we took advantage of the Phylofish database (ANR Project, 2011-2015), to find perch orthologs for the zebrafish most differentially expressed genes. Phylofish aimed at analyzing gene evolution and gene expression by sequencing the transcriptome of 24 species of major economic and environmental interest. For each species, they constructed separate libraries for more than 10 different tissues, which allowed obtaining a significant amount of transcriptomic resources. For Eurasian perch, about 40.000 mRNA sequences are available (Pasquier et al., 2016).

Instead of interrogating this database directly using the zebrafish sequence, we first used NCBI BLAST to retrieve the tilapia (*Oreochromis niloticus*) orthologs genes, then the translated sequences, and we used this last one to query the perch transcriptome within Phylofish database. This was necessary because tilapia is phylogenetically closer to perch than zebrafish, and then it should have more homology between sequences. Once found the perch orthologs, primers were designed for each gene of interest (GI). The same method was employed to design primers for potential reference genes (RG) that would be used to normalize the RT-qPCR results.

We started working with the 16 DEG from the zebrafish study. Initially, we were using the entire mRNA sequence obtained from Phylofish database to design the primers and most of them were not producing a unique amplicon. Thus, we tried to find the exons on each sequence and design forward and reverse primers in different exons in order to avoid amplification of gDNA or immature mRNA. For so, either we used software to translate the nucleotide sequences and took the longest sequence between stop codons or we aligned the perch sequence against the tilapia sequence, for which it is know the position of exons and introns, and by homology, we assigned the coding DNA sequence (CDS). We used the CDS to look for primers. Not all primers designed using these methods produced the expected results, no being specific for the targeted sequence. At the end, from the 16 genes from zebrafish, we were able to design and validate primers couples for 11 genes.

2.3. *Validation of reference genes for Eurasian perch*

We started selecting 15 genes commonly used in the literature as RGs. From these, five primers couples were validated because some genes were not present in the phylofish database, or because the primers proposed by the software used to design had high homology with many other Eurasian perch sequences in the database. The validated primers were: *actin*, *tubulin*, *lsm14*, *hprtl* and *tbp*. In addition, another primer pair targeting *actin*, that has been previously used for a study in the laboratory, was evaluated in our samples using RT-qPCR. None of them presented a sufficient stability between egg samples, meaning that we find significant statistical differences in their expression between the groups of high and low egg quality. Noteworthy, the samples we have available for Maternal Legacy experiment come from fish populations presenting diverse characterists, including different origins and raising systems These features have potential to contribute for modifications in gene expression, thus it adds more difficulty to find realiable reference genes since these are expected to be stably expressed across samples.

In parallel with Maternal Legacy experiment, a microarray analysis was performed in 31 Eurasian perch egg samples from two fish populations and presenting varied quality. The results of this analysis will be presented in details in the next chapters. But we also used the microarray results to help finding reliable reference genes to be used for Maternal Legacy experiment. For this end, we looked for the most stably expressed genes in the analysis. This was done by filtering the list of expressed genes according to the coefficient of variation (CV), and those presenting variation lower than 2%, were chosen for further analyses. This list contains 45 genes. We designed and validated primers for the six first genes on this list (those showing lower CV) to check their expression by RT-qPCR (as described below). The respective results were submitted to a Mann-Whitney-Wilcoxon test after confirming the absence of normality, using the Shapiro-Wilk test, and the absence of homogeneity of variance, using the Levene's test (RStudio software version 1.0.143). No significant differences were found between egg quality groups for the three following genes: *adenosine kinase-like* (Phylofish sequence ID: MPF_LOC101464997.1.1), *40S ribosomal protein S27a* (Phylofish sequence ID: MPF_LOC100697017.2.2) and *ELAV-like protein 1-like* (Phylofish sequence ID: MPF_LOC100695900.1.2) (Figure 16). They were then validated as reference genes and allowed the normalization of the genes of interest we tested in the following.

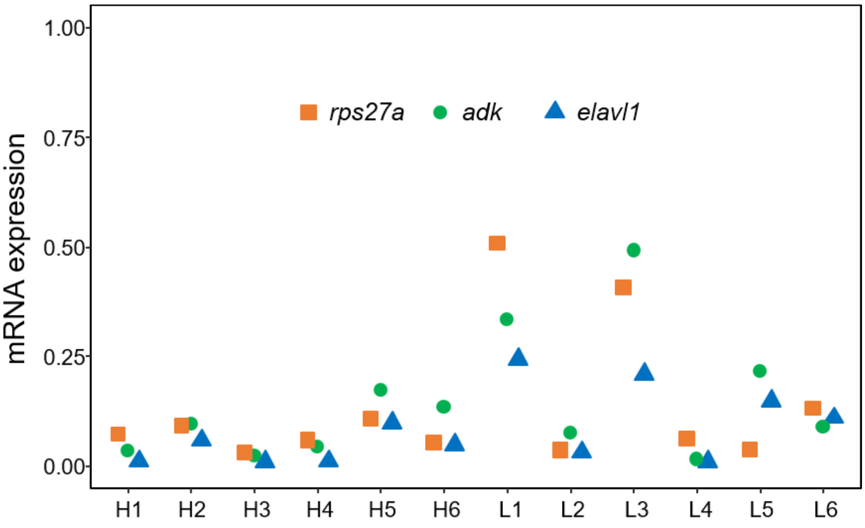


Figure 16. Reference genes expression in high (H1-H6) and low (L1-L6) egg quality samples.

3. Part B – Comparing gene expression between species

3.1. *Expression of the selected genes in Eurasian perch eggs*

3.1.1. RT-qPCR analysis

Here again we used the microarray results to help in Maternal Legacy experiment. This time we looked for the expression pattern of the 11 zebrafish quality-related genes, for wich we already had primers pairs designed, in Eurasian perch eggs. The expression level of four out of 11 was significantly differentially expressed or close to it (p-value ≤ 0.1), in Eurasian perch eggs belonging to high compared to low quality groups. Thus, their expression was checked by RT-qPCR in Eurasian perch eggs. These genes were: equilibrative nucleoside transporter 1-like (*slc29a1a*) (Phylofish sequence ID: MPF_LOC101478767.1.3), ubiquitin thioesterase otulin (*otulin*) (Phylofish sequence ID: MPF_LOC101474680.1.1), inter-alpha-trypsin inhibitor heavy chain H2-like (*itih2*) (Phylofish sequence ID: MPF_LOC100693444.1.1) and ribosome production factor 2 homolog (*rpf2*) (Phylofish sequence ID: MPF_LOC100699686.1.1).

Both, potential reference genes (RGs) and genes of interest (GIs) were studied by RT-qPCR in all samples representing high (n = 6) and low (n = 6) quality eggs. Reverse transcription was performed in a final volume of 20 µl using a M-MLV Reverse Transcriptase (Sigma-Aldrich), 1 µg of RNA and random nonamers (2.5 µM - Sigma-Aldrich) and following the manufacturer’s protocol. Reverse transcript products were diluted 1:27 and 5 µl were used for the RT-PCR, using PerfeCTa SYBR Green SuperMix (Quanta Bioscience) and 5 pmol of each primer. Primers were designed using Primer3Plus or Primer Design Tool-NCBI software (Supplementary Table 15 - Annex). RT-qPCR was performed using a Step One Plus system (Applied Biosystems, Foster City, USA). The PCR program consists of a first step at 95°C for two minutes followed by 40 cycles consisting of a denaturation step at 94 °C for 15 s, an annealing step at 50 °C (at least - depending on the primers pairs) for 15 s and an elongation step at 72 °C for 30 s. The amplification was followed by a melting curve stage, according to manufacturer’s parameters in order to check the primers specificity. The abundance of the target cDNA in each sample was calculated using a serial dilution of a pool of all cDNA samples using the StepOne Software (Applied Biosystems, version 2.1). This dilution curve was used to certify the reaction efficiency (80-120%). All samples were analyzed in duplicate.

The geometric mean of the expression level data of the three RGs previously validated (Figure 16) was used to normalize the data obtained from the GIs. The values obtained after the normalization were analyzed using a Mann-Whitney (RStudio software version 1.0.143) to compare differences of gene expression between the two quality groups ($p<0.05$).

3.1.2. RT-qPCR results and discussion

The expression of the four tested genes was not significantly different while comparing high and low quality Eurasian perch eggs (Figure 17).

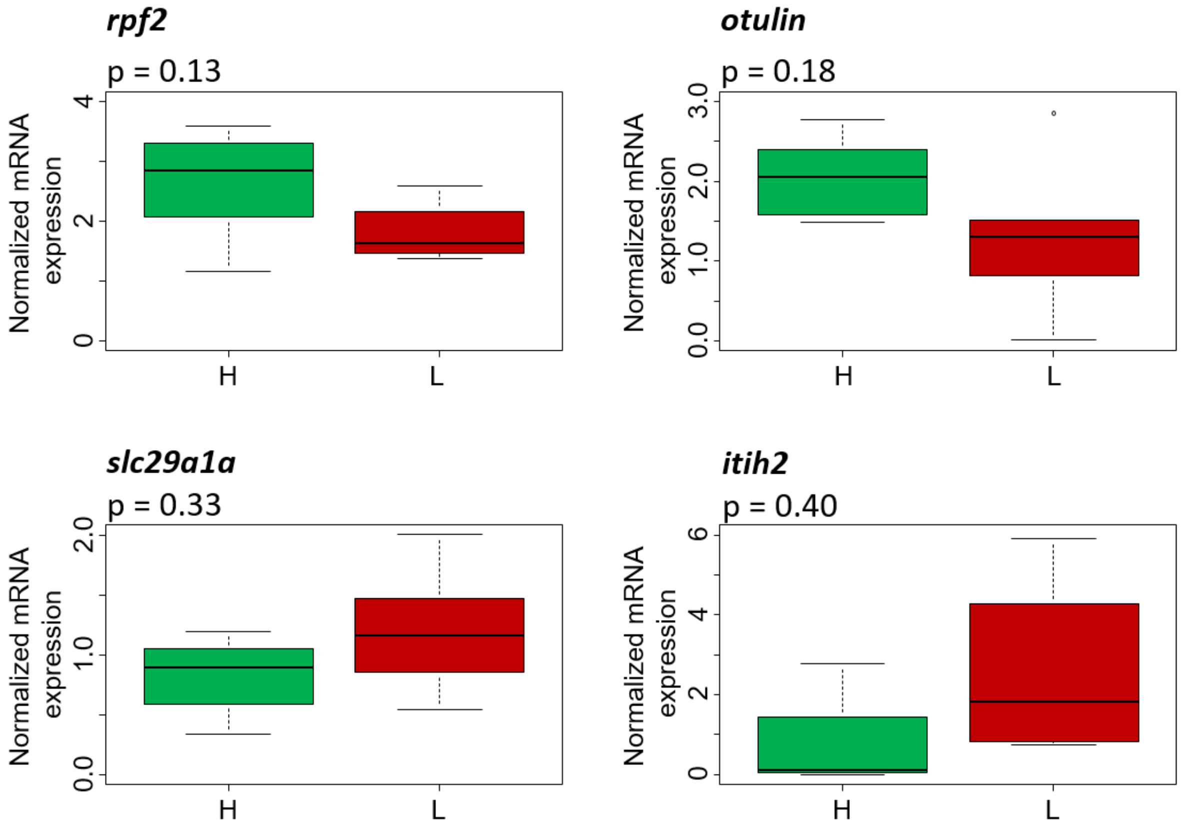


Figure 17. Normalized expression of egg quality-related genes, previously identified in zebrafish, in Eurasian perch eggs. H = high and L = low egg quality groups. p-values shown correspond are in result of a Mann-Whitney-Wilcoxon test (n=6 for each group).

Concerning the results on rainbow trout, no good quality RNA could be successfully extract for this species. As a consequence, no eggs' gene expression study could be performed. With regards to sea bass, a transcriptomic analysis of eggs belonging to high (survival rate >60% at 3 hpf) and low (survival rate <60% at 3 hpf) quality groups was performed also employing microarrays. Authors found 39 DEG between the two groups (Żarski et al., 2017a). However, no common DEG was found between sea bass and zebrafish.

In zebrafish, *slc29a1a*, *otulin* and *itih2* were down-regulated in low quality eggs, while *rpf2* was up-regulated in the same quality group. As observed in sea bass vs. zebrafish comparison, the results of the present study demonstrate that the genes tested did not present the same pattern of expression in the two species compared, Eurasian perch vs. zebrafish. Even if we used the same technique for quantification, closer embryonic developmental stage to assess egg quality and closer thresholds (rates) to limit high and low quality groups. Only *otulin* tended to follow the same pattern of genes expression as in zebrafish, being numerically higher expressed in eggs of higher quality. The other three genes presented inverse tendencies in comparison to the expression pattern in zebrafish. These differences may be explained for species-specific regulations at the transcriptomic level during embryonic development or even may be due to non-controled methodological factors, such as the developmental stage chosen to assess egg quality, that were not the same. However, other genes, belonging to the same pathway, may still be implicated in the differences of egg quality observed. Thus, shared molecular mechanism implicated in embryos proper development remains to be investigated.

The work on this project together with the trainings I attended, gave me the necessary background to perform and interpret the results of most of analysis I would accomplish later during my PhD. It includes many molecular biology and bioinformatic tools, genomics and statistical analysis. In addition, working with Maternal Legacy project, helped us to make some essential choices for the project. The first one was the use microarrays as the technique to perform gene expression profiling, once we saw that RNA-seq was not able to elucidate differences between distinct categories of egg quality in zebrafish. Other contribution from the Maternal Legacy project was the necessity of overthink the stage of embryonic development and threshold chosen to determine egg quality groups, since using the same criteria will allow more reliable comparisons of results obtained in different species. It was also a starting point to build different strategies for egg quality groups comparisons, as presented in **Chapter 2**. Due to the difficults we have to find good reference genes, it also helped in the choice of the samples/fish populations that would be used in the following experiments. And, at the end, it allowed the comparison between populations presenting different levels of domestication (**Chapter 3**). By choosing only two populations, we expected to have less variation in the eggs gene expression and once find, the number of source (s) explaining it would be reduced.

Chapter 1 recapitulation sheet

(PROTOCOL ADAPTATION AND GENE EXPRESSION COMPARISON BETWEEN SPECIES)

Specific objectives

- Define an efficient protocol for high quality total RNA extraction from eggs
- Find suitable reference genes to normalize gene expression on eggs
- Perform gene expression analysis on eggs of high and low qualities
- Compare the expression of quality-related genes between species

Main results

- Improvement of RNA extraction protocol
- Validation of three reference genes
- No differentially expressed quality-related genes between zebrafish and Eurasian perch

Next, in Chapter 2:

- We will investigate the transcriptomic content of Eurasian perch (*Perca fluviatilis*) eggs in order to present an extensive analysis of results variation that can be find when different protocols to assess egg quality are employed either (1) using individual criteria or (2) when a multi-parametric analysis is used.

V. Chapter 2: Impact of the methods employed to assess egg quality on their transcriptomic profile results

1. Part A - Unifying fish egg quality transcriptomic studies. *What can we learn from the Eurasian perch?*

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1.1. *Abstract*

Egg quality is an important issue to be solved in order to improve fish production in captive conditions. It is related to developmental success and thus explains greatly reproduction impairments due to massive early lethality. For several decades many studies have aimed at developing methods to assess egg quality reliably as early as possible. However, these methods are very diverse and depend greatly upon the egg morphology, technical means and authors scientific goals. This heterogeneity of methods leads to difficulties to make efficient comparisons between studies. Today, with the growing success of omics studies, it becomes possible to find common pathways potentially linked to the egg quality in several fish species. However, the accuracy of such techniques and the large number of genes that may be impacted request for reliable methods to assess egg quality. The present study aims at determining whether and how method choice impacts transcriptomic analyses of unfertilized eggs in Eurasian perch (*Perca fluviatilis*). To do so, we compared two by two groups of spawn with various qualities. We tested the impact of criterion of quality (survival rates at 24 hpf and 48 hpf as early criteria and hatching rate or deformities rates at hatching as later criteria) and the impact of thresholds (rates) used to define the limits of one group of spawn within one specific criterion. The study demonstrates that transcriptomic results are related to early developmental failures but not to later failures in this species. In addition, the confrontation of results obtained between comparisons showed that transcriptomic results greatly depend on methods used to define groups of egg quality. Nevertheless, two molecular functions were highlighted and are potentially related to egg quality in most analyses. They correspond to genes involved in immune system and in translation which is in accordance with the literature. Finally, while comparing all results obtained, the expression of *CD68* coding for Macrosialin, is increased in low quality eggs in all analyses performed. Our results thus demonstrate that the methodology employed to define groups of egg quality greatly influence transcriptomic results. It points the need for a consensus way to study developmental impairments in most of fish species. This would help to obtain comparable results between studies involving either one species in various scientific contexts or different species. It may help to define not only conserved molecular pathways affected in egg quality in several species but also interesting ways for intra-species studies.

Keywords: microarray, egg content, gene ontology, mRNA, Teleosts, P*erca fluviatilis*.

1.2. *Background*

Among around 33.000 fish species known today (Froese and Pauly, 2019), just a few are studied by biologists. Many studies are performed in the context of aquaculture, in order to improve fish culture practices. Rearing fish species implies to be able to control their reproduction in captivity and obtain healthy offspring to sustain livestock. Fish farms need, among others, to control the reproductive cycle and obtain good quality gametes leading to well developing embryos and larvae. Consequently, understanding egg quality related mechanisms are of primary importance and many fundamental questions remain to be addressed, among them, what makes a good egg, what may affect egg quality and how precisely assess egg quality. In aquaculture, early developmental failure is one of the major problems in fish breeding programs. High embryonic mortality negatively impacts fish reproductive performance, mostly first developmental stages mortality which highly correlate to gamete’s quality. Thus, the production of high quality gametes is requested to increase aquaculture production (Migaud et al., 2013).

Studies available so far, already show a huge heterogeneity in terms of species reproduction strategies and ways to assess their egg quality. Literature devoted to fish eggs quality is abundant [reviewed by (Bobe, 2015; Schaerlinger and Żarski, 2015; Migaud et al., 2013; Bobe and Labbé, 2010; Brooks et al., 1997; Kjorsvik et al., 1990)], and reflects a huge heterogeneity of practices, depending on species reproduction strategies, egg morphology, technical means of authors and producers and also on the studies scientific context. Consequently, compilation and meta-analyses are complex. It may mainly be due to the use of heterogeneous criteria to assess the egg quality (Bonnet et al., 2007a). Up to now, the most reliable and easiest way to assess egg quality is to measure developmental success. Survival rates are evaluated as early as possible from the first cell divisions to the eyed stage depending on the egg transparency and the parameters reliability in a given species. For example, some species may trigger several cell divisions after egg activation without fertilization, while others need to be fertilized to begin embryogenesis. Hatching and deformities/malformations rates and the swimbladder inflation may also be considered, even if they can be seen as late criteria. If numerous studies use one principal criterion to estimate egg quality, others take into account several of them in the meantime. The studies are diverse within and between species.

Egg’s quality is mainly characterized by their intrinsic properties (Brooks et al., 1997) that could impact their structure and function throughout early embryogenesis. Consequently, any defect of incorporation and/or synthesis of molecules during oogenesis would lead to developmental impairments. In addition, many molecular functions activated in eggs and early embryos are widely conserved through animal kingdom including fish species. Investigating egg content in relation to their quality will (i) help scientists to better understand intrinsic modifications leading to developmental defects and (ii) enable to find reliable molecular parameters allowing predicting egg quality that could potentially be adapted for several fish species.

Some studies focused on yolk proteins and lipids content, with the goal of making links between efficient feeding regimes, egg content and developmental success (Durland et al., 2010; Henrotte et al., 2010; Luo et al., 2015). For almost two decades of increasing technical progress in transcriptomic and proteomic, scientists can investigate other molecules not related to the yolk proteins and lipids. Few studies focused on egg protein content (Castets et al., 2012; Yilmaz et al., 2017); potentially, it is mainly due to technical difficulties because of the high concentration of Vitellogenin-related proteins compared to other proteins. However, studies investigating transcriptomic content of eggs related to their quality and developmental potentiality is increasing rapidly (Bonnet et al., 2007a; Chapman et al., 2014; Cheung et al., 2019; Ma et al., 2019; Mommens et al., 2014; Rise et al., 2014; Żarski et al., 2017a). These studies have been fruitful and identified many maternally-loaded mRNA essential for early development (Bobe, 2015). In common, they employed comparisons of at least two spawn groups which quality is assessed with criteria that are highly variable between species. In addition, authors often define percentage thresholds separating quality groups which therefore mainly depend upon data obtained during the experimentation and are not always accurately explained.

In zebrafish, Knoll-Gellida et al. (Knoll-Gellida et al., 2006) identified more than 11.000 unique sequences tags in fully grown ovary. These sequences probably reflect only part of the RNA expressed at the end of oogenesis. Most of them may probably correspond to maternal RNA accumulated during oogenesis and necessary during the embryonic development. They not only control cellular processes during embryogenesis early steps but may also later impact axes formation or cell differentiation (Pelegri, 2003). Consequently, transcriptomic studies aiming at investigating egg maternal RNA profiles in relation to their quality deal with a large number of differently expressed transcripts. Deregulation of any of these genes may theoretically have a variety of consequences at various steps of embryogenesis. It implies that embryonic phenotypes may theoretically be carefully examined in order to make reliable links between transcriptomic profiles and observed phenotypes.

The present study aimed at investigating how the choice of criteria and thresholds influences transcriptomic data in Eurasian perch (*Perca fluviatilis*). We choose this species because its reproduction can be controlled in captive conditions but still an important heterogeneity of early embryonic developmental success is observed. It appeared thus as a choice model to determine how spawn quality groups definition can impact transcriptomic results even with a unique experimental protocol to assess developmental success. It showed that, in our conditions, the choice of criterion or modifications of one threshold allowing defining egg quality groups already interfere on transcriptomic results. From a larger point of view, our results demonstrate the need of considering methodological differences between studies in order to perform reliable intra- and inter-species studies allowing finding common molecular pathways within and between species.

1.3. *Material and methods*

1.3.1. Broodstock management and eggs sampling

The experiments were performed at the Aquaculture Experimental Platform (AEP, registration number for animal experimentation C54-547-18) belonging to the URAPA lab and located at the Faculty of Sciences and Technologies of the University of Lorraine (France). Breeders originated from "Lucas Perches" fish farm (Hampont, Lorraine) and their oogenesis was induced in recirculating aquaculture systems using a photothermic program (Abdulfatah et al., 2011; Fontaine et al., 2015). Eggs were sampled during a spawning season taking place in 2015. Right after the collection, one part of the unfertilized eggs was frozen in liquid nitrogen and transferred at -80 °C for later molecular analyses. Another part of the spawn was fertilized as described in (Żarski et al., 2012c) using a pool of sperm of 3 males and incubated to assess egg quality.

1.3.2. Study of criteria

In total 28 females were sampled. Four parameters were studied, called criteria in the following parts. The two first criteria were chosen to characterize early developmental stages corresponding to embryonic survival rates at 24 (SR24) and 48 (SR48) hours post-fertilization (hpf). They were estimated in triplicate (3x100 embryos; same samples for both analyses) for each spawn using the following formula: (number of alive embryos/total number of embryos)x100. The two other criteria rather characterized late stages. Hatching rate (HR) was estimated in triplicate (3x100 embryos; for each spawn). Samples were isolated at fertilization and left untouched until hatching. They are different from those used to evaluate SR24 and

SR48, but were coming from the same females. They were estimated using the following formula: (number of hatched/total number of embryos)x100. Deformities rate (DR) was estimated at hatching for each spawn using the formula: (number of abnormal embryos at hatching/total number of hatched embryos) x100. It was done on hatched embryos from the HR measurement (in triplicate). All rates are expressed as percentages corresponding to the mean of the triplicates.

In order to investigate potential differences in survival between the three first criteria, survival and hatching rates were compared using a two-way ANOVA in repeated measurements followed by a pairwise t-test comparison and applying a Bonferroni p-value adjustment. Statistical probability significance was established at 5% (α<5%). Tests were performed using R (v.1.1.423) (R Core Team (2017)).

1.3.3. Quality groups defined according to different criteria

Each criterion was studied and analyzed independently (Figure 18). Each time, spawn groups qualified as low and high qualities were designed. One specific spawn belonged to one group depending on their performance (rate) according to the studied criterion. Thus, thresholds (limits of rates) were chosen in order to design groups with at least five spawn to be statistically robust. Spawn groups were named using the criterion (SR24, SR48, HR and DR) and a reference to the threshold. For example, for survival rate at 24 hpf, the group including spawn with rates >80% is noted SR24_80+ while for the same criterion, spawn with rates <45% are noted SR24_45-. In total, 13 groups were defined. All groups name codes are summarized in Figure 18 and Supplementary Table 1.

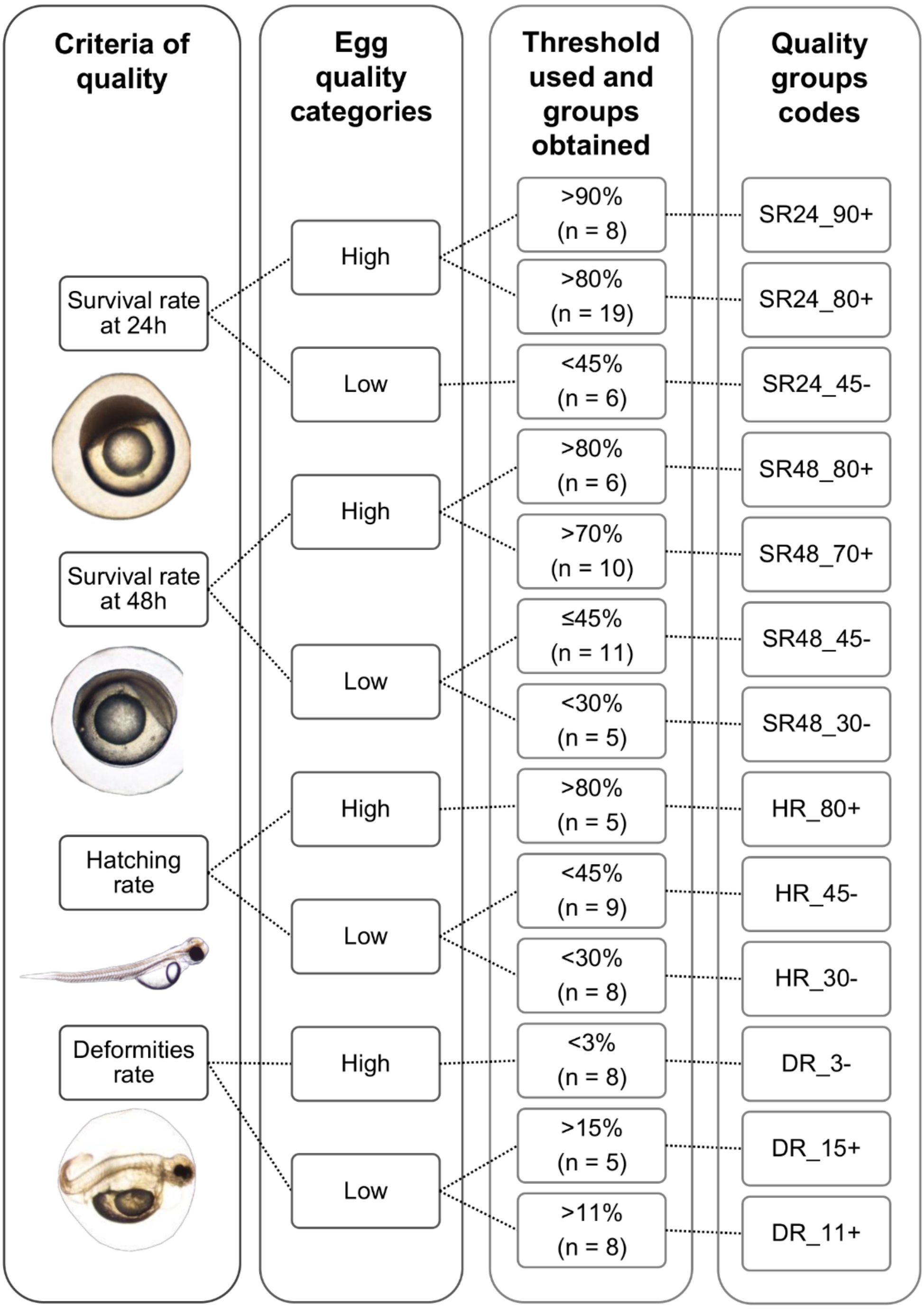

Figure 18. Design and characterization of groups of spawn according to eggs' quality. Different groups of quality were formed using different criteria and thresholds. The first and second columns show the criteria and quality terms used in the text, respectively. The third column presents thresholds used to form each group of egg quality and number of spawn per group (n). The last column summarizes the code names employed in the text for each group.

1.3.4. RNA extraction

Total RNA was extracted from 28 samples of mature, unfertilized and frozen eggs using TRIzol reagent (Life Technologies) at a ratio of 100 mg per mL of reagent and following the manufacturer's instructions with some modification. A step of milling was added in the homogenizing step in order to break the hard chorion characteristic in the eggs of perch. A bullet blender (Next Advance) and zirconium oxide beads 1.0mm were used for milling. Also, a supplementary run of the separation phase step was performed due to eggs' high lipids content. A NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies) was used to evaluate the quantity of total RNA and Agilent 2100 Bioanalyzer (Agilent Technologies) was used to evaluate the integrity of the RNA extracted. Samples exhibiting integrity higher than 7 was used for the microarray analysis.

1.3.5. Microarray analysis

Perch arrays (SurePrint G3 Custom Gene Expression Microarray, 8x60K - Agilent Technologies) contained 48,986 non-redundant probes designed based on the transcriptome available on Phylofish Databases (Pasquier et al., 2016). The “One-Color Microarray-Based Gene Expression Analysis (Low Input Quick Amp Labeling) Protocol” was followed for sample preparation, hybridization, wash and scan of the slides and data extraction. Briefly, 150 ng of total RNA was used in the amplification/Cy3-labeling step. After this process, all samples were purified (RNeasy mini kit, Qiagen) and they were quantified using Nanodrop. Samples exhibiting a yield higher than 1.03 µg of cRNA and a specific activity higher than 10.30 pmol cy3/µg of cRNA were fragmented and used for hybridizing the arrays. A total of 600 ng of Cy3-cRNA of each sample was randomly distributed onto the four slides. After 17 h of hybridization at 65 °C, the slides were washed, dried and scanned with an Agilent Technologies Scanner (G2505C). The scanned images were extracted with Agilent Feature Extraction software. Data were normalized and log(2) transformed for statistical analyses (all data are available in the Gene Expression Omnibus database under the accession code GSE119802). A t-test followed by a Benjamini-Hochberg correction was applied, using GeneSpring software, to identify potential differentially expressed genes (DEG, $p<0.05$) between high and low quality groups.

1.3.6. Analysis of the expression pattern of DEG in high and low quality groups

Using the thirteen groups defined, ten simple analyses were performed in total, in order to potentially obtain DEG. To test the homogeneity of genes expression between the high and low quality groups, a hierarchical clustering analysis (unsupervised average linkage) was performed using Cluster 3.0 software (version1.52) on the different expressed transcripts obtained from the microarray analysis. Pearson correlation (uncentered) was used to measure the similarities. Clusters were visualized using TreeView software (version 1.1.6r4). Then, to evaluate the relationship between the simple analyses, a second round of comparisons, called double comparisons, was performed. Thus, the DEG lists of two simple analyses, were compared using Venn diagrams (Bardou et al., 2014) to identify potential overlapping genes. In total, 6 double comparisons were performed.

1.3.7. Effect of criterion employed to egg quality assessment

The first goal was to check the criterion effect in order to determine how developmental stages at which the survival rates were evaluated may influence transcriptomic results. It was assessed confronting 24 vs. 48 hpf results, taking groups that were designed using the same thresholds. This double comparison involved DEG lists obtained in the two simple analyses: SR24_80+ vs. SR24_45- and SR48_80+ vs. SR48_45-. Venn diagrams allowed identifying potential DEG overlapping between the two lists.

1.3.8. Threshold effect

The same strategy was used to determine the effect of thresholds chosen to limit egg quality groups. Using the same criterion, the double comparison involved simple analyses differing on one threshold qualifying either high or low quality. The double comparison could thus be subdivided into two categories. The first ones involved a variation of the higher threshold while the low quality group was identical. The other ones involved a variation of the lower threshold while the high quality group was identical. Five double comparisons were performed and are summarized in Table 5. Venn diagrams were also used to allow identifying potential DEG overlapping between the lists.

Table 5 . Double comparisons performed using the DEG from all six simple analyses, with modification of thresholds.

Characterization of the double comparisons	**Simple analysis 1**	**Simple analysis 2**
Varying HIGH quality at 24h	SR24_90+ vs. SR24_45-	SR24_80+ vs. SR24_45-
Varying HIGH quality at 48h	SR48_80+ vs. SR48_45-	SR48_70+ vs. SR48_45-

Varying HIGH quality at 48h	SR48_80+ vs. SR48_30-	SR48_70+ vs. SR48_30-
Varying LOW quality at 48h	SR48_70+ vs. SR48_30-	SR48_70+ vs. SR48_45-
Varying LOW quality at 48h	SR48_80+ vs. SR48_30-	SR48_80+ vs. SR48_45-

1.3.9. Identification of DEG common to all comparisons

In addition to the effect of the stage of development and the threshold we were also interested in determining whether some genes did appear as differentially expressed in all comparison in the meantime. For this purpose, we also employed Venn diagrams, using all six DEG lists as input.

1.3.10. Gene ontology (GO)

To functionally annotate probes we aligned them against the perch transcriptome extracted from the genome, provided by (Ozerov et al., 2018), with minimap2 (version 2.7 with -m 20 parameters). Because the gene prediction file had small UTRs, we extended the prediction on both transcript sides by 2 kb. If a probe had a unique alignment, it was assigned to the corresponding transcript. If the probe had two corresponding transcripts located one after the other on the genome, we assigned it to the transcript having the match closest to its center. Probes with no match or over two matches were not assigned to a transcript. We then retrieved the human orthologs from the annotation file provided by (Ozerov et al., 2018), to perform a gene ontology (GO) overrepresentation statistical analysis with the Panther14.0 software (Mi et al., 2019). The lists of DEG corresponded to the inputs and parameters were set at default, meaning that a Fisher’s exact test and a Benjamini-Hochberg correction were applied. As background, we used the complete list of expressed genes already identified in Phylofish, in addition to those ones we were able to identify using the perch genome. We asked for complete Biological Processes (BP) and Pathways and only corrected p-values <0.05 were considered as significant.

1.4. *Results*

1.4.1. Reproductive performance

Survival rates presented variabilities at each developmental stage. However, a higher number of spawn exhibited high survival rates at 24 hpf (19/28 >80% SR24; Figure 19 and Supplementary Table 1) in comparison to other stages. Considering SR48 and HR, the distribution of spawn was homogeneous. A significant difference was observed only between 24 hpf and hatching (Figure 19). Twenty-three spawn presented deformities with rates ranging from 0 to 19% (Supplementary Table 1). Taking into account all these information, we were able to obtain several quality groups with a minimum of five spawn in a group (Figure 18).

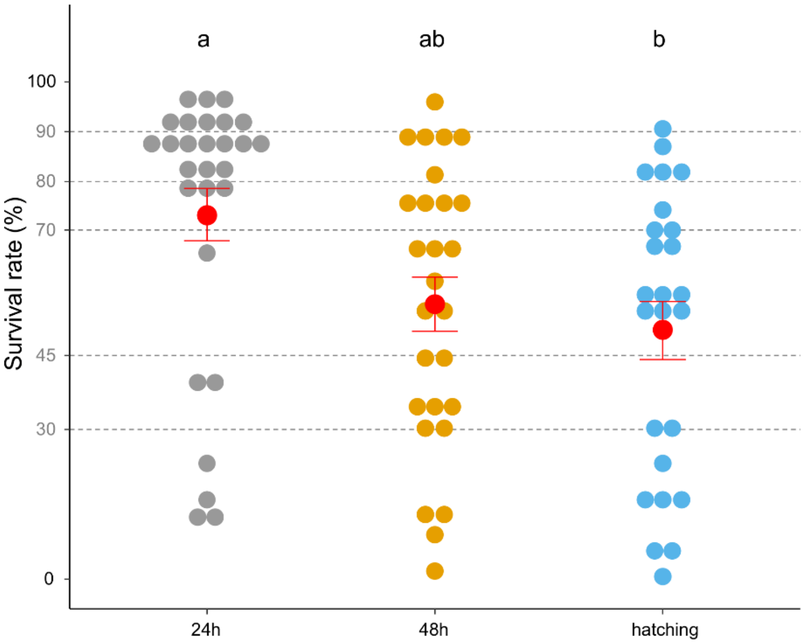

Figure 19. Distribution of spawn according to the embryonic survival rates at 24 and 48 hours post-fertilization (hpf) and at hatching. Red dots represent survival means ± SEM at each observed stage (n= 28, 27 and 25 for 24 hpf, 48 hpf and hatching, respectively). Scatter points correspond to means values for each spawn. Interrupted lines marks the rates used to define the quality groups. Different letters indicate significant differences between observation stage using a two-way ANOVA in repeated measures followed by a pairwise t-test with Bonferroni correction ($p<0.05$).

1.4.2. Effect of the criterion used to egg quality assessment

The first goal was to study the relationship between the criteria used to determine reproduction success and the transcriptomic content on unfertilized eggs. Some parameters concerned early development (SR24 and SR48) while others evaluated late development (HR and DR). At late stages, three groups of spawn were defined for hatching and deformities rates allowing making two simple comparisons for each parameter. They correspond to HR_80+ vs. HR_30- and HR_80+ vs. HR_45- for hatching rate and DR_3- vs. DR_15+ and DR_3- vs. DR_11+ for deformities rate. No statistical difference was observed in any simple analyses, preventing making any relationship between these late criteria and the eggs transcriptomic content or any further comparison.

Similar comparisons were performed using the survival rates at 24 hpf and 48 hpf at the same thresholds (>80% vs. <45%). The comparison performed at 24 hpf showed 11 DEG between the two spawn groups (SR24_80+ vs. SR24_45-; Figure 20A, Supplementary Table 2, Figure 21A). Using the same thresholds at 48 hpf, 351 DEG were identified in the comparison SR48_80+ vs. SR48_45- (Figure 20B, Supplementary Table 2, Figure 21B). No biological process GO term or pathway was highlighted for any of these simple comparisons.

In order to determine whether the 11 DEG found in the first comparison at 24 h are included in the 351 ones found at 48 h, we employed Venn diagrams. Only two genes were common while comparing both DEG lists (Figure 20C, Supplementary Table 3).

A

Survival rates at 24h	>90% (n = 8)	>80% (n = 19)
<45% (n = 6)	671 DEG (a)	11 DEG (b)

B

Survival rates at 48h	>80% (n = 6)	>70% (n = 10)
≤45% (n = 11)	351 DEG (c)	211 DEG (d)
<30% (n = 5)	521 DEG (e)	1480 DEG (f)

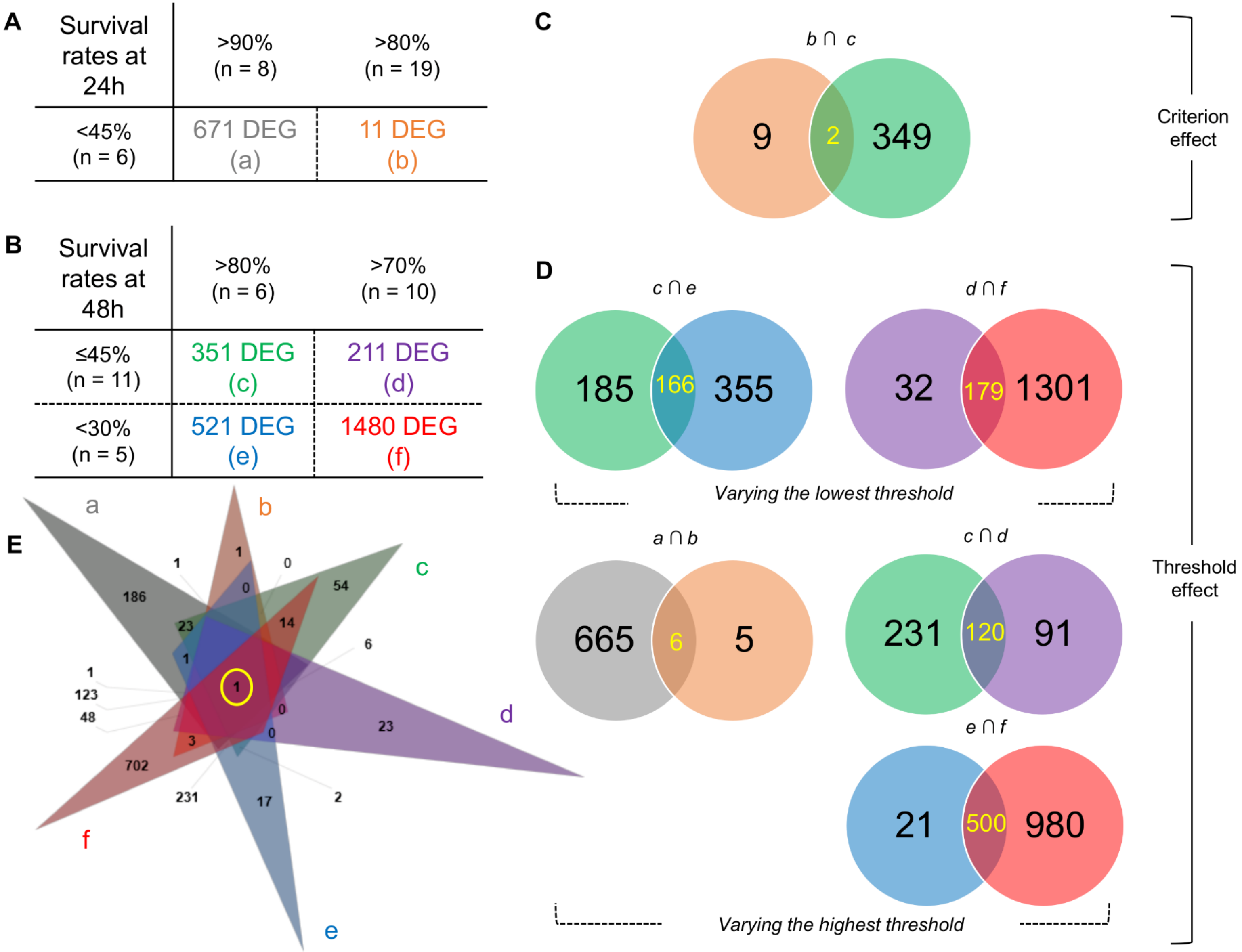

Figure 20. Comparisons of differentially expressed genes (DEG) obtained for simple analyses. Panels (A) and (B) show the number of DEG obtained in simple analyses using different thresholds at 24 and 48 hpf, respectively. Letters between parenthesis under the number of DEG and color codes are used as symbols to simplify identifications of the corresponding simple analyses above each Venn diagrams in (C), (D) and (E). n = number of spawn per group of quality. (C) Venn diagrams showing the number of DEG shared between simple analyses using similar thresholds at 24 and 48 hpf, to study the criteria effect. (D) Venn diagrams showing the number of DEG shared between simple analyses, to study the threshold effect. They were further subdivided into two categories depending whether the highest or the lowest thresholds were modified. Above each circle, italic letters identify the simple analysis used as input in the diagrams, they are also identified by the same color each time. The numbers in the diagram's intersections (in yellow) represents the DEG shared by both simple analyses. (E) Venn diagram of the comparison of all DEG lists shows one gene commonly found in every simple analysis. A t-test followed by a Benjamini-Hochberg correction was used to identify the DEG.

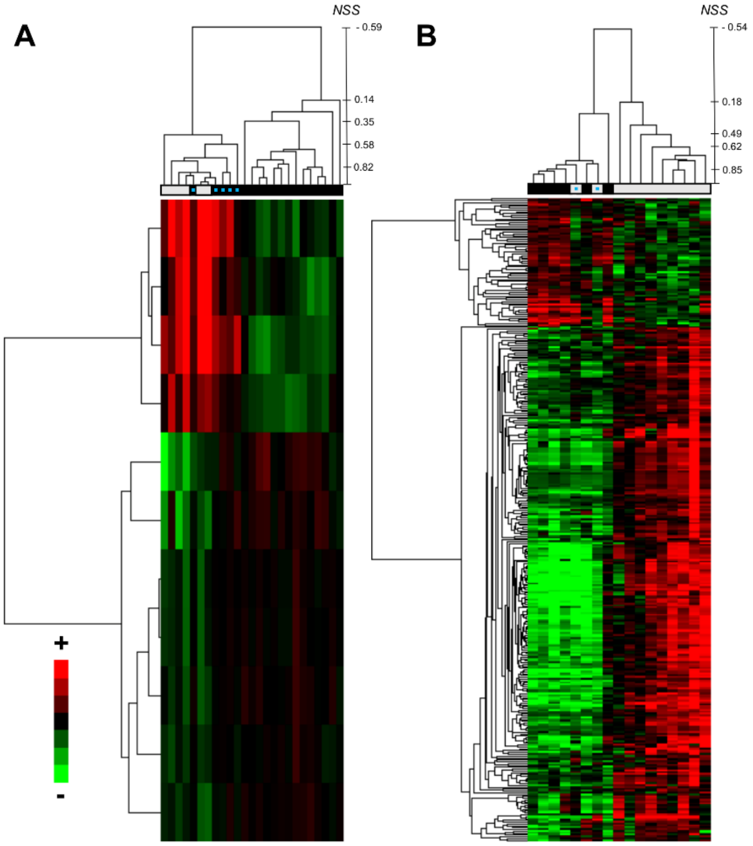

Figure 21. Unsupervised hierarchical clustering analysis of the differentially expressed genes (DEG; $p<0.05$) between groups of high and low eggs quality. (A) DEG from the comparison SR24_80+ vs SR24_45-. (B) DEG from the comparison SR48_80+ vs SR48_45-. In both heatmaps, colors on the top bar indicate the high (black) and low (gray) quality egg samples. Blue dots marking some samples indicate that they clustered with the opposite quality group. Red color indicates the over expression, and green color indicates the under expression while black is used for median expression. The dendrograms on the left and on the top represent correlation distance between genes and samples, respectively. Nodes similarity score (NSS) between samples are shown. It ranges from 1 (identical) to -1 (opposites), while 0 means they are uncorrelated.

1.4.3. Effect of the threshold used to egg quality groups definition

Comparisons of data obtained with groups of spawn defined using the same criterion but with different thresholds were also performed. Using the survival rate at 24 h as criterion, three groups of quality could be defined with at least five spawn (2 of high quality and 1 of low quality). Then, SR24_90+ and SR24_45- groups were compared and led to 671 DEG (Figure 20A, Supplementary Table 2, Supplementary Figure 1A). Surprisingly, the second analysis (SR24_80+ vs. SR24_45-) led to only 11 DEG whereas the number of spawn comprised in SR24_80+ is higher and include spawn belonging to SR24_90+. Results obtained using Venn diagrams show that six genes were common to both DEG lists (Figure 20D, Supplementary Table 3). The SR24_90+ vs. SR24_45- analysis revealed that *immune system* and the *translation* related genes were enriched (Table 6). Most of these genes were up-regulated in low quality group.

Table 6. Overrepresented terms in the DEG list from SR24_90+ vs. SR24_45-. The terms represent Biological Processes. For each term, number of genes represented and corrected p-values are shown.

GO biological process complete	Gene count*	Corrected p-value (FDR)	Direction of the disturbance
SRP-dependent cotranslational protein targeting to membrane (GO:0006614)	11	7.30E-03	Up-regulated in low quality
Translational initiation (GO:0006413)	12	8.97E-03	Up-regulated in low quality
Innate immune response (GO:0045087)	19	9.38E-03	Up-regulated in low quality
Viral transcription (GO:0019083)	11	9.80E-03	Up-regulated in low quality
Nuclear-transcribed mRNA catabolic process nonsense-mediated decay (GO:0000184)	11	1.56E-02	Up-regulated in low quality
Leukocyte migration (GO:0050900)	13	1.67E-02	Both-sides disturbed
Cytokine-mediated signaling pathway (GO:0019221)	19	2.77E-02	Both-sides disturbed

Using the survival rates at 48 h, four groups of spawn were defined. Two of them represented high quality groups with thresholds higher to 70 or 80% while the two others characterized the low quality groups with thresholds below 45 or 30%. All four analyses involving a group of low and high quality were performed to highlight genes differently expressed. The higher number of DEG was observed in the analysis SR48_70+ vs SR48_30- (1480 DEG, Table S2). On the other hand, the lowest number of DEG was obtained in the analysis SR48_70+ vs SR48_45- (211 DEG, Supplementary Table 2). The use of Venn diagrams allowed us to identify variable numbers of DEG shared between analyses (Figure 20D; Supplementary Table 3). The GO analyses showed that, SR48_80+ vs. SR48_30- and SR48_70+ vs. SR48_30- were the only comparisons allowing finding enriched terms at 48 hpf. It corresponded to *immune system* for the first comparison and *translation* and *immune system* for the second one. Most of genes were up-regulated in the low quality groups (Table 7 and 8).

Table 7. Overrepresented terms in the DEG list from SR48_70+ vs. SR48_30-. The terms represent Biological Processes. For each term, number of genes represented and corrected p-values are shown.

GO biological process complete	**Gene count***	**Corrected p-value (FDR)**	**Direction of the disturbance**
Translational initiation (GO:0006413)	19	2.26E-02	Both-sides disturbed
SRP-dependent cotranslational protein targeting to membrane (GO:0006614)	16	2.46E-02	Both-sides disturbed
Activation of immune response (GO:0002253)	31	2.66E-02	Both-sides disturbed
Innate immune response (GO:0045087)	31	2.79E-02	Both-sides disturbed
Viral transcription (GO:0019083)	16	3.53E-02	Both-sides disturbed
Cytokine-mediated signaling pathway (GO:0019221)	33	4.71E-02	Both-sides disturbed

Table 8. Overrepresented terms in the DEG list from SR48_80+ vs. SR48_30-. The terms represent Biological Processes. For each term, number of genes represented and corrected p-values are shown.

GO biological process complete	**Gene count***	**Corrected p-value (FDR)**	**Direction of the disturbance**
Innate immune response (GO:0045087)	20	7.15E-04	Down-regulated in high quality
Cytokine-mediated signaling pathway (GO:0019221)	21	2.24E-03	Both-sides disturbed
Activation of immune response (GO:0002253)	17	1.56E-02	Both-sides disturbed
T cell differentiation (GO:0030217)	9	2.90E-02	Both-sides disturbed

Positive regulation of T cell proliferation (GO:0042102)	7	3.34E-02	Both-sides disturbed
Regulation of adaptive immune response (GO:0002819)	9	4.48E-02	Both-sides disturbed

Interestingly, the unsupervised average linkage clustering analysis showed clear different patterns of gene expression between the groups of high and low eggs quality for all comparisons performed. However, the gene expression within groups present variable correlation between samples with even some samples clustering with the opposite quality group (Figure 21A-B and Supplementary Figure 1A-D).

1.4.4. Common DEG between all comparisons

In order to determine whether some genes were differently expressed in all analyses, a large comparison of all DEG lists coming from all simple analyses was performed. Venn diagrams allowed finding a unique gene that was systematically up-regulated in all low quality groups. It corresponds to the gene CD68, coding for the protein Macrosialin (Figure 20E).

1.5. *Discussion*

1.5.1. Only early survival was related to eggs mRNA content in our conditions

Embryonic development depends upon molecular reserves that are accumulated during oogenesis. After fertilization, only few exchanges occur with the environment (Schaerlinger and Żarski, 2015). Consequently, any defect of incorporation of a molecule may greatly impair developmental progression. Among these molecules, transcripts have largely been studied in developmental biology, demonstrating a precise orchestration of genetic regulations controlling embryogenesis steps. The first players of these regulations are the maternal RNA whose expression is regulated during oogenesis and that are present in the egg before fertilization. Consequently, they may be affected by biotic and/or abiotic factors to which females are submitted and may thus be linked to heterogeneity of developmental success in captive conditions. In several animal species, maternal RNAs are involved in diverse cellular functions such as cell differentiation, regulation of zygotic transcription or embryonic axes definition. Impaired maternal RNAs synthesis during oogenesis may thus theoretically have numerous consequences at various fish embryogenesis stages.

In the present study, differences in egg maternal transcripts abundances were related to early survival rate modifications. This is in accordance with previous studies in other fish species (Chapman et al., 2014; Żarski et al., 2017a). They indicate that maternal transcription impairments have mainly early consequences. Knoll-Gellida et al. (Knoll-Gellida et al., 2006) investigated the ovarian follicle transcriptome in trout and showed that the most abundant mRNA present before fertilization are, among other, mostly related to translation, transcription or cell division functions that are important during early embryogenesis. Genes involved in some of these biological pathways are often found to be affected in transcriptomic studies of egg quality (Cheung et al., 2019; Żarski et al., 2017a). Even if transcripts involved in later processes such as axis formation or cell differentiation would be affected, the embryonic consequences would not be visible because embryos would die early.

On the other hand, late embryonic defects do not seem to be related with transcriptomic defects as no transcript was differently expressed between spawn classified according to hatching rate or deformities rate at hatching. This in accordance with previous results obtained in trout where spawn of high and intermediate quality did not display any gene expression difference (Aegerter et al., 2005; Ma et al., 2019). However, one study found moderate correlation coefficients between hatching rates and some genes expressions (Mommens et al., 2010). Noteworthy, in the same study, no correlation between gene expression and early developmental impairments was observed.

1.5.2. Transcriptomic results depend upon criteria chosen to assess egg quality

Embryonic development is a dynamic process involving at each step the regulation of various molecular pathways. Consequently, our working hypothesis was that developmental impairments observed at various developmental stages may be poorly related because they potentially involve various pathways. Consequently, comparisons of studies involving survival criteria at various developmental stages would not be relevant. In order to test this hypothesis, we performed double comparisons between the DEG lists obtained while using survival rates at 24 and 48 h and the same thresholds. Only two genes were common between both analyses, corroborating our working hypothesis. In Eurasian perch, survival rate at 72 hpf is commonly used to determine early survival because it is easily observed using a low magnificent loupe. A previous unpublished study performed in the laboratory showed a correlation between lethalities observed at 72 and 48 h but no correlation between 72 and 24 h, suggesting different causes or lethalities (M. Alix unpublished data). For this species, the cleavage period lasts for around 24 h while gastrulation lasts from 24 hpf until 51 hpf when the organogenesis begins. The mid-blastula transition (MBT) occurs at around 9 hpf (Alix et al., 2015). Considering that zygotic genome activation (ZGA) would take place at this moment, as it happens for others species, such as zebrafish, developmental defects observed at 24 hpf may directly involve maternal genes but not those at 48 hpf. In order to make intra or inter-species comparisons between studies, one must carefully consider the developmental stage at which the survival rate was evaluated. Current studies have a tendency to give a large importance to fertilization rates assessed some hours after fertilization in order to take into account the exclusively direct effect of the maternal RNAs. This early fertilization checking is also performed in salmonids even if developmental success is more often assessed at the eyed or yolk sac resorption stages (Bizuayehu et al., 2019; Mommens et al., 2015). In the meantime, some studies use more than one criterion to define egg quality (Castets et al., 2012). Even if this practice may probably help to define more reliable spawn groups, obtained data must be carefully analyzed in the light of the type of criterion (survival or deformities occurrence) and the step at which they were observed.

In the present study, despite of the variable number of DEG, two patterns of genes expression can be observed for each comparison. Inside each group, however, the correlations between samples are quite variable. It shows that comparing extreme quality groups, based on early survival (what is commonly the case in many studies), allows to obtain distinct egg gene expression patterns in which high individual variability can be observed.

1.5.3. The threshold chosen affects interpretation of eggs gene expression results

In addition to the criteria used to characterize egg quality *a posteriori*, all studies distinguished at least two drastically different qualities according to the criteria used. These two groups usually result from thresholds set using heterogeneous methods. Indeed, in some studies, authors take into account a limited number of spawn with extreme variations to define the two quality groups and use the extreme thresholds of both groups. In every case, authors mainly depend upon data obtained during the experiment which cannot be predicted. We thus wanted to determine whether the choice of these thresholds may interfere with transcriptomic results.

Our study shows that, using the same criterion to assess egg quality but using different thresholds modifies the transcriptomic results. In addition, no specific pattern of these modifications could be identified. For example, for the double comparison SR24_90+ vs

SR24_45- with SR24_80+ vs. SR24_45-, the reduction of 10% of the threshold for the high quality group (from 90 to 80%) resulted in the increase of the number of spawn and potentially in the gene expression homogeneity within the high quality group. In fact, it resulted in a drastic decrease of the number of the DEG (from 671 to 11, for each of the simple analysis cited above, respectively). In contrast, for the double comparison SR48_80+ vs SR48_30- with SR48_70+ vs SR48_30-, a similar reduction of 10% in the high quality group, resulted also in the increase of the number of spawn rather led to an important increase of the DEG number (from 521 to 1480, for each of the simple analysis cited above, respectively). In this last condition, the increased number of spawn in the high quality resulted in an increase of the gene expression heterogeneity.

These data could be explained by greater survival rates variation in SR48_70+ group that included spawn with survival rates ranging from around 95% to 74% while SR24_80+ group included those presenting survival rates ranging from around 97% to 80% but with a larger number of spawn (19 and 10 in SR24_80+ and SR48_70+, respectively). However, this hypothesis is not confirmed while comparing low quality groups because the most varied spawn group (SR48_45-) includes 11 spawn, with survival rates ranging from 1% to 43%, did not present the same pattern. More accurately, all simple analyses involving this group presented a lower number of DEG in comparison to the same analyses involving SR48_30- that has a less variable survival rage. Surprisingly, the simple analyses involving the most variable spawn groups SR48_70+ vs. SR48_45- led to 211 DEG which corresponds to the lowest number of genes found in comparisons involving groups designed using the survival rate at 48 h.

In any case, using extreme thresholds to define spawn groups we were always able to find DEG. It is the case in almost every published study. However, the relationship between thresholds and the nature of molecular functions found to be deregulated have to be carefully discussed. To our knowledge, the present study is the first one to present such disparities between spawn groups using different thresholds. Further works are needed in several fish species in order to better understand these differences. In future studies, the impact of thresholds should be addressed in order to interpret properly molecular results obtained, in order to make reliable comparisons with the literature.

1.5.4. Gene Ontology

In all comparisons allowing finding enriched GO terms only two functions were affected which correspond to *translation* and *immune system*. These terms are often found to be related with egg quality in some fish species. suggesting that they may be reliably related to egg quality issues.

Concerning *translation*, even if some genes are more abundant in low quality group of the simple comparison SR48_70+ vs. SR48_30-, most of them were down-regulated in eggs of higher quality in this analysis and at 24 hpf. Many of these genes code for ribosomal proteins and are thus involved in ribosome's assembly. Studies on the characterization of zebrafish (*Danio rerio*) gene expression patterns during embryogenesis showed that an increase of ribosomal protein coding mRNA accumulation starts after MBT (Mathavan et al., 2005). Ribosome biogenesis is upregulated during oogenesis, then it is repressed after fertilization with an increased accumulation of ribosomal proteins coding mRNA until late embryogenesis (Thomas, 2000). It is possible to assume that relative low abundance of ribosomal protein coding mRNAs combined with high amount of pre-formed ribosomes as shown in Atlantic halibut (*Hippoglossus hippoglossus*) (Bai et al., 2007) and *Xenopus* [reviewed by (Brown, 2004)] are expected in eggs with good potential to develop properly. In the present study, the high abundance of mRNA coding for ribosomal proteins in eggs of low quality may indicate some impairment during oogenesis, potentially reducing ribosome biogenesis which is essential for early development. Ribosomal proteins synthesis is controlled at translational but not at transcriptional level (Nomura et al., 1984). Thus, mRNA coding for ribosomal proteins may be less required during first cell divisions, when it is expected that inherited maternal ribosome will supply to this function. However, they should be essential later for gastrulation and organogenesis stages, when the translational capacity of embryonic cells will be in high demand. In addition, other genes involved in translation that were differentially expressed in eggs according to their quality have been characterized. In sea bass (*Dicentrarchus labrax*), the expression of eIF-2-alpha kinase activator GCN1 (*gcn1l1)* and mitochondrial translation elongation factor (*tsfm)*, were highly correlated with fertilization rate (Żarski et al., 2017a). Fertilization rate is usually measured at the first cell division in other fish species, thus, comparing transcriptomic profiles of eggs of different quality that were assessed at earlier stages than 24 hpf (earlier step evaluated in the present study) could give already reliable results.

The second function affected was *immune system*. Most of genes represented in this function were down-regulated in higher quality eggs, even if some of them were down-regulated in lower quality eggs. This term has also been found to be affected in other studies. However, the data available in the literature connecting relative abundance of transcripts with fish egg quality does not imply the same genes or gene families. For example, in Atlantic cod (*Gadus morhua*) genes involved in the *interferon* pathway, also involved in the immune response, were highly expressed in eggs regardless of their quality (Rise et al., 2014). While for sea bass (*Dicentrarchus labrax*) (Żarski et al., 2017a) and Atlantic halibut (*Hippoglossus hippoglossus)* (Mommens et al., 2014)*,* genes representing the same pathway were up regulated in eggs of higher quality. Fish embryos and young larvae are almost unable to produce specific antibodies or some other molecules related to adaptive immunity and the maturation of their lymphoid organs is delayed [reviewed by (Swain and Nayak, 2009)]. Consequently, fish embryos that may be highly subjected to environmental pathogens, greatly depend upon the maternal supply of mRNA and proteins involved in this biological function (Seppola et al., 2009; Swain and Nayak, 2009; Zhang et al., 2013). The dynamic regulation of these genes seems complex during oogenesis and authors even proposed that they may be necessary for the proper embryogenesis progression (Seppola et al., 2009). This question needs further investigation to be properly understood.

1.5.5. CD68: a potential new maternal-effect gene

The confrontation of all DEG lists obtained in this study showed an unexpected result in the view of the simple comparisons performed. Indeed, it showed one unique gene, CD68, with a systematically higher expression in eggs presenting lower quality whatever the chosen criterion or thresholds. CD68, coding for the Macrosialin protein, may be an interesting gene potentially linked with the egg developmental ability.

Macrosialin is a heavily glycosylated protein related to the immune system. It is highly expressed in cells of the monocyte/macrophage lineages, and as such, it has commonly been used as a marker of macrophages (Chistiakov et al., 2017). However, its expression has also been detected in lymphoid and non-haemopoietic cells, such as fibroblasts, endothelial and tumor cells (Gottfried et al., 2008; Pulford et al., 1990), as well as in osteoclasts where it seems to be important for bones resorption function (Ashley et al., 2011). It is a transmembrane protein receptor, mainly associated with endosomes/lysosomes, which can migrate to the cell surface (Gottfried et al., 2008).

In zebrafish microglial cells, which are brain resident macrophages, abundantly express *cd68* (Oosterhof et al., 2017). In this species, a primitive macrophages population appears between ~12-24 hpf (Carroll and North, 2014), corresponding to segmentation and beginning of pharyngula periods (Kimmel et al., 1995). Interestingly, CD68 participates in mammals lipids metabolism, acting as a scavenger receptor, allowing macrophages uptake of oxidized low density lipoprotein (LDL) (Ramprasad et al., 1996). Having in mind the ability of CD68 to recognize modified LDL, its expression in non-myeloid cells and considering the sequence homology between lipovitellin, the major yolk protein, with apolipoprotein B-100 (ApoB), a LDL subunit (Anderson et al., 1998), it is possible to hypothesize that CD68 may have a role in lipovitellin endocytosis and/or processing into lysosomes, or be involved on even earlier events, including lipids uptake during oogenesis, as hypothesized by (Hiramatsu et al., 2015). Several works described functional relationships between yolk proteins such as Vitellogenin and its derivatives and the immune system [reviewed by (Zhang et al., 2013)].

1.6. *Conclusions*

The present study strongly supports the idea that early developmental failures are related with defects of synthesis and accumulation of mRNA in oocytes. On the contrary, hatching and deformities rates may rather be linked to other mechanisms, potentially maternally inherited molecules, such as lipids.

This work mainly shows that criterion used to assess egg quality and thresholds used to define egg quality groups are crucial for transcriptomic analyses. Today, the amount of molecular information related to fish egg quality is increasing and authors naturally tend to compare their data with other studies. Our results stress the necessity to consider the way egg quality groups were defined and embryogenesis stages selected in these studies while doing such comparisons.

We showed that GO analyses help to find biological processes that may be related to egg quality, including immune system and translation. These functions were already found to be disrupted in other fish species. Additionally, comparisons of the DEG lists and especially the confrontation of the six lists helped to find common genes that may be related to egg quality. Up to now, CD68 has not been highlighted to be differentially expressed according to egg’s quality in other species than Eurasian perch.

In any case, each study and/or fish species present their own characteristics, leading to a variate range of data authors have to deal with. It prevents to define a restrictive framework allowing unifying methods to assess egg quality. However, it would be beneficial to consider in advance accurately the experimental methods in order to allow reliable comparisons between two studies. For example, by using the same criterion for one species in two different scientific contexts or trying to use the same developmental stage (not timing) for two species in the same experimental condition. If possible, it would be interesting to define groups using similar thresholds. In any case carefully taking into account all these data while preparing an experiment would be beneficial to try to unify as far as possible the studies, allowing defining convergent and divergent molecular pathways in various studies depending on the scientific questions but not due to methodology differences.

1.7. *Acknowledgements*

We thank Mikhail Ozerov and Freed Ahmad from University of Turku for kindly providing the annotated perch genome used in GO analysis. We also thank members of UR AFPA DAC and LPGP Rennes for their support.

1.8. *Financial support*

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1.9. *Ethics statements*

Lorraine Ethic Committee for Animal Experimentation (CELMEA) and the French Ministry of Research approved the animal experiments. CELMEA agreement number: APAFIS#1390-2018031516387833 v2.

1.10. *Supplementary information*

Supplementary Table 1. Description of the characteristics of all spawn analyzed in the study. Survival rates at 24 and 48 hours post-fertilization, hatching rate and deformities rate at hatching from the 28 spawn analyzed are shown. Spawn belonging to high or low quality groups are shaded in different colors (see table footnote).

Spawn number.	SR24 (%)	SR48 (%)	HR (%)	DR (%)
1	93.57	89.20	74.24	2.98
2	90.21	67.16	69.40	1.32
3	95.59	95.90	83.44	2.92
4	90.62	89.75	90.55	4.97
5	88.96	81.37	68.48	1.40
6	97.28	88.04	70.60	9.72
7	83.69	59.96	80.01	2.07
8	88.17	74.85	83.34	4.51
9	87.39	34.58	30.66	15.23
10	78.24	29.01	16.74	11.28
11	77.05	54.70	52.30	19.63
12	87.23	73.88	54.68	11.16
13	85.77	65.20	65.51	18.00
14	95.83	89.33	86.88	18.73
15	81.21	74.95	56.88	11.92
16	65.43	34.65	15.26	15.32
17	38.80	31.33	23.29	3.10
18	40.15	34.50	6.46	0
19	81.1	8.84	4.63	10.00
20	87.38	45.00	29.99	1.48
21	80.16	53.13	57.83	3.15
22	90.83	43.56	15.62	1.45
23	87.98	77.45	55.26	3.02
24	93.47	67.28	56.52	2.02
25	15.89	0	0	ND
26	11.20	13.45	0	ND
27	23.12	1.46	0.60	0
28	13.37	12.55	0	ND

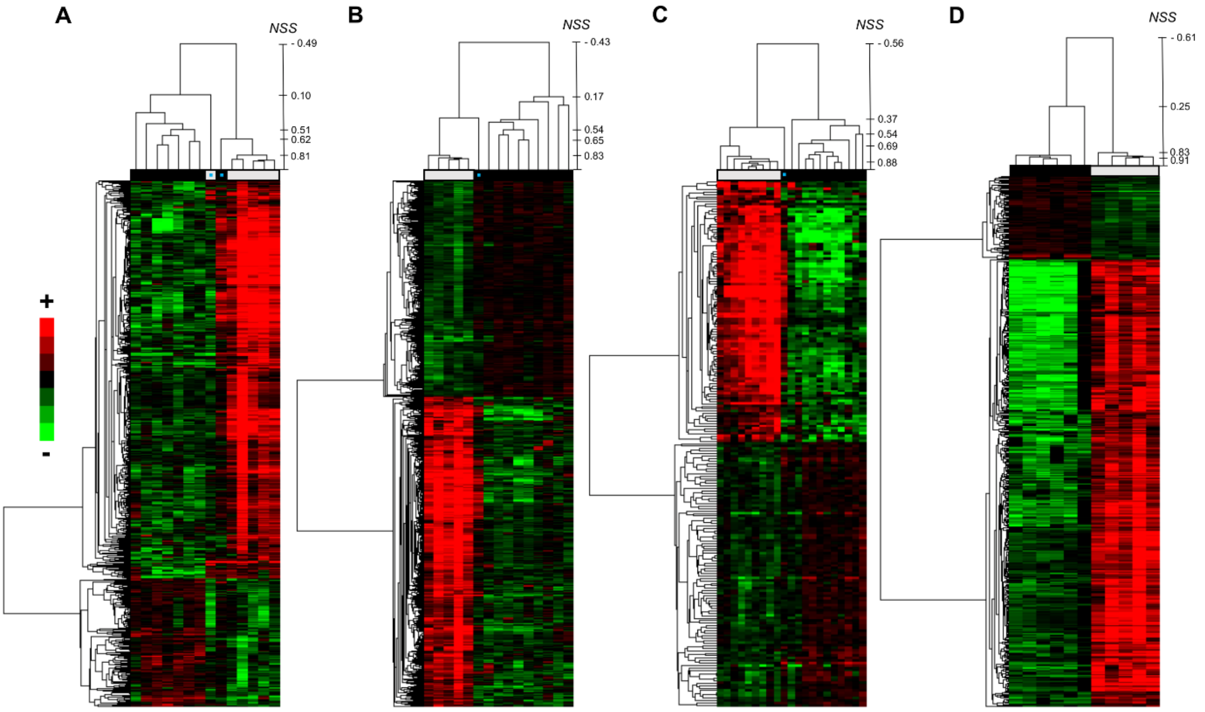
Colors indicate spawn belonging to a specific quality group. As a whole, green shades point to high quality spawn for each criterion, while grey and blue point bad quality ones. For SR24, light green spawn belong to SR24_90+. SR24_80+ contain spawn shaded in light and dark green. Grey spawn belong to SR24_45-. For SR48, light green spawn belong to SR48_80+. SR48_70+ contain spawn shaded in light and dark green. Grey spawn belong to SR48_30-. SR48_45- contain spawn shaded in blue. For HR, green spawn belong to HR_80+. Grey spawn belong to HR_30-. HR_45- contain spawn shaded in gray and blue. For DR, green spawn belong to DR_3-. Grey spawn belong to DR_11+. HR_15+ contain spawn shaded in gray and blue. ND – non-determined.

Supplementary Table 2. Lists of the differentially expressed genes. Phylofish Gene ID, Gene description, Corrected p-value (FDR), Log2 Fold-Change (LogFC) and Regulation of the differentially expressed genes between all the comparisons performed using groups of high and low quality eggs.

Due to the long size of this table, it can be found at the end of this document in the digital version only.

Supplementary Table 3. Lists of the differentially expressed genes shared between different comparisons. Phylofish gene ID and gene description are shown.

Due to the long size of this table, it can be found at the end of this document in the digital version only.



Supplementary Figure 1. Unsupervised hierarchical clustering analysis of the differentially expressed genes (DEG; $p < 0.05$) between groups of high and low eggs quality. (A) DEG from the analysis SR24_90+ vs SR24_45-. (B) DEG from the analysis SR48_70+ vs SR48_30-. (C) DEG from the analysis SR48_70+ vs SR48_45-. (D) DEG from the analysis SR48_80+ vs SR48_30-. In all heatmaps, colors on the top bar indicate the high (black) and low (gray) quality egg samples. Blue dots marking some samples indicate that they clustered with the opposite quality group. Red color indicates the over expression, and green color indicates the under expression while black is used for median expression. The dendrograms on the left and on the top represent correlation distance between genes and samples, respectively. Nodes similarity score (NSS) between samples are shown. It ranges from 1 (identical) to -1 (opposites), while 0 means they are uncorrelated.

2. Part B – Transcriptomic analysis of Eurasian perch eggs assigned to distinct quality groups according to a multi-parametric statistical analysis

2.1. *Context*

The work presented in this Part B was performed before and gave the basis for the one presented in Parte A. It aimed at comparing the transcriptomic profile in Eurasian perch eggs, according to four quality cluster.

In previous study at the laboratory (Alix et al., *In preparation*), 73 spawn were analyzed using a principal component analysis (PCA) followed by an agglomerative hierarchical clustering analysis (HCA) on 12 criteria describing survival, deformities occurrence at hatching and the hatching period. They were able to define three clusters of egg quality, one of high quality and two presenting medium quality. A fourth group was composed by the spawn that failed fertilization or development within the 72 first hours and was thus assigned to a bad quality spawn cluster. They also verified that three criteria (survival rate at 72 hpf, hatching rate and deformities rate) were reliable enough to sort the spawn into the same quality clusters, thus were are going to mention only these three in this Part B.

2.2. *Material and methods*

Material and methods not mentioned in this Part correspond to the same employed in Part A.

2.2.1. Groups of quality using a multi-criteria analysis

Our high quality group, I, presented the highest survival rate at 72 h post fertilization (hpf; mean value: 83.18%) and hatching rates (mean value: 77.51%) with low deformities rate (mean value: 3.74%). The medium quality groups, II and III, showed lower survival rates at 72 hpf (mean values: 55.71% and 43.14%, respectively) and hatching rates (mean values: 47.36% and 31.20%, respectively) in comparison to I. II and III can be differentiated due to a higher deformities rate presented by group II (mean value: 15.16%) compared to the group III (mean values: 3.03%). The fourth (IV) presented survival rate lower than 8.00% at 72 h and almost no hatching (Table 9).

Table 9. Mean ± SE of the main parameters identified as sufficient to define relevant clusters of spawn. Different letters on the top indicates statistical difference between the clusters using a non-parametric Kruskal-Wallis test followed by a Mann-Whitney-Wilcox test ($p < 0.05$). ND = no determined.

Parameters	Clusters of spawn quality			
	I	II	III	IV*
Survival rate at 72 hpf	83.18 ± 3.49^a	55.71 ± 7.58^b	43.14 ± 7.34^b	7.93 ± 3.88
Hatching rate	77.51 ± 2.84^a	47.36 ± 8.77^b	31.20 ± 7.97^b	0.15 ± 0.15
Deformities rate	3.74 ± 0.97^a	15.16 ± 1.21^b	3.03 ± 1.07^a	ND

* The cluster IV was not defined using the same analysis. Instead, it was composed by the spawn that show lack or bad developmental performance from the very beginning. ND – non-determined.

The 32 spawn used in the present analysis comprises the 28 used in the analysis describe in Part A, plus four spawn that presented worst quality and were excluded from that analysis (Supplementary Table 1). Each cluster (I, II, III and IV) contained eight spawn.

2.2.2. Microarray analysis

RNA extraction, samples preparation, arrays hybridization, wash, scan and data extraction and transformation were performed as described in Part A. As said, the clusters were represented by eight samples each, however, one sample from cluster IV failed labeling, thus this cluster had seven samples. A one-way ANOVA followed by a Benjamini-Hochberg correction was used to identify the differentially expressed genes between the four clusters as a whole and a Tukey HSD was used as a post-hoc test to identify the differentially expressed genes (DEG) between the four clusters of quality ($p<0.05$).

2.2.3. Identification of the differentially expressed genes on each cluster

In the following, we wanted to individualize each cluster based on their gene expression, to be able to make connections between gene expression and the embryonic developmental phenotype associated to each of them. Thus, it was important to identify the genes that were differentialy expressed only in one cluster in comparison to the others. Those genes will then be characteristic of one cluster. To this end, we used Venn diagrams [jvenn (Bardou et al., 2014)] to compare the respective DEG lists (blue boxes in Table 10).To characterize the cluster I, for example, we used the differentially expressed genes between groups IxII (set of 13 genes), between IxIII (set of 70 genes) and IxIV (set of 3343 genes) in the mean time (Figure 23). Since the group I is the only common cluster appearing in the three datasets, we reasoned that the genes present in the middle intersection of the diagram may be specific and thus characterize the cluster I. In order to be confirmed, we used a Tukey HSD test to compare their expression in the cluster I in comparison to the three others (p<0.05). The same process was done for the four clusters.

2.3. *Results*

2.3.1. Differentially expressed genes among the four egg quality clusters

The *analysis of variance* performed using the frour clusters of quality revealed 3.485 DEG ($p < 0.05$) between the clusters as a whole (Supplementary Table 4). The differences were higher between the cluster IV and the other three ones and lower in clusters I, II and III compared together (Table 10). This fourth group corresponds to the embryos that failed fertilization or died within the 3 first days (before the beginning of the organogenesis) in comparison to the others that went through it.

Table 10. Number of genes differentially expressed between the clusters. In total, 3485 were differentially expressed (p<0.05). Blue boxes represent genes differentially expressed between clusters, while orange boxes represent the number of genes which are not differentially expressed. Tukey HSD test (n= 31; p<0.05).

Groups	**II**	**III**	**I**	**IV**
II	***3485***	53	13	3285
III	3432	***3485***	70	2080
I	3472	3415	***3485***	3343
IV	200	1405	142	***3485***

A supervised average linkage clustering analysis was also performed using the expression data of the 3.485 DEG. The clustering analysis shows no clear different pattern of gene expression between the clusters. However, it can be seen a huge number of genes that are down- or up- regulated in most of the samples representing the cluster IV in comparison to other ones (Figure 22).

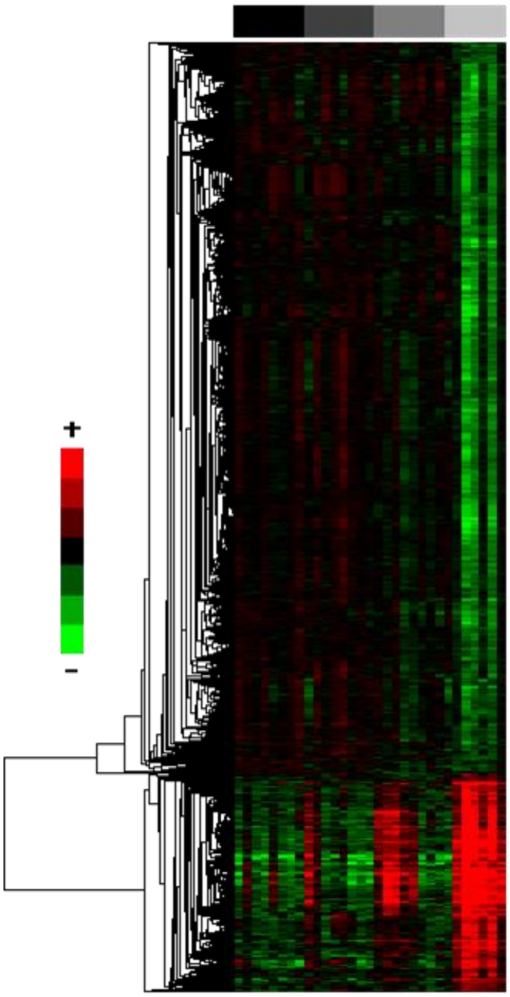


Figure 22. Supervised hierarchical clustering analysis of the 3485 differentially expressed genes ($p < 0.05$) among the four clusters of quality (I, II, III and IV). Colors on the top bar from black to the lighter gray represent the cluster I to IV, respectively. Red color indicates the over expression, and green color indicates the under expression while black is used for median expression. The dendogram on the left represents correlation distance between the genes on which we can distinguish 2 patterns of gene expression. In one of them, most of the genes are low expressed in the cluster IV.

2.3.2. Characterizing the differentially expressed genes on each cluster

Confirming the pattern showed in the clustering analysis (Figure 22), the Venn diagrams analysis leaded to the confirmation of only few exclusive DEG genes in the three first clusters. In the Figure 23 (I), the intersection containing 50 genes represents the number of genes differentially expressed shared by the datasets IxIV and IxIII, meaning that these genes appear in at least one of these groups (I, III or IV) as differentially expressed. The same way of reasoning can be applied to the other two peripherical intersections. Finally, the intersection of the center of the diagrams corresponds to common genes differentially expressed between the three datasets used as inputs for the diagrams. As said in the methods section, since the cluster I is the only common group appearing in the three datasets, we inferred that these five genes could characterize the cluster I. A Tukey HSD test confirmed that four of the five genes identified by the Venn diagrams were differentially expressed in the cluster I in comparison to the three others (p<0.05; Supplementary Table 5). In the same way, one gene characterized the cluster II, two the cluster III (Figure 23, Supplementary Table 5). Still in agreement with the clustering analysis, it was possible to confirm that 1903 genes were differentially expressed in the cluster IV in comparison with the three others (Figure 23; SupplementaryTable 6), from the 1911 identified in the Venn diagrams.

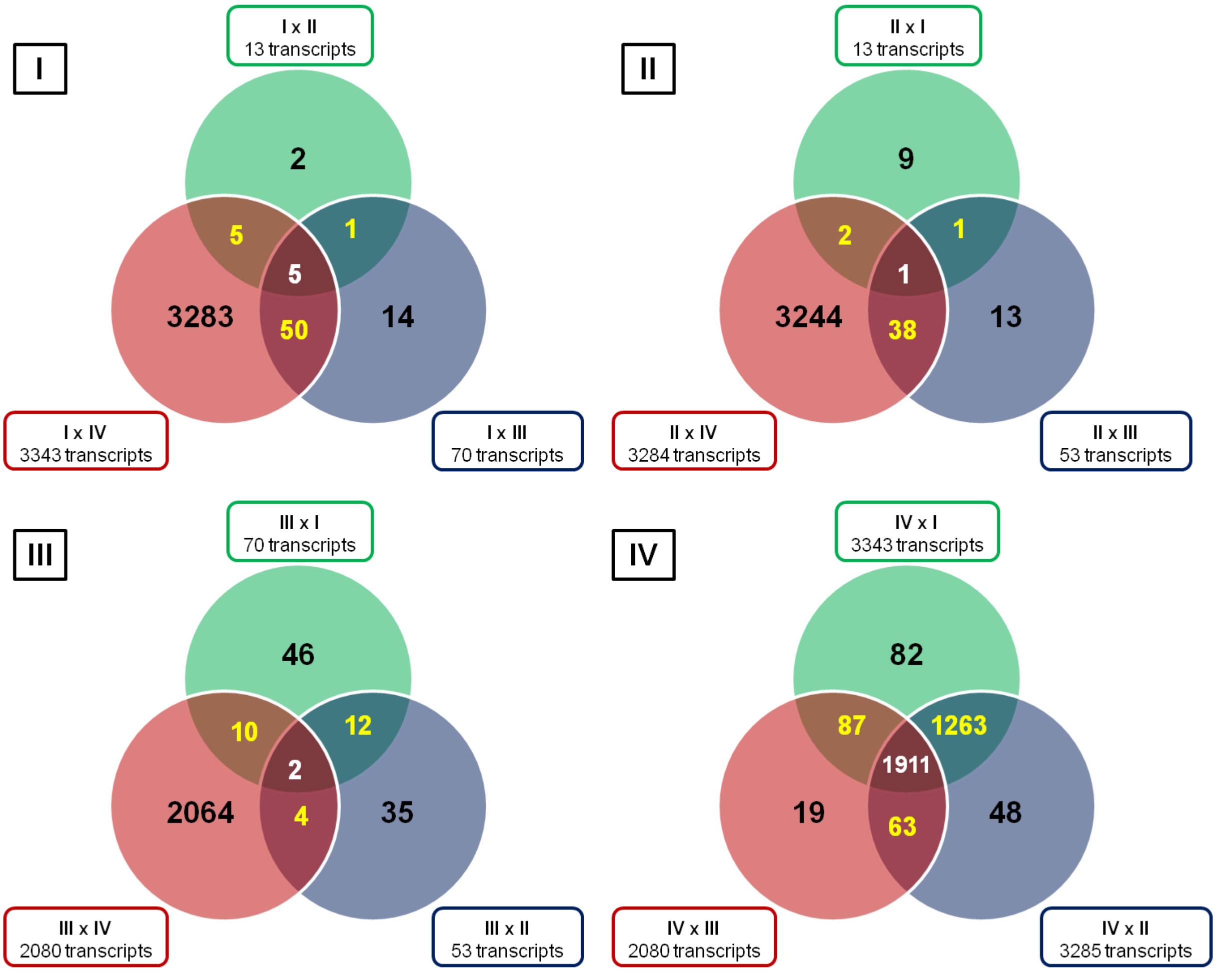


Figure 23. Venn diagram showing the number of overlapping (shared) differentially expressed genes (DEG) between the quality clusters. The round boxes show the number of transcripts in each dataset used as input for the Venn diagrams. I, II, III and IV indicate the cluster for which the analysis was performed. The numbers in yellow, in the peripherical interceptions between circles, indicate the shared DEG between two pairs of comparisons only. And those in white, in the center of each diagram, represent the number of genes with potential to be differentially expressed only in one of the clusters (I, II, III or IV) in comparison with the others.

In clusters I, the four identified genes were up-regulated in comparison to the three others (Log2FC ≤ 0.96 for all genes and comparisons). Same direction of regulation was observed in the gene identified for the cluster II (Log2FC ≤ 2.21 for all comparisons). In in cluster III, the two genes were down regulated in comparison to I, II and IV (Log2FC ≤ 1.68 for all genes and comparisons). In cluster IV 406 genes were up- and 1505 were down-relulated in comparison to the others.

2.3.3. Confimation by RT-qPCR of the genes characterizing the clusters II and III

The genes presenting higher Log2FC were chosen to have their expression confirmed by RT-qPCR. Thus, primers were designed for the characteristic genes from clusters II (*kcng4*) and III (*scn8a*; Table 11). Hydrolysis probes were added in each essay to increase the specificity of the primer’s pairs. Data was log2-transformed before statistical analysis.

Table 11. Genes characteristic of each of the groups the GO terms they belong and the primer sequences used for the Real-Time qPCR study of 4 of them and the two reference genes used for normalization.

Target gene	**Abbreviated name**	**Phylofish / GenBank Gene ID**	**Primer forward 5'-3'**	**Primer reverse 5'-3'**	**Hydrolysis probe 5'-3'**
Group II					
Potassium voltage-gated channel subfamily G member 1-like	*kcng4*	MPF_LOC101471721.1.1	GCCCTGTAAGCTTCTCGTTG	TAAACGCCCTTGATGGTCTC	6-FAM-TCCTCCTCCTAACCTCCCGTGAACT-TAMRA
Group III					
Sodium channel protein type 8 subunit alpha-like	*scn8a*	MPF_LOC100703813.1.2	GTGCCAAAGCCCAACACTAT	TCTGGCAGAGACATCCTCCT	6-FAM-CGATCGCATTCACTGCCTAGACATC-TAMRA
Reference genes					
ELAV-like protein 1-like	*elavl1*	MPF_LOC100695900.1.2	GATCGTGAACTACCTGCCCC	TTACCTGCCACTTTGTCCCG	-
18S rRNA	-	FJ710875	CCTGCGGCTTAATTTGACTC	CTCAATCTCGTGTGGCTGAA	-

No significant differences have been observed between cluster using an Analysis of variance (Figure 24).

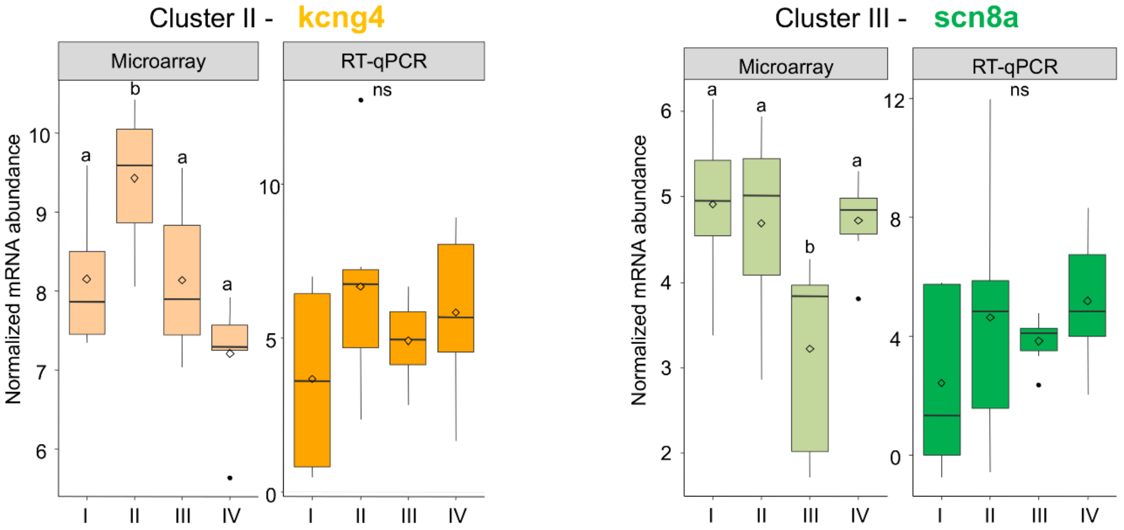


Figure 24. Compared analysis of genes characterizing the cluster II and III presenting the highest Log2FC between clusters in microarray and RT-qPCR experiments. The same egg samples were used to perform both techniques for clusters I-III (n=8) and IV (n=7 for microarray and n=8 for RT-qPCR). An ANOVA was applied to verify significant differences on results from both techniques. In microarray results, this test was followed by a multiple testing correction Benjamini-Hochberg. Results are presented in classical boxplot. Differente letters indicate significante differences between clusters ($p < 0.05$). ns = non-significant.

2.3.4. Gene ontology analysis for the cluster IV

The results of the GO Overrepresentation Analysis performed on the set of genes specific from the cluster IV revealed that Biological Process terms related with *transcription* were enriched (Table 12). In all terms, more than 80% of the genes represented, were down-regulated in the fourth cluster.

Table 12. Overrepresented terms in the exclusively DEG from cluster IV. The terms represent Biological Processes. For each term, number of genes represented, and corrected p-values are shown.

GO biological process complete	**Gene count***	**Corrected p-value (FDR)**	**Direction of the disturbance**
Regulation of RNA metabolic process (GO:0051252)	151	2.47E-02	Both-sides disturbed
Regulation of gene expression (GO:0010468)	180	1.78E-02	Both-sides disturbed

Regulation of cellular biosynthetic process (GO:0031326)	164	2.49E-02	Both-sides disturbed

*Genes can be shared between terms.

2.4. *Discussion*

2.4.1. Cluster I to III do not present a specific gene expression profile

The existence of only few DEG between the cluters I-III may indicated that the phenotypic differences between them are not a result of difference at the transcriptomic level. In other words, differences on later criteria (hatching and deformities at hatching) and limited differences in survival (until 40%) could not be related to the eggs' transcriptomic content in our conditions. However, other mollecules, such as lipids and proteins could still be related to these differences and should be investigated.

A recent study in rainbow trout (*O. mykiss*) evaluated the transcriptomic profile of three distinct egg quality groups that were formed based on the embryonic survival rate until eyed stage. High quality group presented survival rates higher than 80%, in the intermediate one it was between 30 and 50% and for the low quality one survival was not higher than 5%. Authors found that the group presenting intermediate survival was closer to the high-quality group, not producing huge differences in the transcriptomic profile between these two. On the other hand, the low-quality group presented more marked differences in comparison to the two others (Ma et al., 2019). This example agrees with our results and shows that intermediate egg quality groups do not present a characteristic transcriptomic profile.

2.4.2. Cluster IV shows a huge defect of accumulation of the maternal mRNA

Contrasting with the results from cluster I-III, the marked phenotypic differences observed in cluster IV in comparison to the others were followed by a global clear difference in its transcriptomic profile. Because this group was made considering just those spawn that lack fertilization or failed their development before 72hpf, an extensive deregulation at mRNA level seems to be impacting embryonic development at earlier stages. However, despite of the overall contrast between the clusters I-III in relation to IV, a closer observation of the expression patterns on this last cluster, allows to constate that not all samples show the same pattern of genes expression. It points to a high influence of individual variability within the cluster.

Regarding the GO analysis, *Transcription* related terms were enriched in the fourth cluster of egg quality. This cluster encompasses all spawn that presented precocious developmental failure. Interestingly, more than 80% of the genes represented in each term were down-regulated in eggs of lower quality and many of them code for transcription factors proteins. Transcription, together with translation contributes to gene expression. Both are regulated according to the cell's needs. Impairments on the regulatory process will interfere in cells fate. Considering oocytes and eggs, deregulation on transcription may impair the proper accumulation of transcripts, necessary to support embryos early development up to ZGA. Since no transcription takes place in developing embryos before ZGA, the absence of transcriptional and post-transcriptional regulators may block embryonic development at some stages after fertilization.

In addition, in the Part A, we showed that the gene CD68 was up-regulated in eggs presenting lower quality, no matter the criteria or the threshold chosen. Interestinly, the same gene was also up-regulated in the cluster IV (Log2FC between 1.2-2.01 for all three comparisons). This result reinforces that the potential implication of CD68 in embryonic development should be further investigatigated.

2.5. *Conclusions*

We showed that when egg quality groups, defined using a multi-parametric analysis, present differences in survival rate of about 40% between different quality groups, such as those between clusters I, II and III, this difference is not associated to their respective eggs' gene expression profiles. In the same way, deformities rates differences of about 10% between the three first cluster did not reflect difference in the eggs' transcriptomic profiles.

We also showed that cluster IV, formed only based on survival rates at 72 hpf, presented the most important transcriptomic differences that could be related to the phenotype observed in this cluster.

Taken together, these finds showed that not only earlier embryonic developmental stages could be more related to the eggs transcriptomic profile but also that the differences between quality groups should be larger enough to be in consequence of differences in eggs' gene expression. Thus, it leaded us to define new egg quality groups, based on the different criteria/stages individually and taken different threshold to limit the quality groups. The results concerning this new analysis were presented in the Part A of this Chapter.

2.6. *Supplementary tables*

Supplementary Table 4. Phylofish Gene ID, Gene description, Corrected p-value (FDR) and Regulation of the 3485 genes differentially expressed between the four clusters of quality.

Due to the long size of this table, it can be found at the end of this document in the digital version only.

Supplementary Table 5. Phylofish Gene ID, Gene description, Corrected p-value (FDR) and Regulation of the genes differentially expressed only in the cluster I, II or III in comparison with the three others.

Group I

GeneName	**Description**	**p (Corr)**	**p**	**Regulation ([I] vs [II])**	**Regulation ([I] vs [III])**	**Regulation ([I] vs [IV])**	**Regulation ([II] vs [III])**	**Regulation ([II] vs [IV])**	**Regulation ([III] vs [IV])**
MPF_LOC100701795.2.5	XM_003460324.1 PREDICTED: Oreochromis niloticus tripartite motif-containing protein 16-like (LOC100701795), mRNA	0,04	0,00	up	up	up	up	down	down
MPF_LOC101475797.6.6	XM_004567406.1 PREDICTED: Maylandia zebra RING1 and YY1-binding protein B-like (LOC101475797), mRNA	0,03	0,00	up	up	up	down	down	up
MPF_LOC100685053.1.1	XP_003434657.1 PREDICTED: polyubiquitin-like [Canis lupus familiaris]	0,04	0,00	up	up	up	up	up	up
MPF_UBIQP.10.13	UBIQP_XENLA (sp|P62972) Polyubiquitin (Fragment) OS=Xenopus laevis PE=1 SV=2	0,03	0,00	up	up	up	up	up	up
Group II									
MPF_LOC101471721.1.1	XM_004565738.1 PREDICTED: Maylandia zebra potassium voltage-gated channel subfamily G member 1-like (LOC101471721), mRNA	0,02	0,00	down	up	up	up	up	up
Group III									
MPF_LOC100703813.1.2	XM_003448149.1 PREDICTED: Oreochromis niloticus sodium channel protein type 8 subunit alpha-like (LOC100703813), mRNA	0,04	0,00	up	up	up	up	down	down
MPF_contig_004910	-	0,04	0,00	down	up	down	up	down	down

Supplementary Table 6. Phylofish Gene ID, Gene description, Corrected p-value (FDR) and Regulation of the genes differentially expressed only in cluster IV in comparison with the three others.

Due to the long size of this table, it can be found at the end of this document in the digital version only.

Chapter 2 recapitulation sheet

(METHODS TO ASSESS EGG QUALITY AND THEIR IMPACT ON EGGS TRANSCRIPTOMIC RESULTS)

Specific objectives

- Evaluate the relationship between the transcripts eggs' content and the embryos developmental potential
- Evaluate whether the use of different methods to assess eggs quality affects the results when analyzing their mRNA content

Main results

- Marked differences on the gene expression profiles is found between high and low quality eggs
- Changes in the method directly affect the results obtained and thus their interpretation
- mRNA eggs' content may be the source of issues mostly on earlier embryonic developmental stages than in later ones
- Genes related to translation, transcription and immune system are differentially expressed between high and low quality eggs
- *cd68* is up-regulated in all groups of low quality eggs analyzed

Next, in Chapter 3:

- In addition to the variability found in gene expression according to egg quality, we investigated whether an intrinsic factor, such as females' domestication level, could modulate the transcriptomic content of eggs.
- Thus, we will present an embracing overview of the reproductive performance of Eurasian perch (*Perca fluviatilis*) females having different stories of domestication. Morphological, endocrine, histological and genetic data of the broodstock will be presented in addition to the characterization of the embryonic development in relation with their respective eggs' mRNA content.

VI. Chapter 3: Domestication and eggs' transcriptome

Domestication may affect the maternal mRNA profile in unfertilized eggs, potentially impacting the embryonic development of Eurasian perch (*Perca fluviatilis*)

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1. Abstract

Domestication is an evolutionary process during which we expect populations to progressively adapt to an environment controlled by humans. It is accompanied by genetic and presumably epigenetic changes potentially leading to modifications in the transcriptomic profile in various tissues. Reproduction is a key function often affected by this process in numerous species, regardless of the mechanism. The maternal mRNA in fish eggs is crucial for the proper embryogenesis. Our working hypothesis is that modifications of maternal mRNAs may reflect potential genetic and/or epigenetic modifications occurring during domestication and could have consequences during embryogenesis. Consequently, we investigated the trancriptomic profile of unfertilized eggs from two populations of Eurasian perch. These two populations differed by their domestication histories (F1 vs. F7+ – at least seven generations of reproduction in captivity) and were genetically differentiated (F_{ST}=0.1055, $p<0.05$). A broad follow up of the oogenesis progression failed to show significant differences during oogenesis between populations. However, the F1 population spawned earlier with embryos presenting an overall higher survivorship than those from the F7+ population. The transcriptomic profile of unfertilized eggs showed 358 differentially expressed genes between populations. In conclusion, our data suggests that the domestication process may influence the regulation of the maternal transcripts in fish eggs, which could in turn explain differences of developmental success.

Keywords: microarray; egg content; fish populations; reproductive cycle; gonadogenesis; egg quality.

2. Introduction

Domestication is an evolutionary and continuous process enabling wild animals to adapt to humans and anthropogenic environments (Price, 1984, 1999). It involves the combination of several genetic and potentially epigenetic modifications driving gene expression and phenotypic changes. Differences in gene expression due to rapid adaptation to new environments were already reported from the first generation of reproduction in captivity in steelhead trout (*Oncorhynchus mykiss*) (Christie et al., 2016). Thus, the regulation of genes expression may change early during domestication. The main genetic mechanisms involved are inbreeding, genetic drift and natural, relaxed and artificial selections (Price, 1984, 1999). The two first mechanisms have important consequences when founder populations are small because they rapidly lead to important changes in allelic frequencies (Beaumont et al., 2002). The relaxed selection consists of a reduction of selection pressure on traits which are not necessary anymore in captive conditions. The artificial selection results from the selection of breeders according to phenotypes chosen by humans. Finally, the natural selection occurs and usually eliminates animals which are not adapted to anthropogenic environments (Mignon-Grasteau et al., 2005). Studies suggest a relationship between epigenetic modifications and phenotypic plasticity in response to the environment in some animal and plant species (Vogt, 2017). In fish, the current knowledge shows a modification of the epigenetic signature in individuals reared in hatcheries in comparison to their wild counterparts in salmonids and the European sea bass (*Dicentrarchus labrax*) (Anastasiadi and Piferrer, 2019; Gavery et al., 2018; Luyer et al., 2017; Rodriguez Barreto et al., 2019). These modifications affect somatic and germinal cells (Gavery et al., 2018) and may play a role during the first steps of domestication (Anastasiadi and Piferrer, 2019). However, the relationships and timeline between genetic and epigenetic modifications remain unclear (Vogt, 2017).

All these mechanisms depend greatly on the breeding practices. Indeed, independent trials of domestication may lead potentially to various types of modifications that may have either beneficial (adaptation) or deleterious (maladaptation) effects on various biological functions of the new domesticated populations. The artificial selection, for one or several phenotypes is specific to the domestication process and has consequences that may not be predicted, since morphological, behavioral and physiological traits of animals are intrinsically related (Dobney and Larson, 2006). The consequences of modifications of the balance between these traits are not yet properly understood. Indeed, it appears that the artificial selection of specific phenotypes may have deleterious effects on other biological traits because most of resource intakes are dedicated to the selected traits. This imbalance often leads to a decrease of reproduction abilities (Mignon-Grasteau et al., 2005; van der Waaij, 2004), commonly seen in numerous terrestrial and aquatic species. A recent meta-analysis investigating the effect of birth-origin (captive vs. wild) on the reproductive success of animals reared in different anthropogenic environments was performed. For all of the 44 analyzed species, the offspring survival success was decreased in "captive-born" animals compared to their "wild-born" counterparts (Farquharson et al., 2018). It usually involves developmental failures characterized by fertilization issues, embryonic lethalities or the occurrence of deformities. They often ensue from defects of incorporation or synthesis of the eggs' molecular content. Indeed, the abundance of these molecules, controlling embryogenesis process after fertilization, can directly be affected by modifications of extrinsic or intrinsic factors faced by females during oogenesis (Pelegri, 2003). Among them, the maternal mRNA expression profile may thus result from genetic and epigenetic changes in the breeders' ancestors during the domestication process. It could potentially help to make the link between mechanisms described above and the reproductive success of captive populations in comparison to their wild counterparts.

There are two main ways to study the domestication process (Mignon-Grasteau et al., 2005). First, longitudinal studies allowing a continuous follow up of a population throughout the domestication process across generations. This method is the most efficient to understand phenotypic and molecular modifications occurring at each step of the domestication process. However, it is long and difficult to perform logistically. The second way, which is commonly used, corresponds to a comparison between wild and domesticated populations. Such method has been previously used and successfully highlighted differences in several fish species, such as steelhead trout (*O. mykiss*) (Christie et al., 2016), Atlantic salmon (*Salmo salar*) (Bicskei et al., 2014, 2016; Yeates et al., 2014), Atlantic cod (*Gadus morhua*) (Lanes et al., 2012, 2013), greater amberjack (*Seriola dumerili*) (Zupa et al., 2017) and Eurasian perch (*Perca fluviatilis*) (Khendek et al., 2017; Křišťan et al., 2012). However, numerous pieces of information are often lacking (genetic relatedness between populations, rearing conditions and history of the domestication process) and thus prevent drawing accurate conclusions. Indeed, as previously explained, phenotypic modifications potentially leaded by genetic/epigenetic modifications, depend on rearing practices. Such information is not always tracked properly by farmers. For example, for several domesticated fish stocks, wild breeders are introduced to keep a sufficiently high genetic diversity (Teletchea and Fontaine, 2014) without keeping track of these introductions leading to incomplete traceability (Ben Khadher et al., 2016). Today, with the increasing knowledge accuracy and the development of molecular tools, such information becomes important to draw proper conclusions. One way to overcome this issue consists in investigating the genetic differentiation between wild and farmed studied populations. This preliminary step would help understanding differences between populations.

In the context of fish production diversification, numerous efforts are done to domesticate a large number of new species (Teletchea and Fontaine, 2014). However, the lack of knowledge on biological and physiological needs of some species may lead to inadequate domestication attempts with deleterious consequences on the biological traits described above. The Eurasian perch *(P. fluviatilis)* is a promising species in aquaculture for the production diversification. It is a freshwater fish species widely distributed in Europe and in the Northern part of Asia (Stepien and Haponski, 2015). It has a niche market with a traditional demand in several European countries (Overton et al., 2015; Steenfeldt et al., 2015). The Eurasian perch is a synchronous early spring spawner and its oogenesis induction and progression are mostly controlled by temperature and photoperiod variations (Abdulfatah et al., 2011; Fontaine et al., 2015; Gillet and Dubois, 1995; Migaud et al., 2013; Sulistyo, 1998; Wang et al., 2010). Consequently, manipulation of these two factors allowed defining a photothermal program largely used in Eurasian perch farms for out-of season reproduction in recirculating aquaculture systems (RAS) (Abdulfatah et al., 2011). Despite this successful control of its reproductive cycle allowing out-of-season spawning, the reproduction success remains variable even if the same rearing conditions are applied to the broodstock (Schaerlinger and Żarski, 2015). It is probably due to the lack of knowledge on potential intrinsic and/or extrinsic modulating factors, including the history and details of the domestication progression experienced by populations.

In the present study, we chose to compare two Eurasian perch populations, reared in the same conditions but with different histories of domestication. We hypothesized that the level of domestication may modulate the accumulation of maternal mRNA in eggs during oogenesis, potentially impacting the embryos early development after fertilization.

3. Material and Methods

3.1. *Origin of fish and broodstock management*

Fish were handled in accordance with national and international guidelines for animal welfare protection (*Directive* 2010/63/*EU. Agreement number: APAFIS#1390-2018031516387833 v2 accepted by the Lorraine Ethic Committee for Animal Experimentation (CELMEA) and the French Ministry of Research*). Two populations of three years old Eurasian perch originating from artificial reproductions in November 2011 were used. They correspond to (i) fish at an advanced stage of the domestication process coming from breeders reared in RAS for at least seven generations (F7+ population) and (ii) Eurasian perch originating from breeders collected in the Geneva Lake at the embryonic stage and reared in RAS conditions (F1 population). All animals came from the fish farm "Lucas Perches" (Hampont, France), which provided us the information of the presumable number of generations of the F7+ population and that their ancestors had supposedly been caught in Geneva Lake. Fish were transferred to our indoor facilities after weaning period in February 2012 (mean weight of 3.78 ± 1.07 g). Both populations were reared separately in different tanks but under the same RAS conditions (constant photoperiod (L:D - 16:8), 300 lux at the water surface during the lighting period and at 20-21°C) to avoid oogenesis stimulation (Abdulfatah et al., 2011; Migaud et al., 2004) until they reached mean weight of 287 ± 89 g.

About two months before the experiment began (May 2014), 654 Eurasian perch (313 from the F7+ and 341 from the F1 populations) were transferred to the Aquaculture Experimental Platform (AEP, registration number for animal experimentation C54-547-18) belonging to the URAPA lab and located at the Faculty of Sciences and Technologies of the University of Lorraine (France). They were divided into six independent groups (three per population with an equivalent number of fish in each group). Fish were put into six identical rooms consisting of independent RAS with 3000 liters tanks. Temperature, photoperiod and light intensity were accurately controlled in each room using dedicated software. Environmental conditions were the same during acclimation phase and growing period. In order to induce gonadogenesis, breeders were submitted to a photothermal program allowing effective induction and control of the reproduction cycle (Fontaine et al., 2015) from August 18th 2014 to June 22nd 2015 (day 1 to day 309, Figure 25). Water levels of dissolved oxygen (9.53 ± 0.07 mg/L and 9.73 ± 0.12 mg/L), pH (7.55 ± 0.10 and 7.47 ± 0.00), nitrite (0.29 ± 0.14 mg/L and 0.09 ± 0.01 mg/L) and ammonium (0.67 ± 0.22 mg/L and 0.27 ± 0.02 mg/L) were monitored twice a week and kept under the respective thresholds in breeders' tanks (for F1 and F7+ populations, respectively). At the beginning of the experiment, all animals were individually tagged with P.I.T. tags (Transponder ISO 2 x 12 mm, Biolog-id) to monitor individuals all along the experiment. All fish were fed twice a day to satiation five days a week. In alternation, they were fed three days with commercial pellets (Sturgeon Grower N°5, Le Gouessant) and two days with frozen squids and shrimps (Pomona). On Saturdays and Sundays, they were fed once with commercial pellets to satiety.

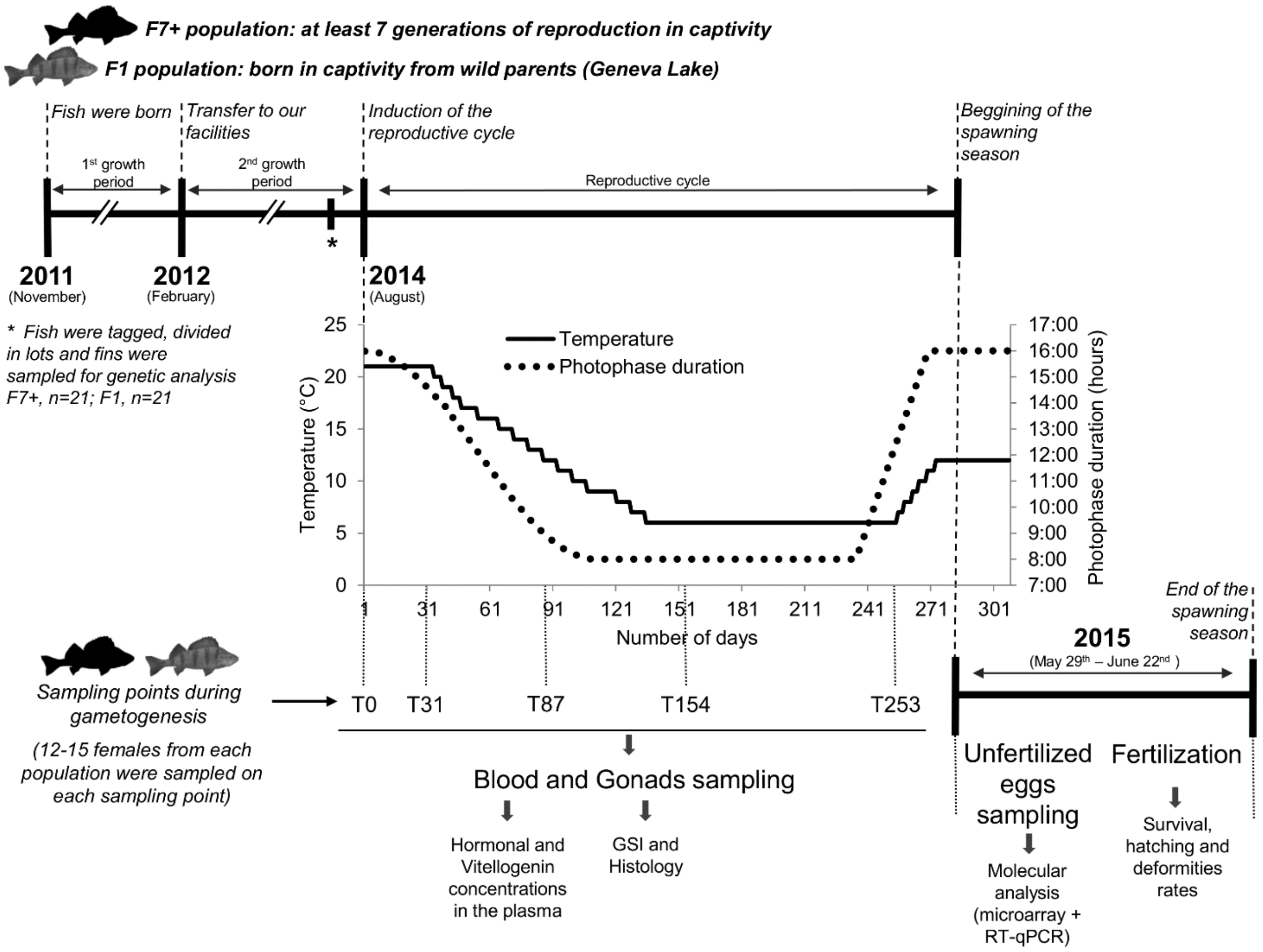


Figure 25. **Graphic summary of the experimental design.** The photothermal program was used to control each step of the reproductive cycle and spawning of Eurasian perch. Fish sampling was performed at T0, T31, T87, T154 and T253 days after the beginning of the photophase initial decrease (induction of the reproductive cycle). For each sampling point, sexual steroids and Vitellogenin levels were measured in the plasma and a histological follow up of the oogenesis progression was performed. During spawning, each spawn was split into two parts. The first one was not fertilized and frozen for further molecular analyses while the other part was fertilized to assess the developmental progression. All details are given in the method paragraph.

3.2. *Experimental design, tissue sampling and morphometric measures*

In order to follow the oogenesis process, five sampling points of females were performed throughout the reproduction cycle: T0 at the beginning of the experiment allowed us to determine the initial status of breeders, T31, T87 and T154 sampling points allowed us to check the oogenesis along its progression and T253 the final status of the gonads before the spawning season (Figure 25). Four to five females per tank were collected at each sampling point. Firstly, fish were anesthetized by immersion into a Tricaine methanesulfonate solution (120 mg/L; Sigma-Aldrich) for five minutes to collect blood from the caudal vein. Blood was centrifuged at 8000 rpm for 10 minutes in previously heparinized (4.5 mg heparin sodium salt from porcine intestinal mucosa 100KU, Sigma-Aldrich) microtubes. Plasma aliquots were conserved at -80 °C for further evaluation of sexual steroids and Vitellogenin concentrations measurements.

After blood sampling, fish were killed using an overdose of Tricaine methanesulfonate (240 mg/L; Sigma-Aldrich) in accordance to European Ethical guidelines (Directive 2010/63/UE). Total weight was measured before collecting the gonads which were weighted to calculate the gonado-somatic index (GSI=gonad weight/total weight*100) and fixed as described below for histological studies.

3.3. *Evaluation of the Steroids and Vitellogenin concentrations in the plasma*

The 17-β-estradiol (E2, ng/mL) and testosterone (T, ng/mL) assays were performed on 50 µL of plasma of each sampled female for all sampling points (around 15 females per population/sampling point) using the DIAsource E2-ELISA kit (KAP0621, DIAsource) and the DIAsource Testosterone ELISA kit (KAPD1559, DIAsource), respectively. Samples were diluted from 1/1 to 1/50 for E2 and from 1/1 to 1/10 for T measurements depending on the oogenesis developmental stage. The E2 assay sensitivity was 5±2 pg/mL and the range of use was from 0 to 880 pg/mL with an intra assays CV varying from 4 to 17% and an inter assay CV of about 27%. Concerning T, the sensitivity was 0.083 ng/mL and the range of use was from 0 to 16 ng/mL. The intra assays CV varied from 7 to 19 % and the inter assay CV was about 16%.

The Vitellogenin plasmatic concentration was indirectly estimated in 80 µl of plasma by measuring concentrations of the alkali-labile phosphate level as described by Ben Ammar et al., (2015).

3.4. *Gonads histology*

Female gonads from all sampling points were fixed in Bouin's solution for one week before being washed in 70% alcohol. Samples were then dehydrated in ascending series of ethanol (70-100%) before being embedded in paraffin with an orientation allowing transversal cuts. Five micrometer sections were performed with a Leitz Wetzlar microtome and collected on glass slides. Masson's trichrome staining was done according to a protocol adapted from (Gabe, 1968) as follows: Hematoxylin solution modified according to Gill III (Merck) was used from five to ten minutes; Phloxine (VWR) was diluted in water at 0.5% and used for five minutes; Light Green (Sigma) was diluted in water at 0.5% and used from three to five minutes. Stained sections were examined, photographed and analyzed using a light upright optical microscope (Nikon Eclipse Ni-U) associated with a DS-Fi1 digital camera and the software NIS BR (Nikon France, Champigny-sur-Marne, France) at low magnification (x2 and x4).

Oocytes stages were determined according to Rinchard and Kestemont, (1996) and classified into six classes: primary growth (PG), early cortical alveoli stage (ECA), late cortical alveoli stage (LCA), early vitellogenesis (EV), late vitellogenesis (LV) and atresia (A). Oogonia (O) stages were also identified.

The gonadal maturation state was determined by counting all oocytes of each class on one complete and representative transversal stained sections of the ovary for T0-T154 and three representative transversal sections for T253 because the gonads were then too large to be laid on one slide.

3.5. *Gametes collection and fertilization*

Before the spawning season, all females were caught to take some oocytes using a catheter and determine their oocytes maturation according to Żarski et al., (2011b). On May 13rd and 15th 2015, females from all tanks were examined and were allocated to separate tanks for the spawning season, according to their oocyte maturation stage and regardless of their original population. Thus, one tank contained the females having oocytes at stages I and II, another tank contained the females at stages III and IV (which were all coming from the F1 population), and another tank contained females that could not be staged reliably. Males from F7+ and F1 populations were kept apart in two tanks depending on their origin. When one female spawned, all females of this tank were monitored daily to identify ovulation and collect the eggs by stripping them. This procedure was always performed between 4am and 5am and each spawn was treated individually. The first spawn observed in each tank was not considered for the experiment because once in the water, the eggs are activated and their ability to be fertilized decrease rapidly. The spawning season took place from May 29th to June 22nd 2015 and each female stripped was identified as to its original population by its P.I.T. tag. Eggs were fertilized as described in Żarski et al., (2012c) with sperm from three males (total volume of 100 µl sperm/g dry eggs). Eggs stripped in the same day were fertilized using the same pool of sperm and at the end of the spawning season no day effect was seen in the reproductive performance. All males used to perform fertilization came from the F1 population, that presented a higher quality (motility estimated under a light upright optical microscope (Nikon Eclipse Ni-U)). The other part of each spawn (18 individual samples of about 200mg) was immediately frozen in liquid nitrogen and kept at -80°C for subsequent transcriptomic analysis.

3.6. *Study of reproductive performance*

In total, 32 spawn, corresponding to 32 females (13 from F7+ population and 19 from the F1), were treated as described above. A previous study performed in our team showed that cell cleavage timetable can be highly variable between embryos even within the same spawn (Alix et al., 2015). Thus, we choose to perform our first evaluation of the embryonic survival at 24 hours post fertilization (hpf) because it was the earliest stage to establish a relevant estimation of survival. We were thus not able to make a distinction between non-fertilized eggs and dead embryos. Eurasian perch eggs are surrounded by a jelly coat that protects embryos from the outside environment (Gillet and Dubois, 1995). This jelly coat prevents to sort the eggs depending on their survival at each stage as it is currently performed with other fish species for which eggs are not attached. Thus, we performed the following protocol to evaluate the survival in the same ribbon samples at several timepoints.

Just after fertilization, three ribbon fragments (samples) of around 500 eggs were randomly cut from each spawn/ribbon and incubated to determine the percentage of embryos alive at different timepoints. We considered that the borders of each fragment should be avoided since embryonic development in this region could be impacted by the cutting. At each specific timepoint, around 100 embryos were counted and, among them, the number of alive embryos (those reaching the proper developmental stage) was counted to evaluate the percentage of alive embryos. These evaluations were performed in the middle of each fragment at 24, 48, 72 and 120 hpf to avoid potential border effects described above. The percentage of embryos alive was estimated using the following formula: (number of alive embryos at one stage/total number of embryos studied at that stage) x 100. In addition, three other fertilized samples of around 100 eggs/sample were kept apart, without manipulation, until the hatching period. They were used to determine the percentage of embryos hatching using the following formula: (number of hatched embryos/total number of embryos in the fragment) x 100 and deformities rates according to Alix et al., (2017). The global deformities rate (Dr) and specific deformities rates allowed studying defects in the axis (Ad), yolk (Yd), cardiac (Cd), mouth (Md), eyes (Ed) and others (Od) as described in Alix et al., (2017).

3.7. *RNA extraction*

Total RNA was extracted from unfertilized frozen eggs from the 32 spawn (mean weight of 100 mg, 10-15 eggs) using TRIzol reagent (Life Technologies) at a ratio of 100mg per mL of reagent and following the manufacturer's instructions with some modifications. Indeed, a milling step was added during the homogenization step to get rid more easily of the gelatinous envelope and chorion surrounding eggs. To do so, a bullet blender (Next Advance) and zirconium oxide beads 1.0 mm were used. In addition, a supplementary centrifugation (4 °C, 30 min. 13000 rpm) was performed before the addition of the chloroform to remove the lipid content in eggs. A NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies) was used to evaluate the quantity of total RNA and an Agilent 2100 Bioanalyzer (Agilent Technologies) was used to evaluate the integrity of the RNA extracted. Samples exhibited an integrity score higher than 7 and were used for the microarray analysis.

3.8. *Microarray analysis*

The Eurasian perch array (SurePrint G3 Custom Gene Expression Microarray, 8x60K - Agilent Technologies) contains 48,986 non-redundant probes previously identified and available from the PhyloFish Database (Pasquier et al., 2016). The "One-Color Microarray-Based Gene Expression Analysis (Low Input Quick Amp Labeling) Protocol" was followed for samples preparation, hybridization, washing and scanning of slides and data extractions. Briefly, 150 ng of total RNA were used for the amplification/Cy3-labeling step. After this step, samples were purified (RNeasy mini kit, Qiagen) and quantified using a NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies). Samples exhibiting a yield higher than 1.03 µg of cRNA and a specific activity higher than 10.30 pmol of Cy3/µg of cRNA were fragmented and used to hybridize arrays (one sample failed the labeling step and was excluded from the experiment). Samples (600 ng of Cy3-cRNA) were randomly distributed onto four slides. After

17 h of hybridization at 65 °C, slides were washed, dried and scanned with an Agilent Technologies Scanner (G2505C). Scanned images were extracted with Agilent Feature Extraction software.

Data extracted from scanned images were normalized and log(2) transformed for statistical analyses (all data are available in the Gene Expression Omnibus database under the accession code GSE119802). Using the GeneSpring software, an unpaired t-test followed by a Benjamini-Hochberg correction was used to identify genes differentially expressed (DEG) between the two populations ($p<0.05$). Then, a hierarchical clustering analysis (unsupervised average linkage) was performed using Cluster 3.0 software (version1.52). Clusters were visualized using TreeView software (version 1.1.6r4).

3.9. *Gene ontology analyses*

In order to give an overview of gene ontology (GO) terms represented among differentially expressed genes between F1 and F7+ populations, they were functionally annotated and classified using Blast2GOv4.1.9 software (Gotz et al., 2008). Default parameters were used for blastx and GO annotations.

In the following, we performed a GO overrepresentation analysis in which we compared the list of DEG to a reference list corresponding to all expressed genes in the microarray. To retrieve this reference list, we first filtered all genes present in the array. Genes were considered as expressed when they presented a signal above background in at least 75% of the samples and in at least one of the populations. In a second time, as the Eurasian perch genome is not yet available in any databases allowing performing GO analyses, we chose to retrieve human orthologs identifiers for the reference and DEG lists. It allowed us to perform the analysis. In order to find these identifiers, we aligned probes designed for the array corresponding to each sequence in the lists against the Eurasian perch transcriptome extracted from the genome, provided by (Ozerov et al., 2018), with minimap2 (version 2.7 with -m 20 parameters). Because the gene prediction file had small UTRs, we extended the prediction on both transcript sides by 2kb. If a probe had a unique alignment, it was assigned to the corresponding transcript. If the probe had two corresponding transcripts located one after the other on the genome, we assigned it to the transcript having the match closest to its center. Probes with no match or over two matches were not assigned to a transcript. We then retrieved the human orthologs identifiers from the annotation file provided by (Ozerov et al., 2018). The genes still missing identifiers in the DEG list were manually annotated using UniProt accessions. In total, among the 358 DEG, 265 human orthologs identifiers were found. The

GO overrepresentation analysis was performed using Panther14.0 (Mi et al., 2019). Parameters were set at default, meaning that a Fisher's exact test and a Benjamini-Hochberg correction were applied. We asked for GO-Slim Biological Processes (BP) and Pathways and only corrected p-values <0.05 were considered as significant.

3.10. *Real-time PCR analysis*

Genes presenting a log(2) fold change (log(2)FC) > 4 in microarray were additionally studied by real-time qPCR in all samples previously used for the microarray. After RNA extraction, a DNase treatment (DNase I, RNase free - Thermo Scientific) was applied to 5 µg of all samples (n=32) following the manufacturer's protocol. The reverse transcription was performed in a final volume of 20 µl using a M-MLV Reverse Transcriptase (Sigma-Aldrich), 1 µg of RNA and random nonamers (2.5 µM - Sigma-Aldrich) and following the manufacturer's protocol. Reverse transcript products were diluted 1:27 and 5 µl were used for the real-time PCR, using PerfeCTa SYBR Green SuperMix (Quanta Bioscience) and 5 pmol of each primer. Primers were designed using Primer3Plus or Primer design Tool-NCBI software (S1 Table). The real-time qPCR was performed using a Step One Plus system (Applied Biosystems, Foster City, USA). The PCR program consists of a first step at 95°C for two minutes followed by 40 cycles consisting of a denaturation step at 94 °C for 15 s, an annealing step at 50-58 °C depending on the primers pairs for 15 s and an elongation step at 72 °C for 30 s. The amplification was followed by a melting curve stage, according to manufacturer's parameters in order to check the primers specificity. The abundance of the target cDNA in each sample was calculated using a serial dilution of a pool of all cDNA samples using the StepOne Software (Applied Biosystems, version 2.1). This dilution curve was used to certify the reaction efficiency (80-120%). All samples were analyzed in duplicate and the geometric mean of the expression level data of the *adenosine kinase-like*, *RNA18s*, *TATA-box binding* and *ELAV-like protein 1-like* (S1 Table) was used as reference to normalize the data obtained. These genes were found as stable in microarray and preliminary real-time qPCR analyses in all samples. The values obtained after normalization were analyzed using a Mann-Whitney test (RStudio software version 1.0.143) to compare differences of gene expression between populations (p<0.05).

3.11. *Genetic variability between populations*

Genomic DNA was extracted from 42 fin samples representing the two populations (21 F1 and 21 F7+), using the universal salt-extraction method, according to (Aljanabi, 1997). Purity and quantity of genomic DNA were assessed using a NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies). Eight microsatellites previously used on *P. fluviatilis* (Ben Khadher et al., 2015) were selected: *PflaL1, PflaL2, PflaL4, PflaL6* (Leclerc et al., 2000), *SviL7* (Wirth et al., 1999), *Svi17* (Borer et al., 1999), *YP60* and *YP111* (Li et al., 2007). Two multiplex amplifications were done using fluorescently labeled primers. The first multiplex (A) contained *PflaL2* (FAM), *PflaL4* (PET), *SviL7* (VIC), *Svi17* (FAM) and *YP111* (PET). The second one (B) contained *YP60* (FAM), *PflaL1* (VIC) and *PflaL6* (FAM). Polymerase chain reaction was carried out using the Multiplex TEMPase 2X MasterMix (VWR), 10 pmol of fluorescent primer mix, genomic DNA and water for a final volume of 30 µl. PCR conditions for multiplex A were: 95 °C for five minutes, 28 cycles at 95 °C for 30 seconds, 55 °C for 90 seconds and 72 °C for 30 seconds, and a final extension of 45 seconds at 60 °C. For multiplex B, PCR conditions were: 95 °C for five minutes, six cycles at 95 °C for 30 s, 48 °C for 90 s and 72 °C for 30 s, 22 cycles at 95 °C for 30 s, 50 °C for 90 s and 72 °C for 30 s, and a final extension at 60 °C for 45 s. PCR products were diluted (1:151) with deionized water and added Hi-Di™ Formamide (Applied Biosystems) and GeneScan 600 LIZ Size Standard (Applied Biosystem). The fragment analysis was performed on a 3500 Genetic Analyzer (Applied Biosystems HITACHI) and alleles were scored with Geneious 11.0.2 (Kearse et al., 2012).

Genetic diversity was estimated through calculation of observed (Ho) and expected (He) heterozygosities in GENETIX (Belkhir et al., 2004). Population differentiation was assessed by estimating the "global" F_{ST} statistic on populations through an analysis of molecular variance (AMOVA when considering only one group of populations) performed in Arlequin with 10000 permutations. Divergence between populations was estimated with a F_{ST}-pairwise test (10000 permutations).

3.12. *Statistical Analysis*

Differences in GSI, sexual steroids and Vitellogenin concentrations, oocytes stages abundance on histological cut and specific deformities were estimated using a non-parametric Wilcoxon-Mann-Whitney. Normality and homogeneity of variance were tested using respectively Shapiro-Wilk and Levene's test.

In order to investigate possible differences of embryonic development between populations, percentage of embryos alive at 24, 48, 72 and 120 hpf and at hatching were compared between populations using a one-way repeated-measures ANOVA. The statistical model included as fixed effect the percentage of alive embryos for F1 and F7+ populations. It has been controlled by the introduction of the females as covariate. This model was chosen after comparison with a second one without a covariate. They were ranked according to their Akaike information criterion and the one having the lowest criterion was chosen (Cavanaugh and Neath, 2019). A TukeyHSD was performed to identify differences between populations at different times individually.

For all tests, a p-value ≤ 0.05 was considered statistically significant. All values given are represented as means ± standard error of mean (SEM). All tests were performed using R (v.1.1.423) (R Core Team (2017)). The package *stats* was used to perform Shapiro-Wilk, Wilcoxon-Mann-Whitney, ANOVA and TukeyHSD tests. While *car* was employed for Levene's test.

4. Results

Two Eurasian perch populations (F1 and F7+) were used in the present study. Analysis of their genetic differentiation using microsatellites revealed a F_{ST} of 0.1055 ($p < 0.001$). In addition, the F7+ population presented a higher observed heterozygosity (mean=0.440) compared to the F1 (mean=0.348), indicating a larger genetic diversity of the F7+ population.

4.1. *Follow up of the gonadogenesis progression reveals few differences between populations*

Five sampling points of females were performed as shown in Figure 25. The GSI of both populations increased progressively all along gonadogenesis to reach close to 13% one month before the spawning season (Supplementary Figure 2A). The only difference between populations can be seen at T31 with a higher GSI (p = 0.02) for the F7+ females (0.91 ± 0.05%) compared to the F1 ones (0.69 ± 0.06%). A follow up of the hormonal status of females did not present any significant difference of the testosterone level between populations. At T253 a higher level was recorded for the F1 (50.35 ± 5.89 ng/mL) compared to the F7+ (35.81 ± 6.49 ng/mL, p = 0.06 – Supplementary Figure 2B). Similar data were obtained for the 17-β-œstradiol (E2), except for the T253 for which the hormonal level was higher (p = 0.03) for F7+ (8.71 ±

0.34 ng/mL) than for F1 (7.39 ± 0.44 ng/mL), no other statistical difference was found (Supplementary Figure 2C). The follow up of the Vitellogenin level in the blood did not present any significant difference between F7+ and F1 populations (Supplementary Figure 2D).

These data suggest that the oogenesis progression for both populations was similar. However, the histological study of gonads revealed that F1 females presented higher percentage of late vitellogenesis oocytes (57 ± 6%) at the end of the oogenesis in comparison to the F7+ ones (41 ± 4%; T253, Figure 26A and B), suggesting that oogenesis was slightly more advanced in the F1 than in the F7+.

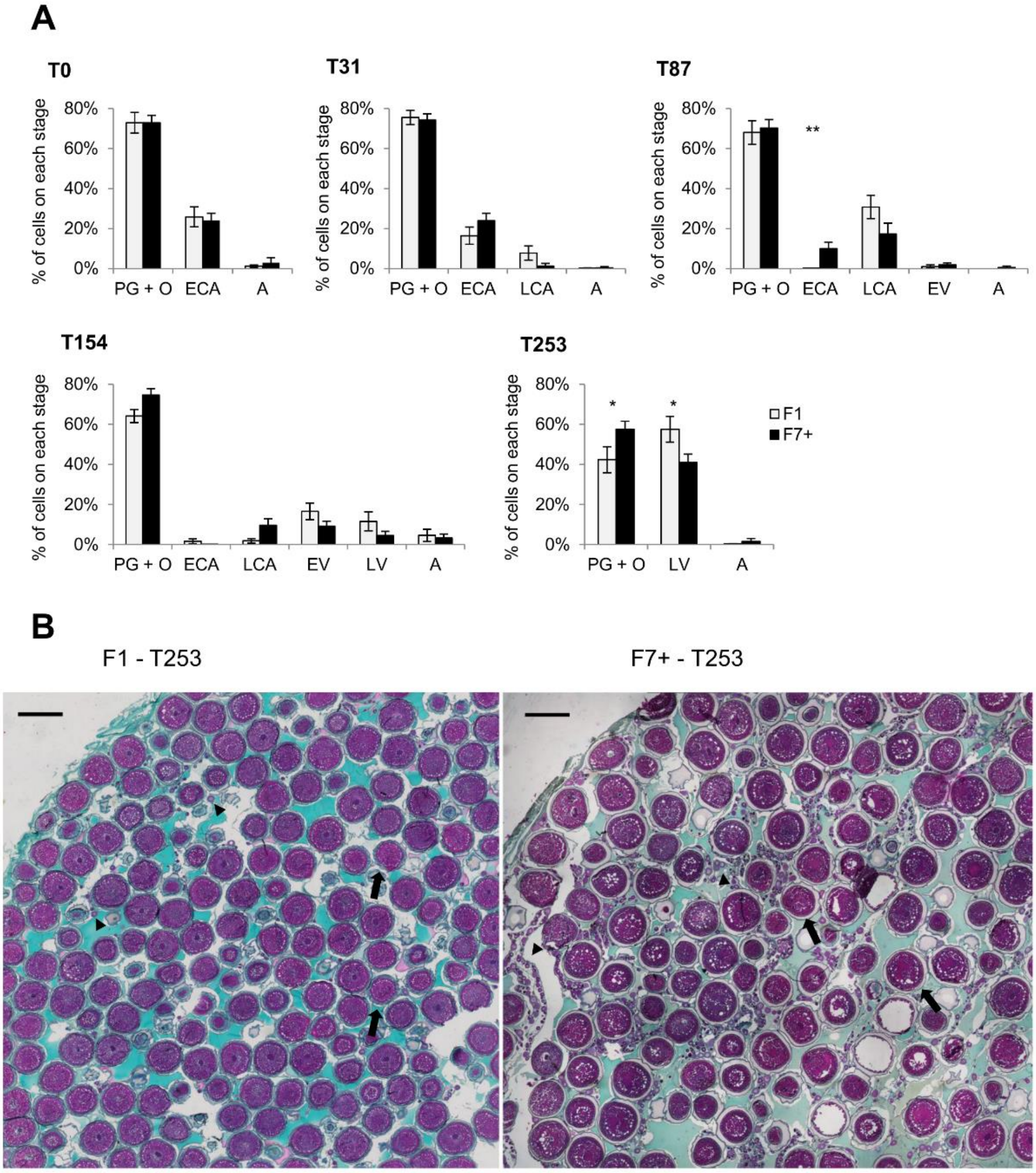


Figure 26**. Histological follow up of the oogenesis progression.** (A) Percentage of each cellular stage in gonads belonging to F7+ and F1 populations during oogenesis period. Stages are represented as: primary growth and oogonia - PG+O, early cortical alveoli - ECA, late cortical alveoli stage - LCA, early vitellogenesis - EV, late vitellogenesis - LV and atresia - A. Differences between the two populations were tested using non-parametric Wilcoxon-Mann-Whitney test ($p<0.05$). Significance levels are represented as follows: *, p = 0.05–0.01; **, p = 0.01–0.001; ***, p = 0.001–0.0001; and ****, $p < 0.0001$. (B) Histological section of gonads representative of F7+ and F1 ovaries at T253. Arrows points to LV stages and arrowheads indicate the PG+O stages. Scale bars represent 1000 µm.

4.2. *Embryonic survival is higher in the F1 than in the F7+ spawn*

Following the observation of a slightly faster oocytes development in F1 population, the first spawning was more precocious for F1 than for F7+ fish. F1 females, coming from all three original replicate tanks, spawned between thirteen and seven days earlier than F7+ first spawner (Figure 27).

The main effect for population yielded an F ratio of F(1,30) = 4.266, p = 0.0476, indicating a significance difference on the number of embryos alive depending on the population. Since an overall population effect on the percentage of embryos alive was observed, TukeyHSD tests were performed between populations and revealed significant differences between them at 48 (p = 0.02), 72 (p = 0.03) and 120 hpf (p = 0.05) and at hatching (p = 0.03). Consequently, embryonic survivorship was significantly higher in F1 than in F7+ population from 48 hpf (Figure 28A and Supplementary Table 8). Interestingly, more heterogeneity of survivorship is seen in F7+ population at all timepoints (coefficient of variation (CV) = 62%, 88%, 95%, 90% and 121% at 24, 48, 72 and 120 hpf and at hatching, respectively) in comparison to F1 in the same stages (CV = 51%, 56%, 56%, 59% and 64% at 24, 48, 72 and 120 hpf and at hatching, respectively). The overall occurrence of deformities and that of specific deformities were comparable between populations and did not present any statistical difference (Figure 28B and Supplementary Table 9).

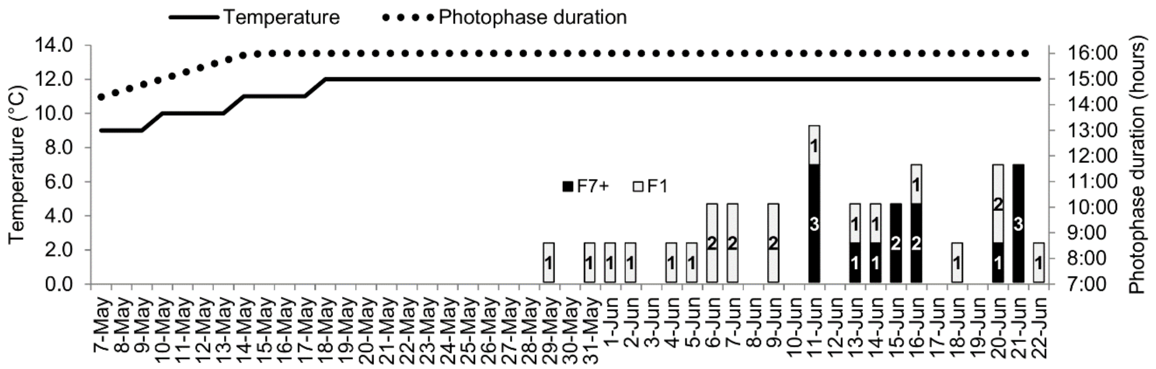


Figure 27**. Timetable of the spawn obtained for both populations during the spawning season in relation to temperature and photophase increase.** Bars with numbers correspond to the number of spawn obtained each day for F1 and F7+ females.

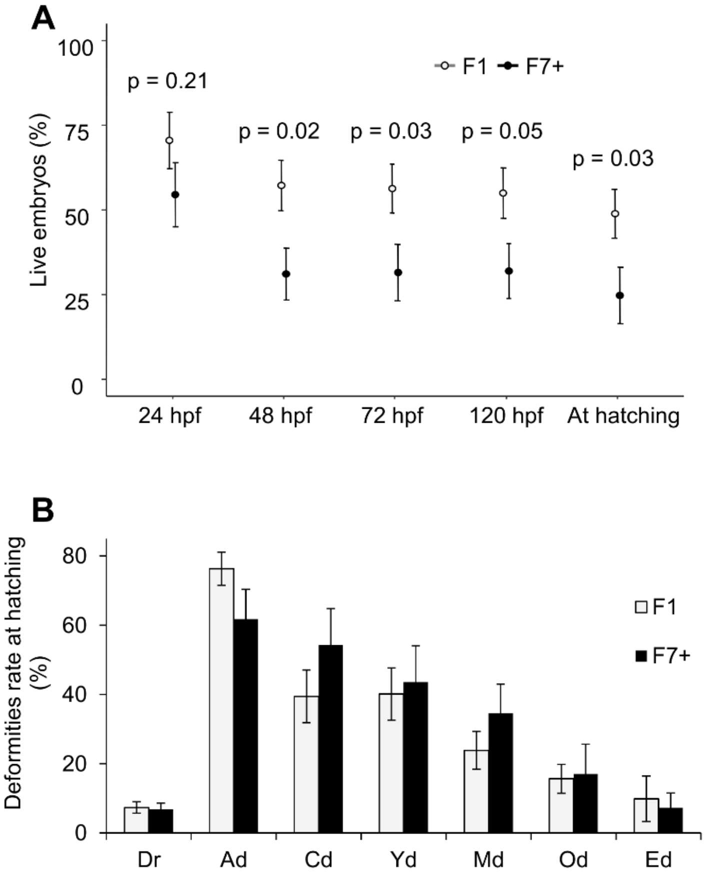


Figure 28. **Evaluation of the embryonic developmental success in F1 and F7+ populations.** (A) Percentage of embryos surviving at 24, 48, 72 and 120 hours post-fertilization (hpf) and at hatching in F1 (light gray dots) and F7+ (black dots) populations estimated based on the total number of studied embryos (about 100 embryos). In (A), dots represent population means ± SEM at each observed time (n= 19 and 13 for F1 and F7+, respectively). P-values presented represent comparisons between populations at each time of observation obtained using a TukeyHSD preceded by a significant one-way ANOVA in repeated measures ($p \leq 0.05$ were considered as significant). (B) Total deformities rates (Dr) and specific rates in various tissues at hatching in F1 and F7+ populations (Ad - Axis, Cd - Cardiac, Yd - Yolk, Md - Mouth, Od – Other, Ed - Eyes). No significant difference has been identified between populations using non-parametric Wilcoxon-Mann-Whitney test ($p<0.05$; n=23).

4.3. *Eggs transcriptomic analysis*

A large scale analysis was performed on 31 spawn to compare the maternal transcriptomic profiles of non fertilized eggs. The statistical analysis revealed 358 differentially expressed genes (DEG) between populations (Supplementary Table 10). An unsupervised average linkage clustering analysis was performed using the expression data of these 358 DEG. It allowed splitting apart both populations revealing that 172 genes were over-expressed in the F7+ population and 186 genes were over-expressed in the F1 population (Figure 29A and Supplementary Table 11).

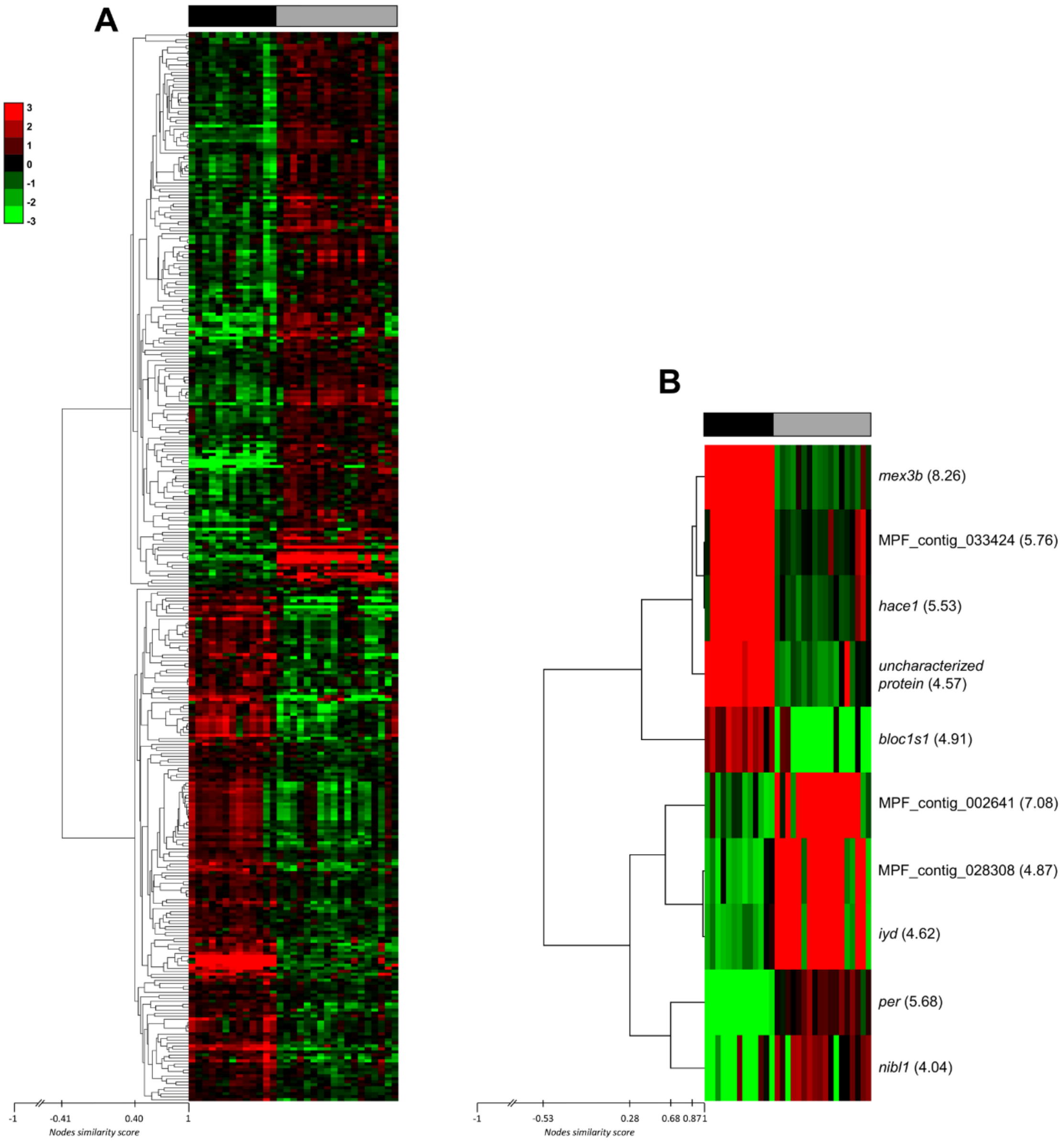


Figure 29**. Heatmaps showing differentially expressed genes between F1 and F7+ populations.** (A) Unsupervised hierarchical cluster analysis of 358 differentially expressed genes ($p < 0.05$) between populations. The dendrogram on the left represents gene correlation distances between the genes. (B) Unsupervised hierarchical cluster analysis of the 10 most differentially expressed genes ($p < 0.05$) with a log(2)FC >4, between populations. Gene abbreviated name and log(2)FC are shown between parentheses on the right. In both parts of the figure, red color indicates over-expression, and green color indicates under-expression while black is used for median expression. Top bar indicates the origin of the samples: black for F7+ samples and gray for F1 ones. Node similarity score bars represents the similarity between tree branches. It ranges from 1 (identical) to -1 (opposites), while 0 means they are completely uncorrelated.

A functional annotation of these 172 and 186 over-expressed genes allowed mapping 86 genes for each population, among which 73 and 76 genes containing specific GO annotations were identified for F7+ and F1 populations, respectively (Supplementary Tables 12 and 13).

Using Panther software, no Pathways was enriched and the term “immune system” was overrepresented (FDR p-value = 0.00251; Supplementary Table 14). Four of the genes represented belong to the butyrophilin or the butyrophilin-like family but two of them were up-regulated in the F1 population while the others were down-regulated in this population. For three of these genes, the log(2)FC was >2 and were thus among the 16% most differentially expressed genes between the two populations.

Indeed, among the 358 DEG only 60 presented a log(2)FC > 2 between the two populations. Fifty DEG showed a log(2)FC between 2 and 3-fold (Supplementary Table 10) and 10 genes had a log(2)FC higher than 4-fold (5 over-expressed in the F7+ population and 5 in the F1; Figure 29B). We choose to check the expression level of the genes having a log(2)FC > 4 by real-time qPCR. Among them, three sequences could not be identified because the probes actually recognized contigs grouping numerous unidentified genes in the Eurasian perch transcriptomic database (Figure 29B). Among the remaining genes, four were more expressed in the F7+ population: *mex3b* (log(2)FC = 8.26), *bloc1s1* (log(2)FC = 4.91), an *uncharacterized protein* (log(2)FC = 4.57) and *hace1* (log(2)FC = 5.53). In the same way, *per2* (log(2)FC = 5.68), *nibl1* (log(2)FC = 4.04) and *iyd* (log(2)FC = 4.62) were more abundant in the F1 population.

Expression level differences were confirmed for *mex3b* (log(2)FC = 7.26 for the RT-qPCR), the *uncharacterized protein* (log(2)FC = 1.65 for the RT-qPCR), *hace1* (log(2)FC = 1.65 for the RT-qPCR) and *per2* (log(2)FC = 3.13 for the RT-qPCR; Figure 30). However, for *bloc1s1* and *nibl1* the expression levels between both populations were not significantly different by RT-qPCR even if they followed the same profile than in the microarray (Figure 30). In addition, concerning *iyd* not only no significantly different expression was observed, but also the profile observed by RT-qPCR was in favor to a higher expression in the F7+ population, which is in contradiction with the microarray data.

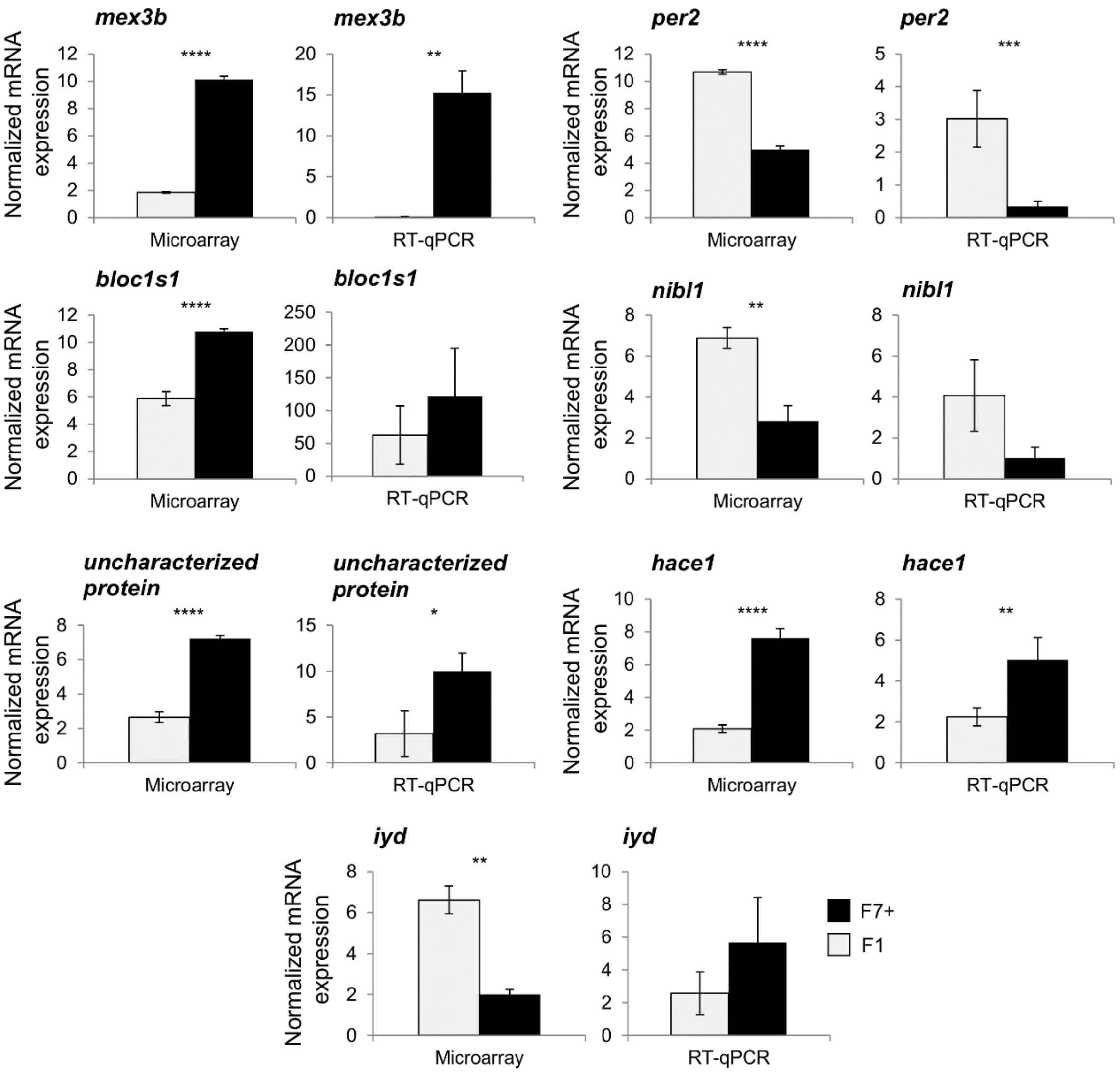


Figure 30**. Compared analysis of 7 genes among the most differentially expressed (log(2)FC >4) between microarray and RT-qPCR experiments.** The same egg samples were used to perform both techniques for F7+ (n=13) and F1 (n=18 for microarray and n=19 for RT-qPCR) populations. An unpaired t-test followed by a multiple testing correction Benjamini-Hochberg was applied on microarray results while a Mann-Whitney-Wilcoxon test was used on RT-qPCR results. Bars correspond to the means ± standard error. Significance levels are represented as follows: *, p = 0.05–0.01; **, p = 0.01–0.001; ***, p = 0.001–0.0001; and ****, p < 0.0001.

5. Discussion

The Differentiation Index (F_{ST}) illustrates a genetic divergence between populations ranging from 0 (gene flow between populations) to 1 (isolated populations without any gene flow). In the literature, a lower F_{ST} (0.002, $p < 0.0023$) was found between various samples of Eurasian perch all around the Geneva Lake (Ben Khadher et al., 2015) and authors considered that there was only one population in the lake. The same authors showed a minimum F_{ST} of 0.45 ($p < 0.0001$) between a wild and nine farmed populations of Eurasian perch that were all supposed to originate from the same geographic location (Ben Khadher et al., 2016). They were considered as distinct populations. In comparison, our F_{ST} (0.1055, $p < 0.0001$) is in between the above mentioned examples. The interpretation of significant differences when using highly variable loci, such as microsatellites, has to be very carefully analyzed since its biological meaning can often be weak (Hedrick, 1999). In the present study, we selected the most variable microsatellites according to literature on Eurasian perch microsatellite differentiation. In addition, the higher heterozygosity index for the F7+ (0.440) compared to the F1 (0.348) shows a higher heterogeneity in the F7+ population compared to the F1. Our F7+ population came from a partner fish farmer but first originated from the transfer from another fish farm. The initial stock was supposedly from Geneva lake but it was difficult to obtain a reliable traceability. Consequently, it is possible that some individuals from different geographic locations may have been introduced in the F7+ stock, which is a common practice in aquaculture (Ben Khadher et al., 2016). Alternatively, the random independent sampling process to create each population stock (F1 and F7+) could have led to different degrees of genetic drift in each stock. In our conditions, none of these hypotheses can be ruled out.

5.1. *Control of the reproductive cycle*

The oogenesis progression was similar between populations even if females from the F1 population seemed to respond faster to the photothermal stimulation and kept a slight non-significant advance all along the process. This advance became significant one month before the spawning with a higher proportion of late vitellogenesis oocytes and may contribute to explain the early onset of the spawning season of F1 females (thirteen to seven days before the F7+ ones). For technical reasons it has not been possible to determine the end of the spawning season of F7+ fish. The short spawning season of F7+ population in comparison to F1 is thus not relevant. It is worthy to note that at the end of the experimental period all remaining females that did not spawn presented developed gonads, once they were all slaughtered at the end of the experiment.

In this study, sexual steroids and Vitellogenin levels were either slightly or not different during the reproduction cycle between populations. The same pattern has been observed for the GSI. Differences found may either be mediated by yet unknown mechanisms or very subtle variations of hormone levels controlling the oogenesis progression. From the current knowledge, it remains difficult to precisely point which of these parameters imposed these modulations between the two populations.

Concerning the developmental success, results showed that F1 population presented an embryonic survival higher than the F7+ one with differences ranging from 16 to 26% of survival depending on the timepoint. This difference is the lowest at 24 hpf (16%), leading to a non-significant result at this timepoint. In any case, differences between populations may be due to egg quality issues that led either to fertilization impairments or higher mortality occurrence. These results enable us to conclude that the overall egg quality was higher in F1 than in F7+ population. Egg quality relies greatly upon its intrinsic content and some molecules may have very early and essential effect during embryogenesis, including pronuclear congregation and mitotic spindle assembly (Dekens et al., 2003). In addition, only few exchanges occur between the developing embryos and the environment (Schaerlinger and Żarski, 2015) reinforcing the importance of the egg content during early embryogenesis. Moreover, the F7+ population shows more heterogeneous survivorship, mainly at 48 hpf, with a higher number of low quality spawn. It is potentially related to individuals' history in the tank during the oogenesis (e.g. behavioral difference). In any case this difference of egg quality may be explained by the resource allocation theory (van der Waaij, 2004). Even if domestication of Eurasian perch begun 20 years ago, numerous questions remain to properly achieve their breeding in recirculating aquaculture systems. Since no selective program has begun yet for this species (Teletchea and Fontaine, 2014), the artificial selection driven by farmers remains empirical. In addition, rearing conditions are not fully optimized and fish farmers continue to make changes in their practices. Consequently, an imbalance between biological functions may occur in this species because resource intakes are allocated toward certain traits at the expense of other functions, such as reproduction. No zootechnical practices may be undertaken to compensate the lack of intake that may occur at each generation. This data is in accordance with numerous studies showing a decrease of the reproductive success in domesticated populations. Indeed, lower fertilization and hatching rates in farmed Atlantic cod (*G. morhua*) (Lanes et al., 2012, 2013), lower survival rate at the eyed stage in farmed Atlantic salmon (*S. salar*) (McGinnity et al., 2003), lower hatching rate in cultured common sole (*Solea solea*) (Lund et al., 2008) and oogenesis impairments in captive-reared greater amberjack (*S. dumerili*) (Zupa et al., 2017) were described in comparison with their respective wild counterparts. Therefore, this problem is widely observed in fish species and further studies are needed to test the hypotheses proposed in the resource allocation theory during fish domestication. If these hypotheses are confirmed, it means that a more accurate knowledge of metabolic needs for each biological function at each step of the life cycle is required before starting any selection program. Farmers should then take this information into account in order to implement a compensation program when the resource allocation is imbalanced. In this manner, all biological functions may beneficiate from an increase of the global resource intake. In addition, the choice of selected biological traits in addition to the follow up of the fitness of individuals should be assessed properly in order to detect early any deviation.

Concerning the Eurasian perch (*P. fluviatilis*), other studies showed that wild populations had higher reproductive performance than captive ones but with even more drastic differences than in the present work (Khendek et al., 2017; Křišťan et al., 2012). Differences between our study and these ones may be due to accumulation of the domestication effect on oogenesis and spermatogenesis, since in those studies developmental performance of embryos was evaluated from pure crosses from each population. In the present study, our goal was to investigate exclusively the effect of the domestication on females' performance. Consequently, we chose to reduce the potential effect of sperm quality and fertilized all spawn with sperm from F1 males. Another explanation could be that rearing conditions using in other studies were different (tank size and colour, first spawn or not…) from ours and influenced differently wild populations in the different studies.

Variations of gene expression profiles between wild and "domesticated" populations have been demonstrated in whole larvae and embryos of Atlantic salmon (*S. salar*) (Bicskei et al., 2014, 2016), fertilized eggs of Atlantic cod (*G. morhua*) (Lanes et al., 2013) and whole larvae of steelhead trout (*O. mykiss*) (Christie et al., 2016) but no study investigated the maternal mRNA profile. These observations strengthen the necessity to better understand the contribution of maternal mRNA to the embryonic early development in our conditions.

5.2. *Eggs transcriptome*

Our working hypothesis was that the domestication process may impact the maternal mRNA content of the eggs and thus the transcriptomic profile of unfertilized eggs coming from F1 and F7+ populations. In total, 358 genes presented a significant difference of expression between populations.

The GO analysis revealed one biological process term overrepresented among the DEG list that we analyzed, suggesting that this function may be affected by the domestication process. This biological process corresponds to the "immune system" grouping proteins usually involved in the regulation of the adaptative immune response such as activation and proliferation of effective T cells and cytokine production (Huang and Wange, 2004), controlling inflammation. However, these genes can be expressed in several tissues and may thus be involved in other biological functions. In fish, the T cell receptor signaling pathway seems to be as complex as in mammals but remains yet to be understood (Laing and Hansen, 2011; Partula, 1999). Some transcriptomic studies in eggs, embryos and early larvae showed that genes related with the immune system are often differentially expressed depending on egg quality or the domestication level. Concerning studies on the egg quality, genes representing the immune system are mostly down-regulated in eggs presenting lower potential to properly develop (Mommens et al., 2014; Żarski et al., 2017a). Concerning domestication comparisons, several genes involved in the immune system were down-regulated in a domesticated population of Atlantic salmon (*S. salar*) compared to their wild counterparts (Bicskei et al., 2014, 2016). In the latter case, the populations used were selected for their growth abilities and authors proposed the existence of a trade-off between growth and immune response during the selection process. In another study performed in the steelhead trout (*O. mykiss*) (Christie et al., 2016), authors proposed that it could simply reflect an adaptation of individuals to the captive environment, implying an up-regulation of genes involved in this function in domesticated fish. However, no information on the direction of perturbations (up- or down-regulation of genes in domesticated or wild populations) was given. In our study, the term "immune system" involved genes that were up-regulated either in the F1 population (five genes) or in the F7+ population (four genes). Additionally, most of the highlighted genes code for Butyrophilin proteins involved in several biological functions, on top of their role in the immune system. More particularly, they regulate the oil droplets secretion in the milk produced by mammals (Robenek et al., 2006). Eurasian perch eggs contain a large oil droplet necessary for proper embryonic development since impairments in its formation have been correlated to embryogenesis defects (Żarski et al., 2011c). It would be interesting to further investigate a potential role of these proteins in the formation of oil droplets in fish eggs.

In addition, some of the genes presenting the wider variations of expression between populations are known to be involved during the early embryogenesis and may partly explain developmental defects leading to early lethalities observed in the F7+ population. The *period2* gene (*per2*) codes for a protein belonging to the basic-helix-loop-helix-PAS (bHLH-PAS) protein family and belongs to the clock genes controlling many developmental and physiological events (Crews, 1998). However, in several mammalian species, numerous clock genes, including *per2*, have been observed in the developing oocytes and eggs as maternal mRNA. These mRNA are not controlled by circadian rhythms and disappear after the MZT (Amano et al., 2009, 2010). Authors proposed that *per2* could be involved in the control of meiosis but, up to now, no proof has corroborated this hypothesis and further investigations are needed to study their role in this tissue. Similar data have been observed in the developing spermatogonia in mice in which clock genes are expressed without any link with the circadian rhythm. In this study, authors made the hypothesis that this gene is mainly linked to the differentiation process (Alvarez et al., 2003). Our study shows for the first time that a *per2* gene is expressed in fish eggs, suggesting similarities with mammals. In addition, it is highly expressed in eggs of the F1 population. Our study does not allow making any hypothesis about the role of *per2* or if it is dependent or independent of the circadian rhythm. However, it suggests that *per2* role during the gonadogenesis may be evolutionary conserved.

The gene *hace1* codes for the HECT domain and Ankyrin repeat Containing E3 ubiquitin-protein ligase 1. It was first identified as a potential tumor suppressor in humans (Anglesio et al., 2004). Later, absence or mutation of this gene was related with developmental issues such as some neurodevelopmental syndromes in humans (Hollstein et al., 2015), a shortening of the body axis, an inhibition of eye pigments formation and a delay in neural tube closure in xenopus (Iimura et al., 2016). In this last study, authors compared their data with another work performed with zebrafish and showing no clear phenotype in this species. They argued that the zebrafish study revealed the role of HACE1 by using splice-sites morpholino efficient to repress zygotic but not maternal RNA (Daugaard et al., 2013) while their study involved translational blocking morpholinos blocking both maternal and zygotic RNA. Thus they suggest that phenotypes in xenopus could be linked to the maternal pool of RNA. Recently, a study demonstrated that HACE1 is involved in the normal development and proper function of the heart in zebrafish (Razaghi et al., 2018). However, authors used splice-site morpholinos suggesting that this cardiac phenotype could be due to later zygotic expression of HACE1. Consequently, even if no maternal role of HACE1 has been studied in the zebrafish, studies performed on xenopus suggest that a maternal expression of these mRNA have consequences on the neural tube development. Up to now, two main targets of Hace1 have been identified: Rac1 involved in the cell cycle control and NADPH oxidase regulating the reactive oxygen species production. A previous study showed that some enzymes involved in the control of the oxidative stress present a variation of expression depending on oocytes quality in Eurasian perch (Castets et al., 2012). In some marine invertebrate species, a modification of redox homeostasis may help to avoid the polyspermy during fertilization

(Schomer and Epel, 1998). In our study, the mRNA abundance of *hace1* is higher in the F7+ population, potentially accelerating NADPH oxydase degradation and thus influencing fertilization. With the current knowledge, no transduction pathway could be favored.

Similarly, the mRNA abundance of *mex3b* mRNA was higher in the domesticated population. *Mex3b*, or *muscle excess 3*, codes for an evolutionary conserved RNA-binding protein involved in post-transcriptional regulations (Buchet-Poyau et al., 2007). It is associated to proper embryonic development by establishing antero-posterior patterning in *Tribolium* (Kimelman and Martin, 2012), *Caenorhabditis elegans* (Draper et al., 1996) and *Xenopus laevis* (Takada et al., 2009). As a whole, embryonic patterning is regulated by expression and spatial distribution of many transcripts. In xenopus, *mex3b* mRNA presents a long conserved untranslated 3'UTR involved in its auto regulation (Takada et al., 2009). In turn, the protein is involved in the mRNA stability and regulates the abundance of several genes, involved in diverse cellular functions (Takada et al., 2009). In the present work, the maternal expression of *mex3b* mRNA presents the highest variation of expression level between the two populations (log2FC > 7 in the RT-qPCR). Consequently, the high expression of this transcript in the F7+ eggs may be linked to fine tuning of numerous molecular functions in the embryo and lead to diverse phenotypes.

Finally, a mRNA coding for an *uncharacterized* protein was found to be significantly more expressed in the eggs laid by F7+ females. BLAST analyses against the Uniprot and NCBI databases showed that they are highly homologous to other uncharacterized proteins in other fish species presenting homologies with some domains of ADP ribosylation enzymes. However, these sequences have not been identified yet.

6. Conclusions

Our study showed that reproductive performance of Eurasian perch females may be influenced by the domestication process which is probably closely related to the rearing practices potentially leading to several genetic and/or epigenetic modifications. This study revealed that even if the breeders of two Eurasian perch populations (F1 vs. F7+) were reared and induced in the same conditions, the F1 population started to spawn earlier than the F7+ during the spawning season. In other words, it shows that, in our conditions, the domestication process may influence the responsiveness of females to the reproductive environmental stimuli in captive environment.

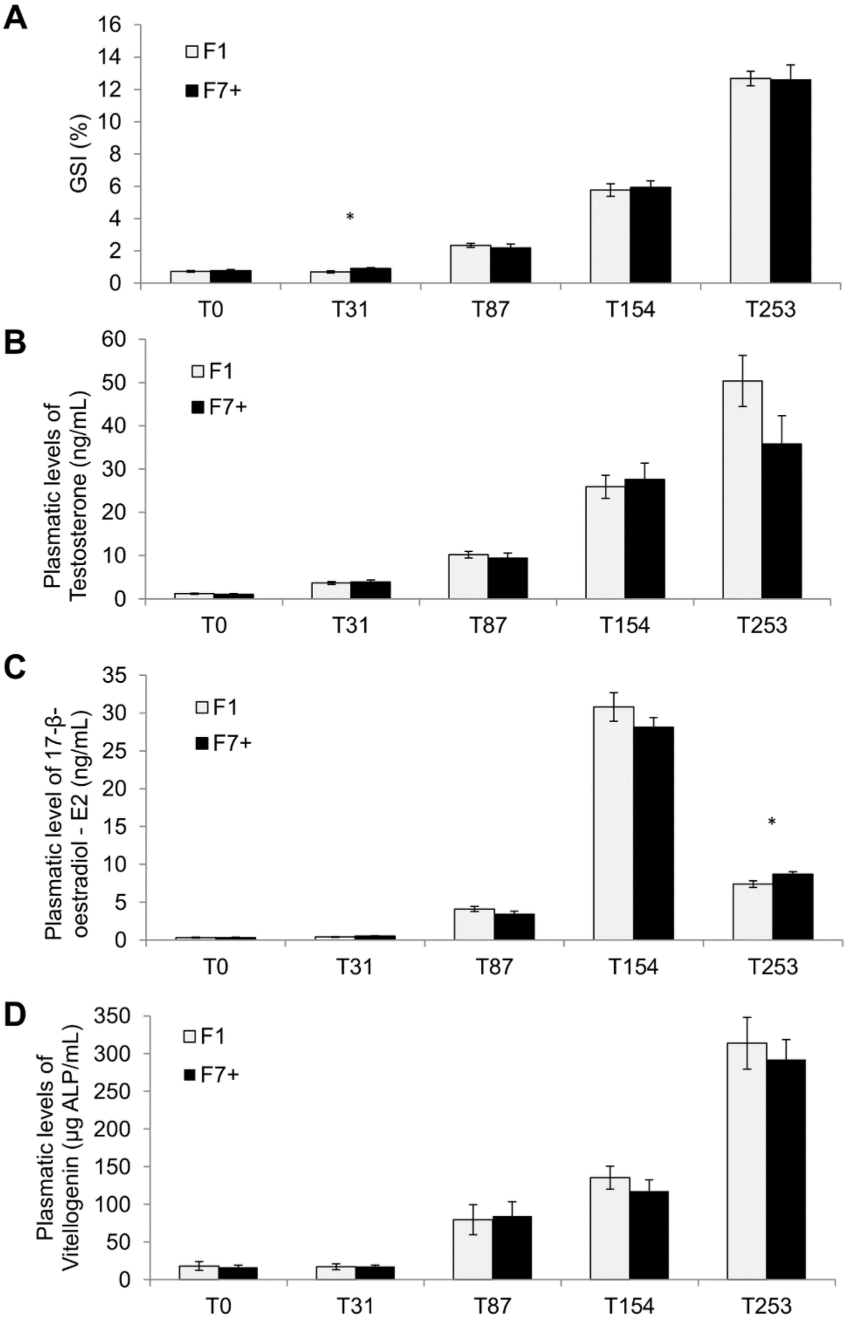
The F1 population produced eggs having a better potential to develop properly until hatching compared to eggs from the F7+ population. These differences in egg quality may be linked with the important variation in the eggs transcriptomic content between populations. The identification of several genes presenting distinct expression between the two populations could open new paths of investigation to understand their role and mechanism of regulation during embryogenesis and depending on the domestication level.

Finally, the genetic differentiation analysis between studied populations did not allow us to isolate the domestication as the only factor explaining our data. It reinforces the necessity of studying populations presenting a clearer life history to further understand the dynamic of modifications occurring during the domestication process. It is particularly important in the perspective of a growing pressure toward fish farmers and scientists to initiate selection programs for several fish species.

7. Acknowledgements

We thank, Paul Georges and Franck Bertrand for their involvement in some experiments as trainees, Alain Iuretig for the care given to the breeders during the growing period and Yves Le Roux for the assistance with the survival statistical analysis. We are also grateful to Mikhail Ozerov and Freed Ahmad from University of Turku for kindly providing the annotated perch genome used in GO analysis and the members of the UR AFPA DAC and LPGP Rennes for their support.

8. Supplementary information



Supplementary Figure 2**. Study of oogenesis progression.** Evolution of (A) gonado somatic index - GSI and plasmatic levels of (B) 17-β-œstradiol - E2, (C) testosterone and (D) Vitellogenin during oogenesis on the populations F1 and F7+. Bars correspond to mean values ± standard error. Asterisks indicate significant differences between populations at $p<0.05$ using non-parametric Wilcoxon-Mann-Whitney test. Significance levels are represented as follows: *, p = 0.05–0.01.

Supplementary Table 7**. Primer sequences used for real-time PCR experiment of the 7 most expressed genes in the two populations and reference genes used for data normalization.**

Target gene	**Abbreviated name**	**Phylofish/GenBank Gene ID**	**Forward sequence**	**Reverse sequence**	**Annealing temperature**
Higher expressed in F7+ population					
RNA-binding protein MEX3B-like	*mex3b*	MPF_LOC101470955.1.1	CTCCACGGACTCCTACTTCG	GGCGAGGAGTCAAAAGTCAG	50°C
E3 ubiquitin-protein ligase HACE1	*hace1*	MPF_HACE1.1.3	GAACGGACACAAAACCACGG	AGGATCTCACAGGTCTCCCC	58°C
biogenesis of lysosome-related organelles complex 1 subunit 1-like	*bloc1s1*	MPF_LOC100710617.1.3	ACGCCTGGGCAACTCTAGTA	GCACCCATGCAGTTATGTTG	58°C
-	*uncharacterized protein*	MPF_NEMVEDRAFT_V1G131035.1.1	GTTTGGTGACAACACCTGGC	CTCGGAGGGGAATTCATGGG	50°C
Higher expressed in F1 population					
period circadian protein homolog 2-like	*per2*	MPF_LOC101485591.1.2	AGGGTGGACCGAGTGTACTG	GGGTTAAGGCCGAGGTTTAG	50°C
iodotyrosine dehalogenase 1-like	*iyd*	MPF_LOC100692784.3.3	TGGTGCTTCGTCTCTGTGTC	GCCTTACTCACCACCACGTT	58°C
Niban-like protein 1	*nibl1*	MPF_NIBL1.1.1	GGTTGGGGGTGTAAGACAGA	GTGCTGCATGAAGACAGGAA	50°C
Reference genes					
Adenosine kinase-like	*adk*	MPF_LOC101464997.1.1	CTTCCTGACCGTCTCTTTGG	CCTTGGTCTCGAAGTCTTGC	50°C
ELAV-like protein 1-like	*elavl1*	MPF_LOC100695900.1.2	GATCGTGAACTACCTGCCCC	TTACCTGCCACTTTGTCCCG	50°C
TATA box-binding protein	*tbp*	MPF_LOC101470168.1.1	CAGGTGCCAAGGTGAGAGCA	ACAACAGCCCTTGCACAGCA	55°C
18S ribosomal RNA	-	FJ710875	CCTGCGGCTTAATTTGACTC	CTCAATCTCGTGTGGCTGAA	55°C

Supplementary Table 8**. Survivorship at 24, 48, 72 and 120 hours post-fertilization (hpf) and at hatching in F1 and F7+ populations.** Columns 2 and 3 correspond to data presented in the Figure 28A. Different letters mean significant differences between populations using an ANOVA one-way repeated measures followed by a TukeyHSD ($p \leq 0.05$; n= 19 and 13 for F1 and F7+, respectively). Population means ± SEM are presented.

	Survival based on the total number of embryos studied (~ 100 embryos)	
	Populations	
Time point	F7+	F1
24 h	54 ± 9% ^{a}	70 ± 8% ^{a}
48 h	31 ± 7% ^{a}	57 ± 7% ^{b}
72 h	31 ± 8% ^{a}	56 ± 7% ^{b}
120 h	32 ± 8% ^{a}	54 ± 7% ^{b}
Hatching (about 15 days)	24 ± 8% ^{a}	48 ± 7% ^{b}

Superscripts refers to the comparisons between populations at each timepoint. Different letters mean significant difference ($p \leq 0.05$).

Supplementary Table 9**. Deformities rates (Dr) and specific rates in various tissues at hatching in F1 and F7+ populations (Ad - Axis, Cd - Cardiac, Yd - Yolk, Md - Mouth, Od – Other, Ed - Eyes).** No significant differences have been identified between the two populations using non-parametric Wilcoxon-Mann-Whitney test ($p<0.05$; n=23). Population means ± SEM are presented.

	Populations	
	F7+	F1
Dr	6 ± 1%	7 ± 1%
Ad	61 ± 8%	76 ± 4%
Cd	54 ± 10%	39 ± 7%
Yd	43 ± 10%	40 ± 7%
Md	34 ± 8%	23 ± 5%
Ed	7 ± 4%	9 ± 6%
Od	17 ± 8%	15 ± 4%

Supplementary Table 10**. Differentially expressed genes list.** PhyloFish gene ID, gene description, False Discovery Rate (p-value) and log(2)FC of the 358 differentially expressed genes on eggs from the F7+ and F1 populations.

Despite of being a long table, I choose to keep it in the printed version because fast data checking may be needed during the manuscript reading.

Genes up regulated in F7+ population			
Phylofish Gene ID	*Gene Description*	*FDR (p-value)*	*Log2 FC*
MPF_LOC101470955.1.1	XM_004565735.1 PREDICTED: Maylandia zebra RNA-binding protein MEX3B-like (LOC101470955), mRNA	0.000	8.270
MPF_contig_033424		0.000	5.769
MPF_HACE1.1.3	HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2	0.000	5.534
MPF_LOC100710617.1.3	XP_003456137.1 PREDICTED: biogenesis of lysosome-related organelles complex 1 subunit 1-like [Oreochromis niloticus]	0.000	4.910
MPF_NEMVEDRAFT_V1G131035.1.1	XP_001625099.1 predicted protein [Nematostella vectensis]	0.000	4.576
MPF_LOC100694351.1.1	XM_003450430.1 PREDICTED: Oreochromis niloticus aryl hydrocarbon receptor nuclear translocator 2-like, transcript variant 1 (LOC100694351), mRNA	0.000	3.674
MPF_LOC100694761.1.2	XM_003442629.1 PREDICTED: Oreochromis niloticus red-sensitive opsin-like (LOC100694761), mRNA	0.001	3.654
MPF_LOC100558617.2.2	XP_003224121.1 PREDICTED: hypothetical protein LOC100558617 [Anolis carolinensis]	0.007	3.622
MPF_contig_036321		0.008	3.313
MPF_LOC100693306.9.13	XP_003458501.1 PREDICTED: protein NLRC3-like [Oreochromis niloticus]	0.000	3.083
MPF_BRAFLDRAFT_92923.9.11	XP_002605501.1 hypothetical protein BRAFLDRAFT_92923 [Branchiostoma floridae]	0.001	2.982
MPF_LOC100711789.5.22	XP_003457783.1 PREDICTED: neural cell adhesion molecule 2-like [Oreochromis niloticus]	0.000	2.881
MPF_LOC100689895.12.13	XP_003459184.1 PREDICTED: coxsackievirus and adenovirus receptor homolog [Oreochromis niloticus]	0.023	2.796
MPF_LOC100689966.1.1	XP_003456465.1 PREDICTED: C-type lectin domain family 4 member M-like [Oreochromis niloticus]	0.000	2.761

MPF_TITIN.3.4	TITIN_HUMAN (sp|Q8WZ42) Titin OS=Homo sapiens GN=TTN PE=1 SV=4	0.001	2.675
MPF_LOC101174554.1.1	XP_004084158.1 PREDICTED: V-set domain-containing T-cell activation inhibitor 1-like [Oryzias latipes]	0.035	2.667
MPF_LOC100707046.6.12	XM_003454686.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100707046), mRNA	0.000	2.662
MPF_contig_042909		0.000	2.644
MPF_HACE1.3.3	[BBH] HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2	0.000	2.455
MPF_TITIN.2.4	TITIN_HUMAN (sp|Q8WZ42) Titin OS=Homo sapiens GN=TTN PE=1 SV=4	0.002	2.452
MPF_LOC100697304.1.3	XP_003458513.1 PREDICTED: hypothetical protein LOC100697304 [Oreochromis niloticus]	0.020	2.386
MPF_contig_038164		0.001	2.275
MPF_contig_044938		0.002	2.258
MPF_LOC101464981.1.1	XM_004574536.1 PREDICTED: Maylandia zebra cyclic AMP-dependent transcription factor ATF-4-like (LOC101464981), mRNA	0.022	2.234
MPF_contig_036939		0.001	2.202
MPF_LOC101479341.5.9	XM_004575727.1 PREDICTED: Maylandia zebra high affinity immunoglobulin epsilon receptor subunit alpha-like (LOC101479341), partial mRNA	0.002	2.178
MPF_LOC101175636.1.1	XP_004067842.1 PREDICTED: leucine-rich repeat-containing protein 24-like [Oryzias latipes]	0.043	2.161
MPF_LOC100689895.9.13	XP_003459184.1 PREDICTED: coxsackievirus and adenovirus receptor homolog [Oreochromis niloticus]	0.001	2.121
MPF_contig_041682	XM_004538959.1 PREDICTED: Maylandia zebra metal transporter CNNM2-like (LOC101472577), transcript variant X1, mRNA	0.000	2.100
MPF_LOC101472577.1.1	XM_004538960.1 PREDICTED: Maylandia zebra metal transporter CNNM2-like (LOC101472577), transcript variant X2, mRNA	0.000	2.054
MPF_LOC100537015.1.4	XR_117933.1 PREDICTED: Danio rerio hypothetical LOC100537015 (LOC100537015), miscRNA	0.004	2.013

MPF_LOC101480464.2.2	XM_004546014.1 PREDICTED: Maylandia zebra uncharacterized LOC101480464 (LOC101480464), transcript variant X4, mRNA	0.002	1.979
MPF_LOC101468624.1.1	XM_004566102.1 PREDICTED: Maylandia zebra charged multivesicular body protein 1a-like (LOC101468624), mRNA	0.002	1.950
MPF_LOC101161271.4.4	XM_004079586.1 PREDICTED: Oryzias latipes Fc receptor-like B-like (LOC101161271), mRNA	0.015	1.941
MPF_contig_028781		0.002	1.928
MPF_LOC101465736.1.3	XM_004549136.1 PREDICTED: Maylandia zebra solute carrier family 45 member 4-like (LOC101465736), mRNA	0.008	1.927
MPF_PCGF1.2.2	PCGF1_DANRE (sp|Q7ZYZ7) Polycomb group RING finger protein 1 OS=Danio rerio GN=pcgf1 PE=3 SV=1	0.026	1.927
MPF_contig_036778	XM_004568351.1 PREDICTED: Maylandia zebra protein kinase C beta type-like (LOC101478005), transcript variant X1, mRNA	0.003	1.899
MPF_LOC101469943.2.2	XM_004576438.1 PREDICTED: Maylandia zebra translocon-associated protein subunit alpha-like (LOC101469943), transcript variant X3, mRNA	0.002	1.898
MPF_contig_048609		0.002	1.888
MPF_UNC89.3.3	UNC89_CAEEL (sp|O01761) Muscle M-line assembly protein unc-89 OS=Caenorhabditis elegans GN=unc-89 PE=1 SV=3	0.002	1.882
MPF_contig_000405		0.007	1.881
MPF_LOC101062260.2.2	XP_003970925.1 PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit alpha-like [Takifugu rubripes]	0.000	1.876
MPF_LOC100704617.1.1	XM_003448236.1 PREDICTED: Oreochromis niloticus putative protein 2-like (LOC100704617), mRNA	0.005	1.866
MPF_LOC100711789.9.22	XP_003457783.1 PREDICTED: neural cell adhesion molecule 2-like [Oreochromis niloticus]	0.002	1.856
MPF_contig_044649		0.017	1.855
MPF_LOC101472722.1.1	XM_004549929.1 PREDICTED: Maylandia zebra zinc finger protein 703-like (LOC101472722), mRNA	0.001	1.848
MPF_NEMVEDRAFT_V1G245263.1.1	XP_001629004.1 predicted protein [Nematostella vectensis]	0.002	1.817

MPF_LOC101160526.1.1	XM_004083816.1 PREDICTED: Oryzias latipes zinc finger protein 395-like (LOC101160526), mRNA	0.044	1.787
MPF_LOC101466800.1.1	XM_004549803.1 PREDICTED: Maylandia zebra kynurenine--oxoglutarate transaminase 1-like (LOC101466800), mRNA	0.014	1.764
MPF_RS17.23.23	RS17_ICTPU (sp|Q90YQ6) 40S ribosomal protein S17 OS=Ictalurus punctatus GN=rps17 PE=2 SV=3	0.001	1.763
MPF_contig_022452		0.003	1.756
MPF_LOC100698039.1.1	XP_003443173.1 PREDICTED: cleavage and polyadenylation specificity factor subunit 4-like [Oreochromis niloticus]	0.006	1.752
MPF_LOC100698625.6.22	XM_003456694.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100698625), mRNA	0.036	1.726
MPF_LOC100698511.1.1	XP_003453540.1 PREDICTED: protein FAM46A-like [Oreochromis niloticus]	0.010	1.721
MPF_contig_036137		0.033	1.695
MPF_LOC101155681.1.1	XP_004069346.1 PREDICTED: uncharacterized protein LOC101155681 [Oryzias latipes]	0.001	1.643
MPF_contig_037954		0.000	1.637
MPF_contig_008939	XM_004563260.1 PREDICTED: Maylandia zebra spermatogenesis-associated protein 13-like (LOC101487877), transcript variant X4, mRNA	0.002	1.624
MPF_LOC101169978.1.1	XP_004079878.1 PREDICTED: Y+L amino acid transporter 1-like [Oryzias latipes]	0.013	1.616
MPF_LOC100692526.3.4	XP_003445246.1 PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1-like isoform 1 [Oreochromis niloticus] ref|XP_003445247.1| PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1-like isoform 2 [Oreochromis niloticus]	0.004	1.605
MPF_PTPRF.1.1	PTPRF_DANRE (sp|A4IFW2) Receptor-type tyrosine-protein phosphatase F OS=Danio rerio GN=ptprf PE=2 SV=1	0.003	1.580
MPF_LOC101075011.4.5	XM_003966867.1 PREDICTED: Takifugu rubripes collagen alpha-5(IV) chain-like (LOC101075011), mRNA	0.018	1.492
MPF_LOC101471603.2.2	XM_004562392.1 PREDICTED: Maylandia zebra MAGUK p55	0.005	1.483

	subfamily member 2-like (LOC101471603), mRNA		
MPF_LOC101483625.1.2	XM_004543147.1 PREDICTED: Maylandia zebra transcriptional enhancer factor TEF-1-like (LOC101483625), transcript variant X3, mRNA	0.004	1.477
MPF_LOC100708882.1.1	XM_003443830.1 PREDICTED: Oreochromis niloticus transcriptional enhancer factor TEF-3-like (LOC100708882), mRNA	0.014	1.471
MPF_TEAD1.1.1	XM_004593777.1 PREDICTED: Ochotona princeps TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), transcript variant X2, mRNA	0.009	1.458
MPF_LOC100712501.1.3	XM_003457496.1 PREDICTED: Oreochromis niloticus coxsackievirus and adenovirus receptor homolog (LOC100712501), mRNA	0.000	1.457
MPF_contig_030303		0.001	1.449
MPF_LOC100711789.8.22	XP_003457783.1 PREDICTED: neural cell adhesion molecule 2-like [Oreochromis niloticus]	0.000	1.418
MPF_LOC101473661.1.1	XM_004568055.1 PREDICTED: Maylandia zebra RNA-binding motif, single-stranded-interacting protein 3-like (LOC101473661), transcript variant X2, mRNA	0.006	1.416
MPF_LOC100692526.1.4	XM_003445199.1 PREDICTED: Oreochromis niloticus NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1-like, transcript variant 2 (LOC100692526), mRNA	0.004	1.383
MPF_PDE1A.1.1	XP_003449629.1 PREDICTED: calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1A [Oreochromis niloticus]	0.031	1.376
MPF_LOC101479843.1.1	XM_004539077.1 PREDICTED: Maylandia zebra mitochondrial dicarboxylate carrier-like (LOC101479843), mRNA	0.002	1.352
MPF_LOC101471273.1.2	XM_004574292.1 PREDICTED: Maylandia zebra dapper homolog 1-like (LOC101471273), mRNA	0.013	1.351
MPF_LOC101477479.1.1	XM_004555047.1 PREDICTED: Maylandia zebra MOB kinase activator 3C-like (LOC101477479), transcript variant X2, mRNA	0.032	1.345

MPF_LOC100711789.2.22	XP_003457783.1 PREDICTED: neural cell adhesion molecule 2-like [Oreochromis niloticus]	0.014	1.333
MPF_contig_016692		0.002	1.328
MPF_CSL2.1.2	CSL2_ONCKE (sp|P86178) L-rhamnose-binding lectin CSL2 OS=Oncorhynchus keta PE=1 SV=1	0.012	1.314
MPF_BT2A3.1.1	BT2A3_HUMAN (sp|Q96KV6) Putative butyrophilin subfamily 2 member A3 OS=Homo sapiens GN=BTN2A3P PE=5 SV=2	0.012	1.311
MPF_LOC101155645.2.2	XP_004081328.1 PREDICTED: villin-1-like [Oryzias latipes]	0.006	1.300
MPF_LOC101071192.1.1	XM_003962722.1 PREDICTED: Takifugu rubripes grainyhead-like protein 3 homolog (LOC101071192), mRNA	0.021	1.300
MPF_EIF4A1.2.3	XM_003458919.1 PREDICTED: Oreochromis niloticus eukaryotic translation initiation factor 4A1 (EIF4A1), mRNA	0.011	1.288
MPF_TBB7.1.1	[BBH] TBB7_CHICK (sp|P09244) Tubulin beta-7 chain OS=Gallus gallus PE=2 SV=1	0.001	1.282
MPF_LOC101468190.1.2	XM_004550947.1 PREDICTED: Maylandia zebra cell adhesion molecule 4-like (LOC101468190), transcript variant X4, mRNA	0.010	1.279
MPF_LOC101475031.1.1	XM_004547318.1 PREDICTED: Maylandia zebra sperm-tail PG-rich repeat-containing protein 2-like (LOC101475031), mRNA	0.025	1.273
MPF_LOC101478741.2.2	XM_004567788.1 PREDICTED: Maylandia zebra CTD small phosphatase-like protein 2-like (LOC101478741), mRNA	0.002	1.269
MPF_LOC101487341.2.3	XM_004547358.1 PREDICTED: Maylandia zebra bladder cancer-associated protein-like (LOC101487341), transcript variant X2, mRNA	0.009	1.255
MPF_contig_018475		0.001	1.248
MPF_contig_012534		0.049	1.241
MPF_LOC101479311.1.1	XM_004547986.1 PREDICTED: Maylandia zebra polypeptide N-acetylgalactosaminyltransferase 12-like (LOC101479311), mRNA	0.016	1.239
MPF_LOC101468018.7.7	XM_004558976.1 PREDICTED: Maylandia zebra dystroglycan-like (LOC101468018), transcript variant X3, mRNA	0.002	1.233
MPF_contig_049139		0.018	1.233
MPF_LOC101469089.4.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S	0.026	1.223

	ribosomal protein S27a-like (LOC101469089), mRNA		
MPF_contig_012824		0.040	1.195
MPF_LOC100711789.3.22	XP_003457783.1 PREDICTED: neural cell adhesion molecule 2-like [Oreochromis niloticus]	0.001	1.188
MPF_LOC100704882.1.2	XP_003447460.1 PREDICTED: bromodomain adjacent to zinc finger domain protein 2B-like [Oreochromis niloticus]	0.046	1.184
MPF_LOC100709351.7.10	XM_003449499.1 PREDICTED: Oreochromis niloticus integral membrane protein 2B-like (LOC100709351), mRNA	0.014	1.179
MPF_LOC101477102.1.1	XM_004575966.1 PREDICTED: Maylandia zebra eukaryotic initiation factor 4A-II-like (LOC101477102), transcript variant X1, mRNA	0.014	1.173
MPF_LOC101075011.1.5	XM_003966867.1 PREDICTED: Takifugu rubripes collagen alpha-5(IV) chain-like (LOC101075011), mRNA	0.001	1.167
MPF_LOC101474632.2.2	XM_004566302.1 PREDICTED: Maylandia zebra integral membrane protein 2B-like (LOC101474632), transcript variant X2, mRNA	0.022	1.148
MPF_LOC100696573.1.4	XM_003458226.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100696573), mRNA	0.035	1.115
MPF_LOC100692711.1.1	XP_003447247.1 PREDICTED: apolipoprotein A-I-binding protein-like [Oreochromis niloticus]	0.022	1.100
MPF_contig_009643		0.014	1.091
MPF_LOC101476415.1.1	XM_004548724.1 PREDICTED: Maylandia zebra prostacyclin synthase-like (LOC101476415), mRNA	0.023	1.075
MPF_contig_005144		0.026	1.038
MPF_LOC100709038.4.4	XM_003439572.1 PREDICTED: Oreochromis niloticus liprin-beta-2-like (LOC100709038), mRNA	0.029	1.014
MPF_LOC100710673.7.7	XM_003447676.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L22-like (LOC100710673), mRNA	0.009	1.011
MPF_LOC100709038.2.4	XM_003439572.1 PREDICTED: Oreochromis niloticus liprin-beta-2-like (LOC100709038), mRNA	0.025	1.008
MPF_LOC100704735.1.2	XP_003457359.1 PREDICTED: ICOS ligand-like [Oreochromis niloticus]	0.002	1.006
MPF_contig_016535		0.022	1.006

MPF_LOC101162073.1.1	XM_004079022.1 PREDICTED: Oryzias latipes protein C21orf2-like (LOC101162073), mRNA	0.007	0.989
MPF_LOC101482296.2.3	XM_004546497.1 PREDICTED: Maylandia zebra transmembrane protein 56-B-like (LOC101482296), transcript variant X2, mRNA	0.002	0.979
MPF_LOC101076755.1.1	XM_003972682.1 PREDICTED: Takifugu rubripes CUGBP Elav-like family member 2-like, transcript variant 1 (LOC101076755), mRNA	0.046	0.974
MPF_LOC101487985.1.1	XM_004543063.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase NEDD4-like (LOC101487985), transcript variant X1, mRNA	0.037	0.970
MPF_LOC100704613.1.1	XM_003447242.1 PREDICTED: Oreochromis niloticus transmembrane protein 170B-like (LOC100704613), mRNA	0.012	0.953
MPF_LOC101476111.3.3	XM_004546755.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase OSR1-like (LOC101476111), mRNA	0.049	0.949
MPF_contig_014271	XM_004552647.1 PREDICTED: Maylandia zebra muscleblind-like protein 2a-like (LOC101474967), transcript variant X10, mRNA	0.037	0.923
MPF_CYYR1.8.19	NM_212882.1 Danio rerio cysteine and tyrosine-rich protein 1 (cyyr1), mRNA gb|BC066606.1| Danio rerio cysteine and tyrosine-rich protein 1, mRNA (cDNA clone MGC:77252 IMAGE:6963826), complete cds	0.015	0.911
MPF_contig_022063		0.007	0.905
MPF_LOC101482280.1.1	XM_004542676.1 PREDICTED: Maylandia zebra protein phosphatase 1 regulatory subunit 7-like (LOC101482280), mRNA	0.037	0.903
MPF_LOC100701098.1.1	XM_003446807.1 PREDICTED: Oreochromis niloticus superoxide dismutase [Cu-Zn]-like (LOC100701098), mRNA	0.010	0.901
MPF_LOC100689895.10.13	XP_003459184.1 PREDICTED: coxsackievirus and adenovirus receptor homolog [Oreochromis niloticus]	0.026	0.900
MPF_LOC101158586.1.1	XM_004086364.1 PREDICTED: Oryzias latipes COMM domain-containing protein 7-like (LOC101158586), mRNA	0.001	0.885
MPF_MUC18.1.2	MUC18_RAT (sp|Q9EPF2) Cell surface glycoprotein MUC18	0.027	0.875

	OS=Rattus norvegicus GN=Mcam PE=1 SV=2		
MPF_LOC101482845.4.5	XM_004538718.1 PREDICTED: Maylandia zebra regulating synaptic membrane exocytosis protein 1-like (LOC101482845), mRNA	0.034	0.861
MPF_LOC100711031.2.4	XM_003445679.1 PREDICTED: Oreochromis niloticus BCL2/adenovirus E1B 19 kDa protein-interacting protein 3-like (LOC100711031), mRNA	0.048	0.859
MPF_ATF1A.1.1	ATF1A_DANRE (sp|A3KNL5) ATPase inhibitor A, mitochondrial OS=Danio rerio GN=atpif1 PE=2 SV=1	0.022	0.858
MPF_contig_035679	WP_002494948.1 Gram-positive signal peptide protein, YSIRK family, partial [Staphylococcus epidermidis]	0.018	0.857
MPF_LOC100692372.1.1	XM_003453719.1 PREDICTED: Oreochromis niloticus serine/threonine/tyrosine-interacting-like protein 1-like (LOC100692372), mRNA	0.007	0.853
MPF_LOC100709659.1.5	XM_003459501.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100709659 (LOC100709659), mRNA	0.009	0.852
MPF_contig_018509		0.039	0.842
MPF_LOC101480816.1.2	XM_004562059.1 PREDICTED: Maylandia zebra breast cancer anti-estrogen resistance protein 3-like (LOC101480816), transcript variant X3, mRNA	0.008	0.837
MPF_LOC100711616.1.1	XP_003457621.1 PREDICTED: rho guanine nucleotide exchange factor 2-like [Oreochromis niloticus]	0.003	0.823
MPF_LOC101465583.2.7	XM_004562463.1 PREDICTED: Maylandia zebra histone H3.3-like (LOC101465583), mRNA	0.012	0.821
MPF_LOC100706345.1.1	XP_003438270.1 PREDICTED: nephrocystin-1-like [Oreochromis niloticus]	0.032	0.817
MPF_MUC18.2.2	MUC18_HUMAN (sp|P43121) Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM PE=1 SV=2	0.018	0.813
MPF_LOC101476898.4.4	XM_004576052.1 PREDICTED: Maylandia zebra microsomal glutathione S-transferase 1-like (LOC101476898), transcript variant X2, mRNA	0.002	0.800

MPF_LSS.1.1	XP_003458413.1 PREDICTED: lanosterol synthase isoform 1 [Oreochromis niloticus]	0.042	0.797
MPF_LOC101474967.2.3	XM_004552650.1 PREDICTED: Maylandia zebra muscleblind-like protein 2a-like (LOC101474967), transcript variant X13, mRNA	0.027	0.797
MPF_LOC100707856.1.1	XP_003458866.1 PREDICTED: transforming growth factor beta-2-like [Oreochromis niloticus]	0.040	0.796
MPF_contig_016233	XM_004575756.1 PREDICTED: Maylandia zebra reticulon-4-like (LOC101464890), transcript variant X2, mRNA	0.001	0.784
MPF_contig_022012		0.010	0.774
MPF_contig_037497		0.031	0.772
MPF_LOC101480422.1.1	XM_004539079.1 PREDICTED: Maylandia zebra tubulin beta-4B chain-like (LOC101480422), mRNA	0.018	0.768
MPF_contig_020169		0.002	0.754
MPF_LOC101467334.2.2	XM_004565719.1 PREDICTED: Maylandia zebra endophilin-A3-like (LOC101467334), transcript variant X1, mRNA	0.007	0.752
MPF_contig_043816		0.002	0.746
MPF_LOC101079355.1.1	XP_003963369.1 PREDICTED: plakophilin-1-like [Takifugu rubripes]	0.014	0.741
MPF_LOC100705304.1.1	XP_003441119.1 PREDICTED: monoacylglycerol lipase ABHD12-like [Oreochromis niloticus]	0.036	0.739
MPF_LOC100710945.1.1	XM_003449087.1 PREDICTED: Oreochromis niloticus interferon-induced protein 44-like (LOC100710945), mRNA	0.012	0.722
MPF_LOC100690684.1.1	XP_003456227.1 PREDICTED: protein FAM173B-like [Oreochromis niloticus]	0.014	0.721
MPF_contig_030312		0.045	0.719
MPF_LOC101473204.1.1	XM_004569842.1 PREDICTED: Maylandia zebra DNA-binding protein SATB2-like (LOC101473204), transcript variant X3, mRNA	0.050	0.710
MPF_LOC101481610.1.4	XM_004568272.1 PREDICTED: Maylandia zebra tetraspanin-9-like (LOC101481610), transcript variant X4, mRNA	0.018	0.693
MPF_LOC101465583.1.7	XM_004562463.1 PREDICTED: Maylandia zebra histone H3.3-like (LOC101465583), mRNA	0.042	0.662
MPF_LOC100706422.1.5	XM_003455990.1 PREDICTED: Oreochromis niloticus trifunctional purine biosynthetic protein	0.046	0.648

	adenosine-3-like (LOC100706422), mRNA		
MPF_LOC101465489.1.1	XM_004561177.1 PREDICTED: Maylandia zebra disintegrin and metalloproteinase domain-containing protein 12-like (LOC101465489), mRNA	0.026	0.640
MPF_LOC101465885.1.2	XM_004539025.1 PREDICTED: Maylandia zebra UPF0390 protein zgc136864-like (LOC101465885), mRNA	0.009	0.638
MPF_LOC101075645.1.1	XP_003978839.1 PREDICTED: alpha-1-antitrypsin homolog [Takifugu rubripes]	0.023	0.638
MPF_contig_047563		0.030	0.607
MPF_LOC100702553.2.4	XP_003450101.1 PREDICTED: hypothetical protein LOC100702553 [Oreochromis niloticus]	0.014	0.597
MPF_LOC100695025.1.1	XM_003443862.1 PREDICTED: Oreochromis niloticus CTD small phosphatase-like protein 2-A-like, transcript variant 1 (LOC100695025), mRNA	0.036	0.580
MPF_LOC101476898.1.4	XM_004576052.1 PREDICTED: Maylandia zebra microsomal glutathione S-transferase 1-like (LOC101476898), transcript variant X2, mRNA	0.046	0.565
MPF_contig_028528		0.033	0.541
MPF_LOC100705178.1.2	XP_003453898.1 PREDICTED: iron-sulfur cluster assembly enzyme ISCU, mitochondrial-like [Oreochromis niloticus]	0.021	0.516
MPF_contig_004526		0.030	0.515
MPF_LOC101471138.1.1	XM_004565562.1 PREDICTED: Maylandia zebra zinc finger E-box-binding homeobox 1-like (LOC101471138), transcript variant X2, mRNA	0.048	0.464
MPF_contig_010528		0.022	0.409
MPF_LOC101464890.4.8	XM_004575765.1 PREDICTED: Maylandia zebra reticulon-4-like (LOC101464890), transcript variant X11, mRNA	0.037	0.405
MPF_contig_002956		0.004	0.393
MPF_contig_012766		0.043	0.352
Genes up regulated in F1 population			
Phylofish Gene ID	*Gene Description*	*FDR (p-value)*	*Log2 FC*
MPF_contig_002641		0.000	-7.083

MPF_LOC101485591.1.2	XM_004542689.1 PREDICTED: Maylandia zebra period circadian protein homolog 2-like (LOC101485591), transcript variant X1, mRNA	0.000	-5.690
MPF_contig_028308		0.001	-4.877
MPF_LOC100692784.3.3	XP_003440743.1 PREDICTED: iodotyrosine dehalogenase 1-like [Oreochromis niloticus]	0.002	-4.621
MPF_NIBL1.1.1	NIBL1_MOUSE (sp|Q8R1F1) Niban-like protein 1 OS=Mus musculus GN=Fam129b PE=1 SV=2	0.009	-4.047
MPF_LOC100706791.1.1	XM_003459845.1 PREDICTED: Oreochromis niloticus centrosomal protein POC5-like (LOC100706791), mRNA	0.000	-3.462
MPF_LOC101463763.2.2	XM_004538649.1 PREDICTED: Maylandia zebra U2 small nuclear ribonucleoprotein B"-like (LOC101463763), transcript variant X3, mRNA	0.001	-3.452
MPF_LOC100692490.4.4	XM_003457423.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L37a-like (LOC100692490), mRNA	0.000	-3.012
MPF_BT3A2.1.1	BT3A2_HUMAN (sp|P78410) Butyrophilin subfamily 3 member A2 OS=Homo sapiens GN=BTN3A2 PE=1 SV=2	0.007	-2.915
MPF_LOC100698021.1.1	XP_003439831.1 PREDICTED: proproteinase E-like [Oreochromis niloticus]	0.022	-2.833
MPF_LOC101476648.1.1	XM_004538345.1 PREDICTED: Maylandia zebra chondroitin sulfate proteoglycan 4-like (LOC101476648), transcript variant X1, mRNA	0.001	-2.828
MPF_LOC101471584.1.1	XM_004556335.1 PREDICTED: Maylandia zebra cytosolic carboxypeptidase 4-like (LOC101471584), mRNA	0.006	-2.703
MPF_LOC100702327.1.1	XM_003459619.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100702327 (LOC100702327), mRNA	0.006	-2.654
MPF_contig_034129		0.007	-2.644
MPF_LOC101485836.1.2	XM_004559956.1 PREDICTED: Maylandia zebra muscle M-line assembly protein unc-89-like (LOC101485836), transcript variant X1, mRNA	0.001	-2.580
MPF_LOC101485836.2.2	XM_004559956.1 PREDICTED: Maylandia zebra muscle M-line assembly protein unc-89-like (LOC101485836), transcript variant X1, mRNA	0.000	-2.558

MPF_contig_037677		0.000	-2.409
MPF_LOC101472409.2.3	XM_004570385.1 PREDICTED: Maylandia zebra formin-2-like (LOC101472409), mRNA	0.006	-2.399
MPF_contig_037687		0.000	-2.324
MPF_LOC100709771.1.1	XP_003443373.1 PREDICTED: insulin-like growth factor-binding protein 2-B-like [Oreochromis niloticus]	0.042	-2.284
MPF_CXAR.1.5	CXAR_DANRE (sp|Q90Y50) Coxsackievirus and adenovirus receptor homolog OS=Danio rerio GN=cxadr PE=2 SV=1	0.002	-2.272
MPF_LOC101481486.1.2	XM_004563678.1 PREDICTED: Maylandia zebra MARCKS-related protein-like (LOC101481486), mRNA	0.017	-2.235
MPF_LOC101482128.1.2	XM_004574739.1 PREDICTED: Maylandia zebra MARCKS-related protein-like (LOC101482128), mRNA	0.027	-2.191
MPF_LOC101073761.1.2	XP_003972246.1 PREDICTED: malate dehydrogenase, cytoplasmic-like [Takifugu rubripes]	0.002	-2.145
MPF_LOC101486920.1.1	XM_004539290.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12-like (LOC101486920), mRNA	0.008	-2.119
MPF_LOC100690589.3.3	XP_003452783.1 PREDICTED: hypothetical protein LOC100690589 [Oreochromis niloticus]	0.002	-2.070
MPF_LOC100705145.1.1	XM_003445077.1 PREDICTED: Oreochromis niloticus phenylserine dehydratase-like (LOC100705145), mRNA	0.000	-2.041
MPF_LOC101483197.2.8	XM_004575580.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12-like (LOC101483197), mRNA	0.007	-2.017
MPF_LOC101479129.2.2	XM_004572164.1 PREDICTED: Maylandia zebra collagen alpha-3(VI) chain-like (LOC101479129), mRNA	0.025	-2.009
MPF_LOC101475558.1.3	XM_004575961.1 PREDICTED: Maylandia zebra pleckstrin homology domain-containing family A member 6-like (LOC101475558), mRNA	0.002	-1.978
MPF_LOC100693266.1.1	XP_003449905.1 PREDICTED: N-lysine methyltransferase SMYD2-like [Oreochromis niloticus]	0.001	-1.954

MPF_contig_002474		0.002	-1.901
MPF_LOC101467899.2.2	XM_004576429.1 PREDICTED: Maylandia zebra uro-adherence factor A-like (LOC101467899), mRNA	0.033	-1.874
MPF_LOC100700049.1.1	XM_003456130.1 PREDICTED: Oreochromis niloticus phosphatidylinositol-glycan biosynthesis class W protein-like (LOC100700049), mRNA	0.022	-1.786
MPF_LOC100693306.12.13	XP_003458501.1 PREDICTED: protein NLRC3-like [Oreochromis niloticus]	0.009	-1.783
MPF_LOC100707240.2.2	XP_003459468.1 PREDICTED: ATPase family AAA domain-containing protein 2-like [Oreochromis niloticus]	0.009	-1.755
MPF_LOC101471998.1.1	XM_004540134.1 PREDICTED: Maylandia zebra MFS-type transporter SLC18B1-like (LOC101471998), mRNA	0.000	-1.732
MPF_LOC101468524.2.2	XM_004540307.1 PREDICTED: Maylandia zebra transcription factor Sp3-like (LOC101468524), transcript variant X2, mRNA	0.022	-1.714
MPF_LOC101169532.11.45	XP_004070110.1 PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Oryzias latipes]	0.001	-1.698
MPF_LOC101477465.2.3	XM_004574488.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 3-like (LOC101477465), mRNA	0.000	-1.691
MPF_LOC101167235.2.2	XP_004078642.1 PREDICTED: putative ferric-chelate reductase 1-like [Oryzias latipes]	0.009	-1.678
MPF_contig_044670		0.000	-1.674
MPF_ATAD2.2.2	ATAD2_PONAB (sp|Q5RDX4) ATPase family AAA domain-containing protein 2 OS=Pongo abelii GN=ATAD2 PE=2 SV=1	0.004	-1.669
MPF_LOC100690779.1.2	XM_003457973.1 PREDICTED: Oreochromis niloticus formimidoyltransferase-cyclodeaminase-like (LOC100690779), mRNA	0.035	-1.659
MPF_LOC100693306.3.13	XP_003458501.1 PREDICTED: protein NLRC3-like [Oreochromis niloticus]	0.015	-1.641
MPF_LOC101472196.2.3	XM_004543012.1 PREDICTED: Maylandia zebra obscurin-like (LOC101472196), mRNA	0.003	-1.630
MPF_LOC101482434.3.5	XM_004575658.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101482434), mRNA	0.002	-1.627

MPF_contig_017105		0.001	-1.617
MPF_LOC100705728.13.17	XM_003459563.1 PREDICTED: Oreochromis niloticus zinc finger protein RFP-like (LOC100705728), mRNA	0.036	-1.603
MPF_LOC101482877.1.1	XM_004569602.1 PREDICTED: Maylandia zebra neuroblast differentiation-associated protein AHNAK-like (LOC101482877), transcript variant X1, mRNA	0.042	-1.602
MPF_LOC101160029.2.2	XM_004081671.1 PREDICTED: Oryzias latipes uncharacterized LOC101160029 (LOC101160029), mRNA	0.022	-1.591
MPF_LOC100706439.1.2	XM_003459417.1 PREDICTED: Oreochromis niloticus kinesin-like protein KIF1C-like (LOC100706439), mRNA	0.009	-1.580
MPF_LOC101470765.1.1	XM_004542729.1 PREDICTED: Maylandia zebra protein SSXT-like (LOC101470765), transcript variant X4, mRNA	0.001	-1.568
MPF_contig_033809		0.000	-1.555
MPF_LOC101480481.1.1	XM_004573155.1 PREDICTED: Maylandia zebra DNA repair protein XRCC3-like (LOC101480481), transcript variant X2, mRNA	0.049	-1.544
MPF_LOC101481352.2.3	XM_004574885.1 PREDICTED: Maylandia zebra kinesin-like protein KIF1C-like (LOC101481352), transcript variant X2, mRNA	0.009	-1.542
MPF_LOC101472196.3.3	XM_004543012.1 PREDICTED: Maylandia zebra obscurin-like (LOC101472196), mRNA	0.002	-1.535
MPF_ZC3HD.1.3	ZC3HD_HUMAN (sp|Q5T200) Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens GN=ZC3H13 PE=1 SV=1	0.048	-1.531
MPF_PTPRT.1.1	XM_003447691.1 PREDICTED: Oreochromis niloticus protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA	0.001	-1.530
MPF_AHNK.15.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.017	-1.528
MPF_contig_049067		0.035	-1.524
MPF_LOC101471516.1.1	XM_004565382.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase OSR1-like (LOC101471516), mRNA	0.004	-1.495

MPF_LOC101167377.1.1	XP_004073716.1 PREDICTED: snRNA-activating protein complex subunit 1-like [Oryzias latipes]	0.002	-1.456
MPF_LOC101465583.5.7	XM_004562463.1 PREDICTED: Maylandia zebra histone H3.3-like (LOC101465583), mRNA	0.006	-1.386
MPF_LOC100701598.3.6	XM_003458636.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100701598), mRNA	0.013	-1.385
MPF_LOC101483197.6.8	XM_004575580.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12-like (LOC101483197), mRNA	0.009	-1.366
MPF_RU17.1.1	RU17_DICDI (sp|Q55FQ0) U1 small nuclear ribonucleoprotein 70 kDa OS=Dictyostelium discoideum GN=snrnp70 PE=3 SV=1	0.004	-1.347
MPF_SC4AB.3.3	SC4AB_DANRE (sp|Q20JQ7) Sodium channel protein type 4 subunit alpha B OS=Danio rerio GN=scn4ab PE=2 SV=1	0.042	-1.341
MPF_contig_042113	XM_004569199.1 PREDICTED: Maylandia zebra eyes absent homolog 3-like (LOC101469709), transcript variant X1, mRNA	0.007	-1.339
MPF_LOC101469709.1.2	XM_004569200.1 PREDICTED: Maylandia zebra eyes absent homolog 3-like (LOC101469709), transcript variant X2, mRNA	0.007	-1.326
MPF_contig_038580		0.002	-1.324
MPF_LOC100712218.1.1	XM_003452499.1 PREDICTED: Oreochromis niloticus potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4-like (LOC100712218), mRNA	0.002	-1.321
MPF_LOC100703514.1.1	XM_003441827.1 PREDICTED: Oreochromis niloticus bifunctional coenzyme A synthase-like (LOC100703514), mRNA	0.018	-1.318
MPF_contig_035430		0.027	-1.300
MPF_LOC101474771.1.1	XM_004556969.1 PREDICTED: Maylandia zebra nuclear pore complex protein Nup98-Nup96-like (LOC101474771), mRNA	0.020	-1.293
MPF_LOC101476997.1.2	XM_004552000.1 PREDICTED: Maylandia zebra microtubule-associated protein futsch-like (LOC101476997), mRNA	0.032	-1.259
MPF_contig_003893		0.038	-1.241
MPF_LOC100701791.2.9	XM_003459617.1 PREDICTED: Oreochromis niloticus class I histocompatibility antigen, F10	0.045	-1.238

	alpha chain-like (LOC100701791), mRNA		
MPF_LOC101464019.2.2	XM_004550084.1 PREDICTED: Maylandia zebra protocadherin-16-like (LOC101464019), mRNA	0.043	-1.235
MPF_LOC101477437.2.3	XM_004545533.1 PREDICTED: Maylandia zebra uncharacterized LOC101477437 (LOC101477437), mRNA	0.010	-1.227
MPF_contig_044426		0.021	-1.224
MPF_LOC101470901.4.10	XM_004574121.1 PREDICTED: Maylandia zebra 40S ribosomal protein S3-like (LOC101470901), mRNA	0.017	-1.223
MPF_contig_034467	XM_004544675.1 PREDICTED: Maylandia zebra CAP-Gly domain-containing linker protein 1-like (LOC101463599), transcript variant X1, mRNA	0.027	-1.219
MPF_contig_019111		0.003	-1.200
MPF_contig_005001		0.012	-1.190
MPF_LOC101469041.3.4	XM_004566363.1 PREDICTED: Maylandia zebra CREB-regulated transcription coactivator 3-like (LOC101469041), transcript variant X4, mRNA	0.035	-1.185
MPF_LOC101468504.2.2	XM_004556227.1 PREDICTED: Maylandia zebra transmembrane protein 170A-like (LOC101468504), mRNA	0.035	-1.181
MPF_LOC100702771.1.1	XP_003459231.1 PREDICTED: WD repeat-containing protein 78-like [Oreochromis niloticus]	0.007	-1.156
MPF_LOC101475777.3.3	XM_004539250.1 PREDICTED: Maylandia zebra dual specificity mitogen-activated protein kinase kinase 7-like (LOC101475777), transcript variant X2, mRNA	0.037	-1.152
MPF_LOC101475192.1.1	XM_004541444.1 PREDICTED: Maylandia zebra probable palmitoyltransferase ZDHHC1-like (LOC101475192), mRNA	0.039	-1.127
MPF_contig_001047	XM_004559756.1 PREDICTED: Maylandia zebra vitrin-like (LOC101482458), transcript variant X1, mRNA	0.001	-1.122
MPF_LOC101482619.1.3	XM_004556458.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase TAO2-like (LOC101482619), transcript variant X2, mRNA	0.009	-1.111
MPF_LOC101161312.2.4	XP_004071113.1 PREDICTED: tumor necrosis factor receptor superfamily member 5-like [Oryzias latipes]	0.010	-1.107

MPF_contig_027614		0.002	-1.106
MPF_LOC100705413.1.1	XP_003445040.1 PREDICTED: protein piccolo-like [Oreochromis niloticus]	0.042	-1.102
MPF_contig_043409	XM_004544675.1 PREDICTED: Maylandia zebra CAP-Gly domain-containing linker protein 1-like (LOC101463599), transcript variant X1, mRNA	0.048	-1.096
MPF_LOC101482458.3.3	XM_004559758.1 PREDICTED: Maylandia zebra vitrin-like (LOC101482458), transcript variant X3, mRNA	0.002	-1.092
MPF_LOC100703705.5.14	XP_003444284.1 PREDICTED: tumor necrosis factor receptor superfamily member 14-like [Oreochromis niloticus]	0.009	-1.089
MPF_LOC101483148.1.1	XM_004567251.1 PREDICTED: Maylandia zebra MAGUK p55 subfamily member 7-like (LOC101483148), mRNA	0.037	-1.089
MPF_contig_036824		0.006	-1.074
MPF_LOC101463599.2.2	XM_004544676.1 PREDICTED: Maylandia zebra CAP-Gly domain-containing linker protein 1-like (LOC101463599), transcript variant X2, mRNA	0.035	-1.074
MPF_contig_024444		0.005	-1.073
MPF_LOC101470901.6.10	XM_004574121.1 PREDICTED: Maylandia zebra 40S ribosomal protein S3-like (LOC101470901), mRNA	0.045	-1.072
MPF_contig_038149	XM_004554086.1 PREDICTED: Maylandia zebra nuclease-sensitive element-binding protein 1-like (LOC101465558), transcript variant X3, mRNA	0.002	-1.068
MPF_contig_026589		0.020	-1.068
MPF_LOC101476322.2.2	XM_004550884.1 PREDICTED: Maylandia zebra ETS domain-containing transcription factor ERF-like (LOC101476322), mRNA	0.037	-1.061
MPF_LOC101466982.2.2	XM_004574455.1 PREDICTED: Maylandia zebra pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial-like (LOC101466982), mRNA	0.041	-1.058
MPF_SELMODRAFT_443953.1.1	XP_002978779.1 hypothetical protein SELMODRAFT_443953 [Selaginella moellendorffii]	0.001	-1.030
MPF_LOC101466982.1.2	XM_004574455.1 PREDICTED: Maylandia zebra pyruvate dehydrogenase E1 component subunit alpha, somatic form,	0.031	-1.028

	mitochondrial-like (LOC101466982), mRNA		
MPF_LOC101463719.6.12	XM_004549308.1 PREDICTED: Maylandia zebra 40S ribosomal protein S3a-like (LOC101463719), mRNA	0.008	-1.015
MPF_MUC14A.1.1	NP_727928.3 mucin 14A [Drosophila melanogaster]	0.041	-1.012
MPF_LOC101479727.6.6	XM_004576138.1 PREDICTED: Maylandia zebra uncharacterized LOC101479727 (LOC101479727), mRNA	0.014	-1.010
MPF_LOC100933241.11.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.024	-1.009
MPF_LOC100693188.1.1	XM_003453806.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693188 (LOC100693188), mRNA	0.009	-1.003
MPF_LOC100699383.1.6	XM_003445310.1 PREDICTED: Oreochromis niloticus translationally-controlled tumor protein homolog (LOC100699383), mRNA	0.005	-1.002
MPF_G6PCA.2.1.1	NP_001157278.1 im:6895556 [Danio rerio]	0.022	-0.996
MPF_LOC101076067.1.1	XP_003972813.1 PREDICTED: src substrate protein p85-like [Takifugu rubripes]	0.000	-0.995
MPF_LOC101467026.1.1	XM_004563273.1 PREDICTED: Maylandia zebra X-linked interleukin-1 receptor accessory protein-like 2-like (LOC101467026), mRNA	0.026	-0.983
MPF_contig_008498		0.003	-0.979
MPF_LOC100712073.1.1	XM_003439241.1 PREDICTED: Oreochromis niloticus 39S ribosomal protein L15, mitochondrial-like (LOC100712073), mRNA	0.002	-0.975
MPF_CCDC57.1.2	NP_001188491.1 coiled-coil domain containing 57 [Danio rerio]	0.005	-0.974
MPF_LOC100697331.4.4	XM_003444214.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100697331 (LOC100697331), mRNA	0.002	-0.961
MPF_contig_036627		0.001	-0.956
MPF_LOC100695404.1.1	XM_003448451.1 PREDICTED: Oreochromis niloticus PDZ domain-containing protein GIPC1-like (LOC100695404), mRNA	0.003	-0.944
MPF_REST.2.2	REST_DANRE (sp|Q2EI20) RE1-silencing transcription factor OS=Danio rerio GN=rest PE=2 SV=1	0.022	-0.943

MPF_contig_024773		0.004	-0.938
MPF_contig_028987		0.029	-0.937
MPF_LOC100696573.2.4	XM_003458226.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100696573), mRNA	0.005	-0.936
MPF_LOC101472023.1.2	XM_004546375.1 PREDICTED: Maylandia zebra mitochondrial import inner membrane translocase subunit Tim17-B-like (LOC101472023), mRNA	0.004	-0.935
MPF_contig_019268	XM_004554085.1 PREDICTED: Maylandia zebra nuclease-sensitive element-binding protein 1-like (LOC101465558), transcript variant X2, mRNA	0.034	-0.922
MPF_contig_032727		0.024	-0.916
MPF_LOC101468599.1.1	XM_004560177.1 PREDICTED: Maylandia zebra uncharacterized LOC101468599 (LOC101468599), mRNA	0.014	-0.913
MPF_LOC100698539.1.1	XM_003459086.1 PREDICTED: Oreochromis niloticus nucleolar protein 7-like (LOC100698539), mRNA	0.021	-0.913
MPF_LOC101465566.2.2	XM_004556315.1 PREDICTED: Maylandia zebra hepatocyte growth factor receptor-like (LOC101465566), transcript variant X2, mRNA	0.032	-0.904
MPF_LOC101474183.2.2	XM_004569039.1 PREDICTED: Maylandia zebra cell adhesion molecule 4-like (LOC101474183), mRNA	0.035	-0.902
MPF_contig_045124		0.016	-0.902
MPF_contig_045852	XM_004566538.1 PREDICTED: Maylandia zebra ral GTPase-activating protein subunit alpha-2-like (LOC101468264), transcript variant X2, mRNA	0.016	-0.899
MPF_LOC101474742.1.1	XM_004570733.1 PREDICTED: Maylandia zebra synaptonemal complex protein 2-like (LOC101474742), mRNA	0.033	-0.898
MPF_contig_002686		0.022	-0.897
MPF_contig_026772	XM_004569431.1 PREDICTED: Maylandia zebra nucleolar protein 7-like (LOC101483852), transcript variant X1, mRNA	0.037	-0.894
MPF_CCDC57.2.2	NP_001188491.1 coiled-coil domain containing 57 [Danio rerio]	0.003	-0.874
MPF_contig_041411		0.047	-0.865
MPF_contig_026051		0.018	-0.841

MPF_LOC100698929.2.2	XM_003442472.1 PREDICTED: Oreochromis niloticus E3 ubiquitin-protein ligase RNF25-like (LOC100698929), mRNA	0.028	-0.840
MPF_LOC101463583.1.1	XM_004542143.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase PAK 7-like (LOC101463583), transcript variant X2, mRNA	0.032	-0.826
MPF_contig_046848		0.037	-0.819
MPF_LOC101473264.2.2	XM_004559813.1 PREDICTED: Maylandia zebra casein kinase II subunit alpha-like (LOC101473264), transcript variant X1, mRNA	0.042	-0.816
MPF_LOC101476812.1.3	XM_004575484.1 PREDICTED: Maylandia zebra DNA-directed RNA polymerase III subunit RPC8-like (LOC101476812), mRNA	0.013	-0.816
MPF_contig_007520	XM_004542664.1 PREDICTED: Maylandia zebra kinesin-like protein KIF1A-like (LOC101479103), transcript variant X2, mRNA	0.022	-0.816
MPF_contig_005437	XM_004542664.1 PREDICTED: Maylandia zebra kinesin-like protein KIF1A-like (LOC101479103), transcript variant X2, mRNA	0.022	-0.809
MPF_contig_047310		0.002	-0.788
MPF_LOC101167402.1.2	XM_004080364.1 PREDICTED: Oryzias latipes uncharacterized LOC101167402 (LOC101167402), mRNA	0.014	-0.784
MPF_LOC101475525.4.5	XM_004547130.1 PREDICTED: Maylandia zebra RING finger protein 165-like (LOC101475525), transcript variant X5, mRNA	0.025	-0.784
MPF_IFIT5.4.9	NM_001142188.1 Xenopus (Silurana) tropicalis interferon-induced protein with tetratricopeptide repeats 5 (ifit5), mRNA gb|BC168560.1| Xenopus tropicalis cDNA clone MGC:184922 IMAGE:7678513, complete cds	0.001	-0.760
MPF_contig_014481		0.021	-0.754
MPF_LOC101474701.1.2	XM_004555778.1 PREDICTED: Maylandia zebra histone H2A.V-like (LOC101474701), mRNA	0.011	-0.754
MPF_contig_027257		0.022	-0.753
MPF_LOC101073532.1.2	XM_003970121.1 PREDICTED: Takifugu rubripes mid1-interacting protein 1-like (LOC101073532), mRNA	0.013	-0.751

MPF_contig_029749		0.005	-0.743
MPF_BTNL2.1.7	BTNL2_HUMAN (sp|Q9UIR0) Butyrophilin-like protein 2 OS=Homo sapiens GN=BTNL2 PE=2 SV=1	0.025	-0.743
MPF_LOC101158032.1.2	XM_004073072.1 PREDICTED: Oryzias latipes ubiquitin-conjugating enzyme E2 A-like, transcript variant 1 (LOC101158032), mRNA	0.033	-0.733
MPF_contig_037127	XM_004550664.1 PREDICTED: Maylandia zebra afadin-like (LOC101467084), transcript variant X1, mRNA	0.030	-0.726
MPF_LOC100699424.5.7	XM_003455807.1 PREDICTED: Oreochromis niloticus deleted in malignant brain tumors 1 protein-like (LOC100699424), mRNA	0.046	-0.709
MPF_contig_025802		0.020	-0.707
MPF_contig_005296		0.046	-0.699
MPF_LOC101477400.4.4	XM_004538536.1 PREDICTED: Maylandia zebra cyclin-G2-like (LOC101477400), mRNA	0.029	-0.679
MPF_contig_036844		0.042	-0.678
MPF_contig_032700		0.027	-0.671
MPF_contig_004690	XM_004556611.1 PREDICTED: Maylandia zebra calcium/calmodulin-dependent protein kinase type II subunit gamma-like (LOC101474026), transcript variant X8, mRNA	0.031	-0.665
MPF_contig_044256		0.035	-0.657
MPF_LOC101484059.1.1	XM_004553703.1 PREDICTED: Maylandia zebra spermatogenesis-associated protein 5-like (LOC101484059), mRNA	0.014	-0.650
MPF_LOC101479656.2.2	XM_004540064.1 PREDICTED: Maylandia zebra beta-taxilin-like (LOC101479656), mRNA	0.032	-0.644
MPF_contig_038890		0.041	-0.641
MPF_contig_014987		0.040	-0.632
MPF_LOC101469710.1.2	XM_004569651.1 PREDICTED: Maylandia zebra DCN1-like protein 5-like (LOC101469710), transcript variant X5, mRNA	0.033	-0.614
MPF_LOC101077981.1.2	XP_003976814.1 PREDICTED: h-2 class II histocompatibility antigen, I-A beta chain-like [Takifugu rubripes]	0.026	-0.608
MPF_contig_000130		0.014	-0.604
MPF_LOC100694829.1.1	XM_003458851.1 PREDICTED: Oreochromis niloticus hypothetical	0.017	-0.603

	protein LOC100694829 (LOC100694829), mRNA		
MPF_THAP1.2.4	THAP1_PONAB (sp|Q5RCE4) THAP domain-containing protein 1 OS=Pongo abelii GN=THAP1 PE=2 SV=1	0.035	-0.598
MPF_LIN1.6.14	LIN1_NYCCO (sp|P08548) LINE-1 reverse transcriptase homolog OS=Nycticebus coucang PE=1 SV=1	0.015	-0.595
MPF_contig_005684		0.033	-0.572
MPF_LOC101078877.1.1	XP_003976004.1 PREDICTED: mitochondrial 2-oxoglutarate/malate carrier protein-like [Takifugu rubripes]	0.046	-0.563
MPF_LOC101484158.1.1	XM_004537991.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase TRIM32-like (LOC101484158), transcript variant X1, mRNA	0.050	-0.526
MPF_contig_006673		0.017	-0.521
MPF_LOC101481611.1.2	XM_004544911.1 PREDICTED: Maylandia zebra elongation factor Ts, mitochondrial-like (LOC101481611), mRNA	0.030	-0.510
MPF_LOC100699959.1.1	XP_003455537.1 PREDICTED: noelin-like [Oreochromis niloticus]	0.039	-0.478

Supplementary Table 11. **Differentially expressed genes listed in the same order as they appear in the clustering analysis.** PhyloFish gene ID is shown for each gene and the numbers 1-358 correspond to their position in the figure resulting from clustering analysis.

Due to the long size of this table, it can be found at the end of this document in the digital version only.

Supplementary Table 12**. F7+ Gene Ontology list.** PhyloFish gene ID, gene description, Gene Ontology Category, ID and Terms represented in the eggs transcriptome of the F7+ population. GO Categories are: P = Biological Process, F = Molecular Function and C = Cellular Component.

Due to the long size of this table, it can be found at the end of this document in the digital version only.

Supplementary Table 13**. F1 Gene Ontology list.** PhyloFish gene ID, gene description, Gene Ontology Category, ID and Terms represented in the eggs transcriptome of the F1 population. GO Categories are: P = Biological Process, F = Molecular Function and C = Cellular Component.

Due to the long size of this table, it can be found at the end of this document in the digital version only.

Supplementary Table 14**. Genes belonging to the enriched term found in the overrepresentation analysis.** PhyloFish gene ID, gene description, Uniprot protein and gene names, Uniprot Acession Number, False Discovery Rate (p-value), Regulation and log(2)FC of the genes represented in enriched function affected in the transcriptome of the eggs belonging to F7+ and F1 population.

Phylofish Gene ID	Gene Description	Uniprot Protein Name	Uniprot Gene Name	Uniprot Accession	FDR (p-value)	Regulation	Log2 FC
MPF_BT2A3.1.1	BT2A3_HUMAN (sp|Q96KV6) Putative butyrophilin subfamily 2 member A3 OS=Homo sapiens GN=BTN2A3P PE=5 SV=2	Putative butyrophilin subfamily 2 member A3	BTN2A3P	Q96KV6	0.012	up in F7+	1.310596
MPF_BT3A2.1.1	BT3A2_HUMAN (sp|P78410) Butyrophilin subfamily 3 member A2 OS=Homo sapiens GN=BTN3A2 PE=1 SV=2	Butyrophilin subfamily 3 member A2	BTN3A2	P78410	0.007	down in F7+	-2.91508
MPF_BTNL2.1.7	BTNL2_HUMAN (sp|Q9UIR0) Butyrophilin-like protein 2 OS=Homo sapiens GN=BTNL2 PE=2 SV=1	Butyrophilin-like protein 2	BTNL2	Q9UIR0	0.025	down in F7+	-0.74259
MPF_LOC100697304.1.3	XP_003458513.1 PREDICTED: hypothetical protein LOC100697304 [Oreochromis niloticus]	Butyrophilin subfamily 1 member A1	BTN1A1	Q13410	0.020	up in F7+	2.386402
MPF_LOC101174554.1.1	XP_004084158.1 PREDICTED: V-set domain-containing T-cell activation	V-set domain-containing T-cell activation inhibitor 1	VTCN1	Q7Z7D3	0.035	up in F7+	2.666751

	inhibitor 1-like [Oryzias latipes]						
MPF_LOC100710945.1.1	XM_003449087.1 PREDICTED: Oreochromis niloticus interferon-induced protein 44-like (LOC100710945), mRNA	Interferon-induced protein 44-like	IFI44L	Q53G44	0.012	up in F7+	0.722237
MPF_LOC100701791.2.9	XM_003459617.1 PREDICTED: Oreochromis niloticus class I histocompatibility antigen, F10 alpha chain-like (LOC100701791), mRNA	HLA class I histocompatibility antigen, alpha chain F	HLA-F	P30511	0.045	down in F7+	-1.2377
MPF_LOC100690589.3.3	XP_003452783.1 PREDICTED: hypothetical protein LOC100690589 [Oreochromis niloticus]	Major histocompatibility complex class I-related gene protein	MR1	Q95460	0.002	down in F7+	-2.07028
MPF_LOC100703705.5.14	XP_003444284.1 PREDICTED: tumor necrosis factor receptor superfamily member 14-like [Oreochromis niloticus]	Tumor necrosis factor receptor superfamily member 14	TNFRSF14	Q92956	0.009	down in F7+	-1.08907

Chapter 3 recapitulation sheet

(DOMESTICATION AND EGGS’ TRANSCRIPTOME)

Specific objectives

- Compare the reproductive cycle and performance of females having different histories of domestication (F1 vs. F7+)
- Evaluate eggs’ transcriptomic profiles and their potential relationship with females’ domestication level.

Main results

- F1 females were precocious spawners than F7+ ones
- F1 females produces eggs of better quality
- Gene expression pattern was clearly different between populations (more than 300 DEG)
- Genes related with immune system were differentially expressed between populations
- *mex3b*, *hace1*, a gene coding for an *uncharacterized protein* and *per2* were identified as new potential maternal-effect genes

Next, in General Discussion:

- Based on the current literature and in the results obtained from the previous chapters, we will point some difficulties faced during the work and also make some suggestions for future studies on fish egg quality vs. eggs’ transcriptomic content.

VII. General discussion

My PhD work allowed identifying a strong relationship between eggs transcriptomic content and embryonic early development in Eurasian perch. In addition, eggs' mRNA content will be the unique source of transcripts to allow normal embryonic developmet until zygotic genome activation (ZGA). As a consequence, a first question that was raised concerned ZGA in this species. From its answer, we will be able to point the moment until when the identified maternal-effect genes would be exclusively controlling embryonic development and allow distinguish between maternal and zygotic transcripts. In addition, we made the hypothesis that low survivals observed already at 24 hpf for some spawn, could result from issues during the maternal to zygotic transition (MZT). We made this reasoning because ZGA is needed for gastrulation in other species and gastrulation starts about 24 hpf in Eurasian perch (Alix et al., 2015). In order to allow future studies to investigate these questions, it became important first to characterize the MZT in this species. In this context, I started investigating and the preliminary results concerning this transition in Eurasian perch will be presented in the following.

1. Maternal control of embryonic development in Eurasian perch

Under the perspective of better understand the transcriptomic dynamic during early embryonic development in Eurasian perch, I begun to compare the expression of known-maternal and -zygotic zebrafish genes in Eurasian perch embryos at different developmental stages. Eurasian perch and zebrafish belong to different phylogenetic groups among the teleostei fish and still they share some similarities during early development. Comparing the timing during their early development, zebrafish will develop faster, the mid-blastula transition (MBT) will happen at the tenth cleavage cycle (3 hpf), followed by gastrulation [about 4.4 hpf; (Kimmel et al., 1995)]. In Eurasian perch, MBT starts from the 128-cells stage (about 9 hpf) and gastrulation at 24 hpf (Alix et al., 2015). Despite of this timing differences, morphological developmental features are quite similar between both species. Concerning ZGA, increase of zygotic transcripts occurs before gastrulation in zebrafish (Harvey et al., 2013). Thus we investigated whether this particular genomic feature would be comparable between this species.

I studied by RT-qPCR the gene expression pattern of four zebrafish known-maternal (*ccnb1, plk1, eml2* and *tbp*) and three known-zygotic (*klf4, id1* and *foxa3*) genes in embryos of Eurasian perch every 2 hours from 5 to 33 hpf (Material and Methods employed are described in Annex section; Figure 31A).

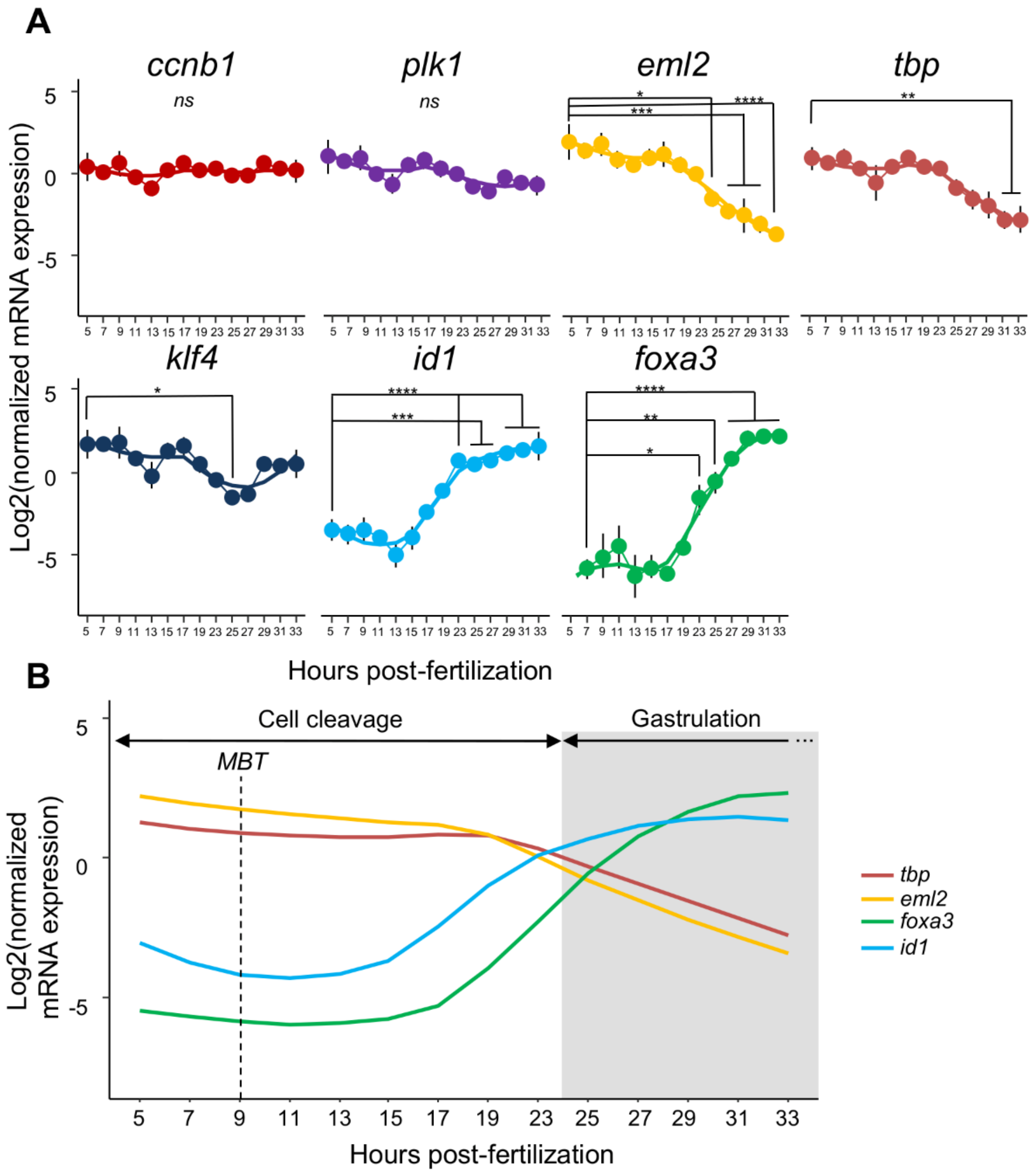


Figure 31. Gene expression patterns of the zebrafish maternal and zygotic genes on Eurasian perch (*Perca fluviatilis*) embryos from 5hpf to 33 hpf. Genes were chosen because they were known to be either maternal or zygotic in zebrafish (Aanes et al., 2011; Harvey et al., 2013; Lee et al., 2013; Vesterlund et al., 2011). (A) Individual expression profile of the six genes tested. Significance levels are represented as follows: *, p = 0.05–0.01; **, P = 0.01–0.001; ***, P = 0.001–0.0001; and ****, P < 0.0001 and were obtained using a linear mixed effects analysis of the relationship between gene expression levels and sampling times. Time points corresponded to the fixed effect, while females constituted the random effect. P-values were obtained through pairwise t-test comparisons between time points followed by a Bonferroni correction. They always represent differences between 5 or 7hpf (for foxa3) and the other time points. ns = non-significant. (B) Superposition of the expression profile of the genes with the indication of MBT, cell cleavage and gastrulation (Alix et al., 2015). Maternal genes: *ccnb1*, *plk1*, *eml2* and *tbp*. zygotic genes: *klf4, id1* and *foxa3*. MBT: mid-blastula transition.

Ccnb1 and *plk1* presented an expression profile quite stable through the development of perch embryos. A decrease of abundance of the maternal genes *eml2* and *tbp* is seen from the first time point evaluated (5hpf), however, significant differences are seen from 25 and 31 hpf, respectively. *Klf4* is a zygotic gene in zebrafish and presented a closely to maternal gene profile in the first 13 hpf. In the following, it presented a slight increase of expression until 19 hpf, then a decrease until 25 hpf and new increase from 27hpf. Expression profiles comparable with those in zebrafish were observed for *id1* and *foxa3* and statistical differences appeared from 23 hpf for both. For *foxa3*, the expression in the first time point (5 hpf) was under detection for three samples, thus 7 hpf was used instead to present the results. Four of the seven genes tested showed pattern of expression closer to maternal and zygotic profiles in perch, as in zebrafish (Figure 31B). The genes *eml2* and *tbp* belong to the maternal pool and *foxa3* and *id1* are detected more likely before ZGA and after gastrulation for both, zebrafish and Eurasian perch.

In these preliminary results we evidenced some divergences and correspondences between Eurasian perch and zebrafish. *ccnb1* and *plk1* did not expressed in a profile expected for the maternal genes in Eurasian perch and *klf4* presented an unclear pattern of expression (Figure 31A). In agreement with the dynamic presented in other vertebrates, we detected an increase of the zygotic genes after MBT (9 hpf) and before gastrulation (24 hpf; Figure 31B). It suggests that some mechanisms leading to ZGA may be conserved between Eurasian perch and other species. Because the zygotic genes detected from 23 hpf, right before the gastrulation, the hypothesis of a connection between high early mortality and ZGA impairments still persists.

Another interesting approach of investigation could be to determine also the localization of other maternal genes and in the following, test the localization and expression of these genes in spawn of variable quality. Changes in the expected expression pattern or in their localization during embryos development according to the eggs' quality, may be one more support that issues in the MZT can contribute for high mortality in early developmental stages. This may help solving impairments by increasing understanding of these events possibly given the high early mortality phenotype described in aquaculture, and confirmed in this study.

The expression profiles that coincided or not between Eurasian perch and zebrafish reinforce that extrapolations between species concerning early development are not always possible. In order to be able to properly discuss similarities and differences between species, many sources of variation in studies should be carefully pondered. For this reason, some of them will be discussed in the following.

2. Sources of eggs' transcriptomic variations

2.1. *Methodological factors potentially affecting transcriptomic results*

2.1.1. Methods employed to assess egg quality

Among many offspring characteristics that are affected by maternal factors, a major and complex one is their ability to survive until some steps during their early life relying on eggs content. For this reason, the relationship between eggs' content and embryos early survival are commonly made and implies egg quality. Our quality study (**Chapter 2**) proved that, as for other species, some aspects of Eurasian perch eggs' quality are related to their mRNA profile. We also demonstrated that the way to assess egg quality influences the results, since assessing quality considering earlier stages and each criterion individually resulted in differentially expressed genes (DEG) between high and low-quality groups. In our study, only one gene, CD68, was up-regulated in bad quality eggs, regardless the methods applied to assess their quality.

In Table 13, I summarized studies connecting egg quality and global transcriptomic modifications. It illutrastes the high variability found in this kind of studies concerning the number of DEG obtained, criteria/developmental stages employed to assess egg quality and thresholds/rates limiting high and low-quality groups, intra- and inter-species. The differences in number and kind of DEG detected by other studies, in comparison with ours, may also reflect the methods employed to assess egg quality. For example, while studying egg quality in sea bass (*Dicentrarchus labrax*), authors used 60% as a threshold to define egg quality and fertilization rate as criteria. They pointed that the difference between the spawn presenting the highest fertilization rate in the lower quality group and the one presenting the lowest rate in the high quality group was of only 10% (Żarski et al., 2017a). These spawn are more likely to have produced "middle performance". Thus, they could have been classified as intermediate quality and it might have retourned more costrastaded results in gene expression profiles between high vs. low quality groups. We showed in our results that groups of spawn presenting intermediate quality did not present characteristic profiles of gene expression in eggs when compared to high quality groups, in Eurasian perch (*P. fluviatilis*). In agreement with our results concerning intermediate egg quality groups, Ma et al. (Ma et al., 2019), while working with rainbow trout (*Oncorhynchus mykiss*), characterized eggs associated to a survival rate until eyed stage >30% and <50% as an intermediate egg quality group and observed that they presented a transcriptomic profile closer to the one saw in their high quality group (>80%), in comparison to a low quality group (<5%) that presented clear transcriptomic differences. It is possible to hypothesize that lowest quality groups, due to their intrinsic deregulations, contribute the most to the differences found at the transcriptomic level. Additionally, it reinforces the idea that extreme groups of quality may be more reliable to study variations in the transcriptomic profile.

Table 13.Summary of transcriptomic studies comparing high vs. low quality eggs‡.

Species	Criteria[1]	Developmental stage[2]	Thresholds[3]	RNA	#DEG[4]	Stage analyzed	Reference
Rainbow trout (*Oncorhynchus mykiss*)	Absence of abnormalities until yolk-sac resorption	Alevins	>90% and <37%	Total	31	Unfertilized eggs	(Bonnet et al., 2007a)
Striped bass (*Morone saxatilis*)	Survival at 4hpf	Mid-blastula	>50% and <30%	Total	233	Ovarian biopsy (+95% were oocytes)	(Chapman et al., 2014)
Atlantic halibut (*Hippoglossus hippoglossus*)	Hatching rate (340hpf)	Hatched larvae	≥86% and ≤7%	Total	20	8-cell stage	(Mommens et al., 2014)
Atlantic cod (*Gadus morhua*)	Survival at 7dpf	Segmentation stage	~84% and <10%	Total	43	2-cell stage	(Rise et al., 2014)
Sea bass (*Dicentrarchus labrax*)	Fertilization rate (3hpf)	4-cell stage	>60% and <60%	Total	39	Unfertilized eggs	(Żarski et al., 2017a)
Zebrafish (*Danio rerio*)	Survival at 48hpf	Hatching period (long-pec)	>98% and <38%	Total	66	1-cell stage	(Cheung et al., 2019)
Rainbow trout (*Oncorhynchus mykiss*)	Survival at 25dpf	Eyed stage	>80% and <5%	Poly(A) retained / rRNA removed	945 / 1	Unfertilized eggs	(Ma et al., 2019)
Eurasian perch (*Perca fluviatilis*)	Survival at 24hpf	Beginning of gastrulation (<30% epiboly)	>90% and <45%	Total	671	Unfertilized eggs	*This study**
			>80% and <45%		11		
	Survival at 48hpf	End of gastrulation/ beginning of organogenesis	>80% and ≤45%		351		
			>80% and <30%		521		
			>70% and ≤45%		211		
			>70% and <30%		1480		

‡Studies investigating the effect of external factor in egg quality or using multi-parametric analyses to assess egg quality were not considered.[1]Criteria defining egg quality. [2]Developmental stage corresponding to the criteria employed. [3]Threshold: rates used to delimit high and low quality groups.[4]#DEG: number of differentially expressed genes. *No DEG was identified using hatching or deformities rates as criteria.

Regarding the criteria chosen to assess egg quality in the studies, most of them consists of early stages, however later stages also produced positive results (Table 13). Studies in Striped bass (*M. saxatilis*), rainbow trout (*O. mykiss*) and sea bass (*D. labrax*) compared survival obtained at distinct stages and concluded that the earliest ones investigated, such as late cleveage, 32- and 4-cell stages, respectively, would be reliable enough to detect poor egg quality in these species (Chapman et al., 2014; Ma et al., 2019; Żarski et al., 2017a). Despite of investigating the reliability of using different criteria to infer about egg quality, authors did not evaluate the possible effect of criteria changes in the transcriptomic results. Indeed, our study seems to be the first one investigating this hypothesis and shown that the choice of the criteria and threshold correspond to an important source of variation in transcriptomic results.

Thresholds to delimit the quality groups and stages of development used as criteria to assess egg quality correspond only to few examples of variations in methods that can interfere in our conclusions about the results. They mainly depend upon data obtained and cannot be anticipated. Survival rates are the most commonly used parameter to assess egg quality in many studies, however, as discussed in the quality chapter, their choice is not standardized even for one species. It appears difficult to try a homogenization between studies because reproductive biology is already variate among fish species. Moreover, attempts of standardization should be flexible enough to consider the results obtained between spawning seasons, which make this process more difficult. Since it is available, we would be more certain of comparing results containing biological meaning instead of those resulting from methodological variations.

2.1.2. Techniques to perform molecular analysis

In addition to the methods applied to define eggs' quality, other methodological factors will interfere in transcriptomic results, such as the technique employed to extract and determine the RNA profiles. During the samples processing, the choice of using total or poly(A) RNA to perform a screening may influence the interpretation of the results. As described in the general introduction, transcripts previously though to correspond to zygotic transcripts (Mathavan et al., 2005), were in fact maternal transcripts that passed through post-transcriptional processing (Aanes et al., 2011; Harvey et al., 2013). It is even more important when investigating early embryos, for which the ability of the methods to make difference between the sources of the mRNA, whether maternal or embryonic, is essential. In eggs, the choice of selecting poly(A) RNA or their selection by size, make difficult to observe other kinds of RNA. In the above mentioned study in rainbow trout (*O. mykiss*), in which authors compared the transcriptomic profiles on three egg quality groups, they also used different techniques to process the RNA. RNA-seq was employed either on rRNA removed or in poly(A) retained RNA. As results, they found only two DEG in the first RNA type, while 1339 were found for the second one between the three egg quality groups. Due to the reduced number of DEG from rRNA depleted RNA, authors argued that, in their conditions, egg quality is not a result of mRNA accumulation and degradation during oogenesis. This is because stored RNAs have smaller poly(A) tail (15-40 nucleotides), and were not detected in the poly (A) retention sequencing, in comparison to the polyadenylated RNA (~80 nucleotides), that were detected. Longer poly(A) tails RNAs imply activation and potential translation (Ma et al., 2019). However, in most of the studies presented in Table 12, differences on the eggs transcriptomic content were found between egg quality groups also when using total RNA for analysis. Thus, early embryonic development, among many others features, depends on the accumulation, degradation and cytoplasmic post-transcriptional processing of maternal RNAs.

In the same way, the technology employed to perform the screening will produce different results. For example, the use of microarrays will allow identifying only known genes while RNA-seq approaches may produce new findings and improve the current knowledge. Both technologies have their advantages and disadvantages and the choice of one or another is based on the type and number of information one wants to obtain. Thus, a balance should be found depending on the goal of the study and kept in mind that they may impose limits in comparisons between species. In summary, despite of some biological processes appear as perturbed with some constancy in egg quality vs. egg transciptomic profile studies, the genes implicated and the direction of the disruptions are quite heterogeneous. It is reasonable then, to grant, at least in part, this the huge variability of results found between studies to methodological variations.

2.2. *Maternal factors affecting transcriptomic results*

2.2.1. Domestication level

Maternal factors are those able to determine offspring phenotype. They will constitute the primary source of actual changes in eggs mRNA content. As a consequence, any condition, intrinsic or extrinsic, affecting females' life may impact oogenesis and eggs composition. Raising system, breeders' management and any stressful agent could constitute an external source of variation potentially influencing oogenesis. In addition to external factors interfering in females' reproductive performance, intrinsic females' conditions might influence the synthesis and accumulation of mRNA during oogenesis and should also be considered. For example, the nutritional status of the breeders is directly related to their ability to reproduce. Thus, comparing species that do not have an appropriated balanced diet with those that have one, may also constitute a bias. This because the absence of an appropriate diet (excess or insufficiency of some nutrients) may challenge the females, cause distress, and thus induce modification in their eggs' content.

In **Chapter 3**, it was demonstrated that the domestication process, may act as an intrinsic factor, influencing the synthesis and accumulation of mRNA in the oocytes. Two populations that had distinct histories of domestication were compared and they presented distinct eggs transcriptomic profiles. In turn, this may have impacted eggs' quality, since differences in embryos early development between these populations were observed. Studies concerning embryos early survival and the domestication process are quite scarce. In the few studies of this kind available, authors are mostly interested in one side of the response, since the performance of both populations are evaluated either in wild or in captivity environment. Authors used to be more interested in embryos performance in the wild because escapees are a big concern in fish farms due to the possibility of introgression and potential interference of captive fish in natural ecosystems.

Results of studies considering the domestication process and transcriptomic analysis, are complex to interpret since domestication corresponds to an evolutionary process and transcriptomic modification are expected to come from many sources, including genomic and non genomic ones. Thus, on one hand, it would be interesting to always have the broodstock genetic background, so authors would be able to discard the genomic origin of their results. On the other hand, authors should completely present their results, because many times more general or even essential information are omitted. For example, GO analyses are usually performed using the DEG lists originating from comparisons of distinct conditions. It happens that pathways are overrepresented and authors do not share with readers the name of the genes representing the pathways or the direction of the changes in expression (in which condition the genes were down- or up-regulated). It complicates more extensive comparisons between studies.

In table 14, studies relating transcriptomic profile in fish at embryonic stages from populations at different levels of domestication are presented. The genetic background of the fish was not investigated for all of them. When this information is available, we are able to get rid of the genetic drift as being the cause for the transcriptomic changes observed, as demonstrated by (Christie et al., 2016). In addition, not all of these studies present the direction of the perturbation when GO terms were overrepresented among the DEG. As said, this is essential for the interpretation of the results because allow making new hypothesis about the causes of this changes and their consequences for the domestication process. In agreement with our study, genes related to immune system functions are up- or down-regulated according to the population. In my case, this function was two-way perturbed, as in other three studies in Atlantic salmon [*S. salar*; (Bicskei et al., 2014, 2016; Lanes et al., 2013)]. These shared results highlight the *immune system* as an important player for embryonic development and yet, much little is known about this system, even in adults, in fish.

Table 14. Embryonic transcriptomic studies comparing “domesticated” and “wild” fish populations.

Species	“Domesticated” features	“Wild” features	Stage analyzed	# DEG	GO terms	Direction of the disturbance (wild as reference)	Genetic background (F_{ST})	Reference
Atlantic cod (*Gadus morhua*)	Parents of 4 year-old farmed fish	Parents caught ~1 month before spawning	2-8-cells stage	427	Cell death and growth; Signal transduction; Translation; Immune system; Lipid metabolism*	Two-way in all	?	(Lanes et al., 2013)
Atlantic salmon (*Salmo salar*)	Parents presenting ~ 10 generations of directional selection	Parents wild caught	Yolk sac fry	574	Cell death and growth; Signal transduction; Translation; Immune system; Lipid metabolism*	Up; Two-way; Up; Two-way; Two-way	?	(Bicskei et al., 2014)
Atlantic salmon (*Salmo salar*)	*Idem to above*	*Idem to above*	Eyed embryos	165	Cell communication; Signal transduction; Immune system; Translation ; Lipid metabolism*	Two-way; Two-way; Two-way; Up; Up	?	(Bicskei et al., 2016)
Steelhead trout (Oncorhynchus mykiss)	Parents born and first year raised in hatchery environment; ~ 4 years in the wild and then caught for experiment	Parents wild-born	Swimming-up fry	723	Wound healing; Immune response; Metabolism	?	0.009 (method: SNP)	(Christie et al., 2016)
Eurasian perch (*Perca fluviatilis*)	Parents raised for ~7 generarions in captivity	Parents wild-born	Unfertilized eggs	358	Immune system	Two-way	0.1055 (method: microsatellites)	*This study*

#DEG: number of differentially expressed genes. F_{ST}: fixation index. SNP: single nucleotide polymorphism. *Only one representant of each KEGG functional group is shown.

2.2.2. Spawn homogeneity

Another interesting intrinsic factor affecting egg composition, is the potential heterogeneity within spawn which may also constitutes a source of variation. Fish present a huge variety of reproductive strategies that should be taken into account when analyzing egg quality versus egg transcriptomic content. For example, the type of ovaries development giving spawn in batches or total, may also use different strategies to produce high quality oocytes. Thus, it is possible that a faster change in the eggs composition between and within spawn under the influence of diverse factors. In our study, the evaluation of egg quality was always done in triplicate. For each female, each replicate was collected from different parts of the ribbon in order to have more representative samples to be averaged later depending on the group, either according to the quality or the population. After analyzing, we verified some important variations between replicates (Figure 32). Regarding all spawn together, more homogeneity of results can be observed at 24 hpf in comparison to the other time points. If we analyze this time point considering the spawn origin (F1 = 1-13 and F7+ = 14-32), more homogeneity can be observed at 24 hpf for the F1 population in comparison to the F7+ one. This difference presented a tendency of significance ($p = 0.057$) when tested using a non-parametric Wilcoxon-Mann-Whitney test ($\alpha < 0.05$). Interestingly, this pattern is almost inverted at hatching rate, when F1 spawn present more heterogeneous results. It reinforces our discussion in **Chapter 3** about the higher homogeneity observed in the F1 populations spawn concerning not only their quality but also the overall results obtained. In opposition, if we analyse these spawn considering their quality (survival rate), no clear pattern regarding heterogeneity/homogeneity is observed.

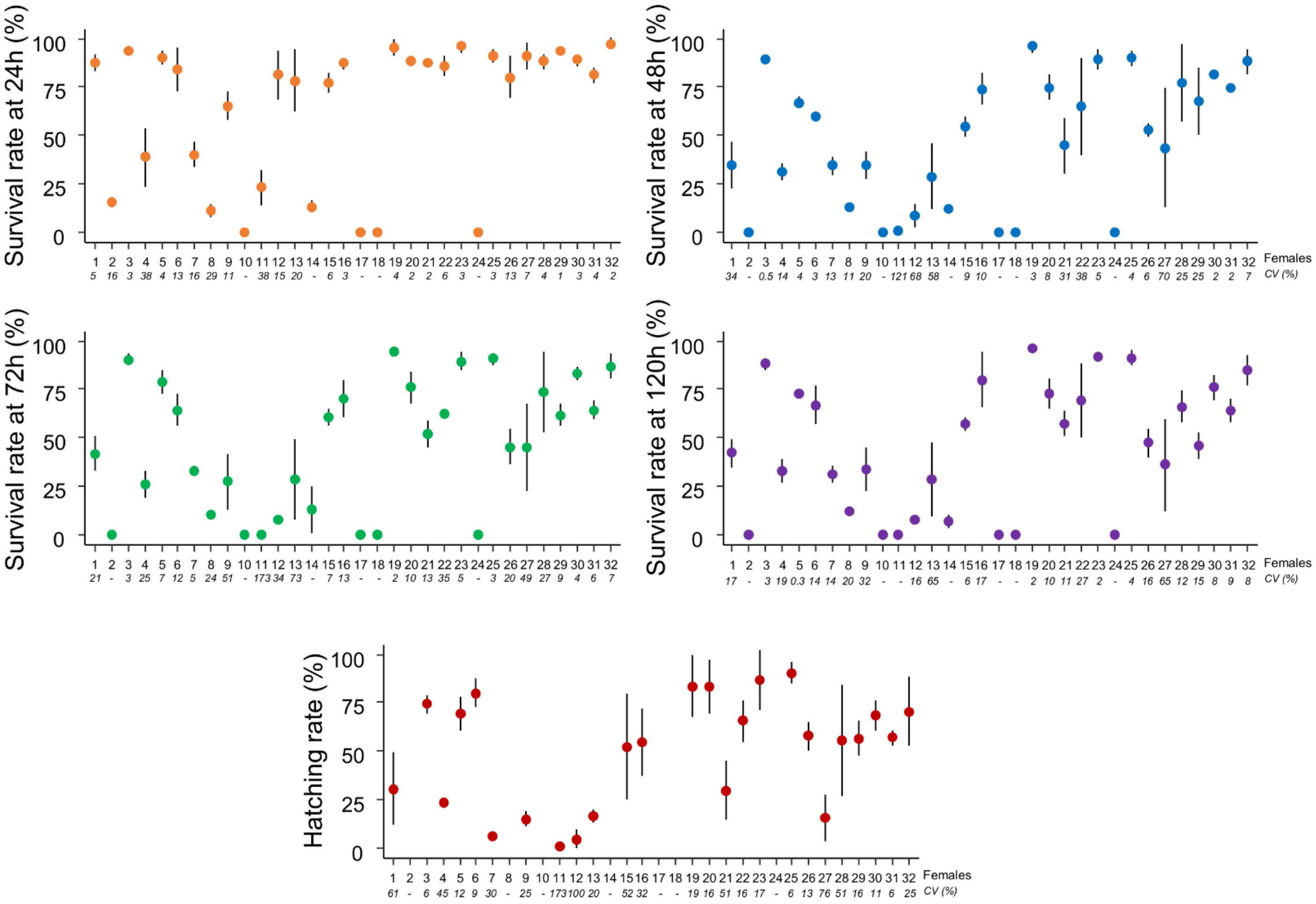


Figure 32. Variations found between replicates when evaluating egg quality of each female on several embryonic developmental stages. The 32 females studied are represented in each individual plot. Points represent the mean and error bars represent the correspondent standard deviation (n=3; except for the female 14, n=2). Females from 1 to 13 belongs to the population F7+, while females 14-32 came from population F1. CV: coefficient of variation is shown for each mean. Ommited CV (-) could not be calculated or are above 100%.

Whether these variabilities came from the methods (human inducing variation during data collection) or from differences already existing in the ribbon, is impossible to determine in our conditions. So far, nothing is known about the homogeneity of oogenesis through the ovary in Eurasian perch. Assuming that differences in quality in the same spawn, come with transcriptomic differences, it is possible that the portion of the spawn sampled also contributes for the transcriptomic results variations. In adult mammals, each ovary has already its pool of oocytes that will be released one by one, or in a reduced number, at each estrus cycle. Differently from mammals, fishes will release a huge number of eggs at once. Thus more difficults are imposed to these species that have to produce new eggs, from the oogonia recruitment stage, at each new reproductive cycle. Mechanisms controlling this process should also be increased and tightly regulated, which raise the potential for more heterogeneity within spawn.

Despite of the above exposed, a study in zebrafish (*Danio rerio*), aiming at comparing the eggs transcriptome between siblings and within clutches revealed that each female was able to give an individual signature to the eggs they produced. This means that major transcriptomic differences were observed between females, in comparison to individual eggs from the same females (Rauwerda et al., 2016). However, in this study, no information about egg quality is given.

3. Eggs’ transcriptome and comparisons between species

3.1. *Shared features*

As highlighted above, high variation in transcriptomic profiles in eggs can come from many sources, which makes challenging to perform comparisons between species. Variations found due to maternal factors will be added to those from the methods applied making their interpretation more complex. Yet, many similarities have already been identified.

The list of common molecular mechanisms necessary for early development identified in different species can be quite extensive and includes not only individual genes but also gene families. One of the most common example is the use of similar gene families, such as *Wnt* signaling pathway, *BMP* pathway and *nodal* signaling that are used for the determination of antero-posterior, dorso-ventral and left-right patterns in chordates, respectively (Brown et al., 2008). This knowledge was achieved thanks to several studies on gene expression profiles and genes localization in embryos during this period in several species. It gave a large overview of the mechanisms involved in patterning and how some small changes could lead to developmental impairments. As for axes patterning, other important embryonic developmental landmarks, such as MZT, MBT, gastrulation and hatching lack much understanding in many species.

In addition, genes related to egg quality have been identified as shared by different species. For example, the gene *npm2,* abundant in oocytes and embryos of vertebrates, became target of loss-of-function analysis in zebrafish embryos after being differentially expressed in rainbow trout (*O. mykiss*) eggs presenting different potential to properly develop (Aegerter et al., 2005). This gene has also been associated with egg quality and good development in xenopus (*X. laevis*) (Onikubo et al., 2015) and in mouse (*M. musculus*) (Zheng and Dean, 2007). Its role was confirmed in zebrafish, for which the absence of maternal-provided *npm2*, resulted in developmental arrest before gastrulation. Author also pointed for the possible involvement of Npm2 in ZGA (Bouleau et al., 2014; Cheung et al., 2019). Following the same pattern, in our multi-parametric quality approach (**Chapter 2 – Part B**) it was also possible to identify nucleophosmin (MPF_LOC100710418.2.4), a nucleoplasmin-family gene that was down-regulated (Log2FC = 1.0) in the fourth cluster of quality in comparison to the other three clusters. In opposition, this gene was not found among the DEG lists from the individual criteria analysis (**Chapter 2 – Part A**). Interestingly, the fourth cluster contained spawn that failed fertilization or presented massive mortality before 72 hpf, while the other low-quality groups excluded these spawn. Thus, as in zebrafish, this gene may be one of the causes of mortality before gastrulation also in Eurasian perch. In this path, the many differentially expressed genes we identified in this study may correspond to starting point for researches also in other species.

3.2. *Suggestions to compare studies within and between species*

Concerning intra-species studies, many methodological issues can be easier solved by properly designing experiments. In this context, the methods used to investigate eggs' quality in relation to their transcriptomic content should allow to isolate the different source of variation, as much as possible. When studying populations, the genetic background may represent an important source of modification on the gene expression profiles, thus, they should be evaluated. So far, most studies on the domestication effect in fish reproduction, comparing farmed vs. wild populations do not give any information concerning the genetic distance between studied populations, as showed above (Table 14). In these cases, there are place for doubts about the domestication being the only source of transcriptomic differences. Another important feature is the level of domestication of fish used in the experiment. Concerning wild populations, whether it is a F1, wild caught and induced in captivity or caugh right before reproductive period, would affect the interpretation of the response obtained. The absence of information on breeders' food intake and their age, for example, could particularly interfere in the studied spawning season and transcriptomic results could reflect diet changes or age differences instead of be in response of the domestication process. Researches ability to control as many parameters as possible would be crucial to make this distinction. In our study using F1 females constitutes an advantage since all external factors could be equated to those faced by F7+ population, including age, food intake and rasing system. An interesting suggestion would also be to follow a fish population from several generations, stating with a wild or a F1, and compare their eggs' transcriptomic content and embryonic developmental performance over time. It is a way to evaluate changes on molecular mechanism potentially causing the previously described reduction on reproductive performance in captivity (Farquharson et al., 2018).

Still in an intra-species point of view, it is also important to be able to distinguish between maternal and paternal contributions for embryonic development and performing reciprocal crosses is a good way to do so (Figure 33). A clear example is the work performed by (Christie et al., 2016). They investigated the domestication process as the cause of changes in the transcriptomic profile of steelhead trout (*Oncorhynchus mykiss*) swimming-up fry. In addition to present genetic evaluation, they performed reciprocal crosses to analyze the maternal contribution for the differences and indeed, the domestication was the main effect. In opposition, (Bicskei et al., 2016) also employed reciprocal crosses to investigate the parental contribution for gene expression changes in domesticated *vs*. wild Atlantic salmon (*Salmo salar*) embryos. In this case, a maternal dominance was seen in addition to the domestication effect. In this study, differently from the previous one, they investigated earlier embryonic stages, which may explain the difference since maternal dominance is expected in earliest stages of embryos development. Despite of any of these studies be interested in egg quality, similar designs could be useful to study the maternal contribution to embryos development.

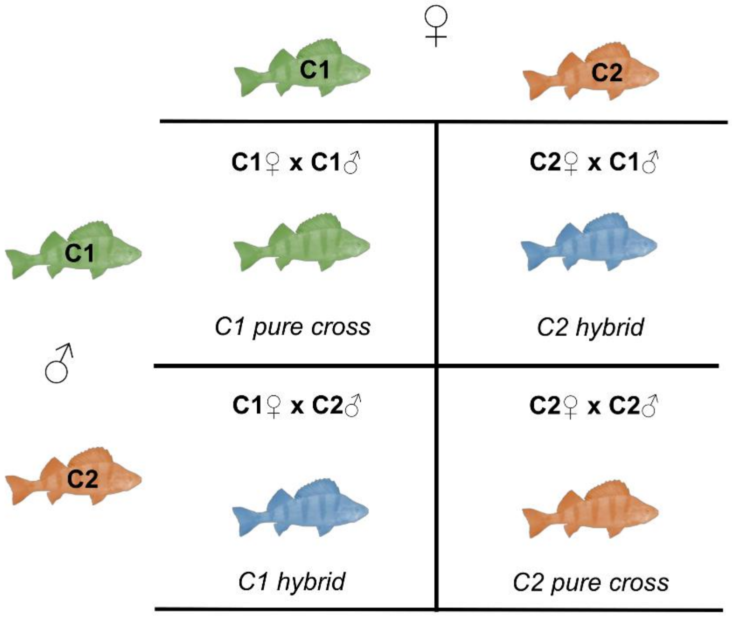


Figure 33. Schematic representation of an experimental design using reciprocal crosses. It corresponds to crosses between individual presenting a determinate condition (C) that will be tested. Individuals from the same condition will be breed to form the pure crosses, while male and females will be reversed breed to form the hybrid crosses. Inspired from: (Christie et al., 2016).

Regarding comparisons between species, in **Chapter 1**, the results comparing three species did not return any common gene differentially expressed according to egg quality. Apart of the differences usually found between species, this lack of common genes can also result from methodological origin. For example, in sea bass (*Dicentrarchus labrax*), authors used fertilization rate (4-cells stage) as criterion and the thresholds to delimit the groups of high and low quality were higher or lower than 60%, respectively. As we presented in our quality study (**Chapter 2 – Part A**), these two parameters directly affected the number and the genes presenting differential expression between high and low quality in Eurasian perch (*P. fluviatilis*). It may also be true in sea bass (*D. labrax*). On the other hand, when comparing zebrafish (*D. rerio*) and Eurasian perch (*P. fluviatilis*), no common gene was identified either, despite of the use of the comparable parameters for both species. For this second comparison, however, the methodology concerning the assessment of egg quality, is not likely to be an explanation for the differences found but mostly be related to maternal factors and the reproductive biology of both species. Inter-species comparisons are more complex if we consider the many biological differences between them. In transcriptomic studies vs. egg quality studies, the developmental stages should be priorized over the time post-fertilization, since the timing can be highly variable between species. At the same time, similar stages may share more features. It could also be interesting to group species according to similar morphological characters. It is not a guarantee of similarities at the transcriptomic level, as we showed in the example of MZT in *Ascaris suum* and *Caenorhabditis elegans,* that present quite comparable morphological development but strong differences on the ZGA (Wang et al., 2014). In fish, it could be a starting point and the presence or absence of eggs' oil droplet could be a first criterion to separate species in groups. This will put apart zebrafish and Eurasian perch, for example.

A complicating factor to study reproductive performance and make comparison between species relies on the fact that reliable information about females' reproductive biology and embryonic proper development are missing for many species. Thus, it would be interesting to first pursue investigations, for given species individually, mainly concerning intrinsic features still lacking information, such as: spawn homogeneity in terms of egg content and egg quality, variations between spawn, variations within a population, variations between populations, only to give some examples. In addition, for each species it is important to know the most reliable way to assess egg quality (e.g. earlier or later stages) and for so, a better knowledge of embryos early development would be necessary. When it is not possible to analyze unfertilized eggs, or even to be able to make reliable correlations (or not) between eggs content and egg quality, the main developmental landmarks during early stages, such as MBT, MZT, gastrulation and others, should be known to allow drawing proper experiments and conclusions.

The absence of comparable protocols to study maternal contribution for embryonic early development is an issue because they produce results not easy to be confronted with what already exists in the literature. Therefore, it not allows to raise more general conclusions. In order to try to overcome this issue, some features should be considered, for example those found in the present study, such as the use developmental stage instead of time post-fertilization. As highlighted in **Chapter 1** and mentioned above, equivalent developmental stages are more likely to share gene expression patterns between species. Another suggestion also demonstrated in this work, is the use of earlier developmental stages to assess egg quality instead of the latter ones (when looking for eggs' content variations). And also a more general feature, which is always designing experiments in order to be able to make distinction between the conditions analyzed. In the future, the use of comparable methods between species will increase meta-analyses feasibility and reliability, in addition to allow going deeper and faster in the understanding of the main landmarks during embryos development. Figure 34 presents a scheme summarizing many factors that nowadays correspond to obstacle to have more comparable methods to study egg quality in association with the eggs' mRNA content.

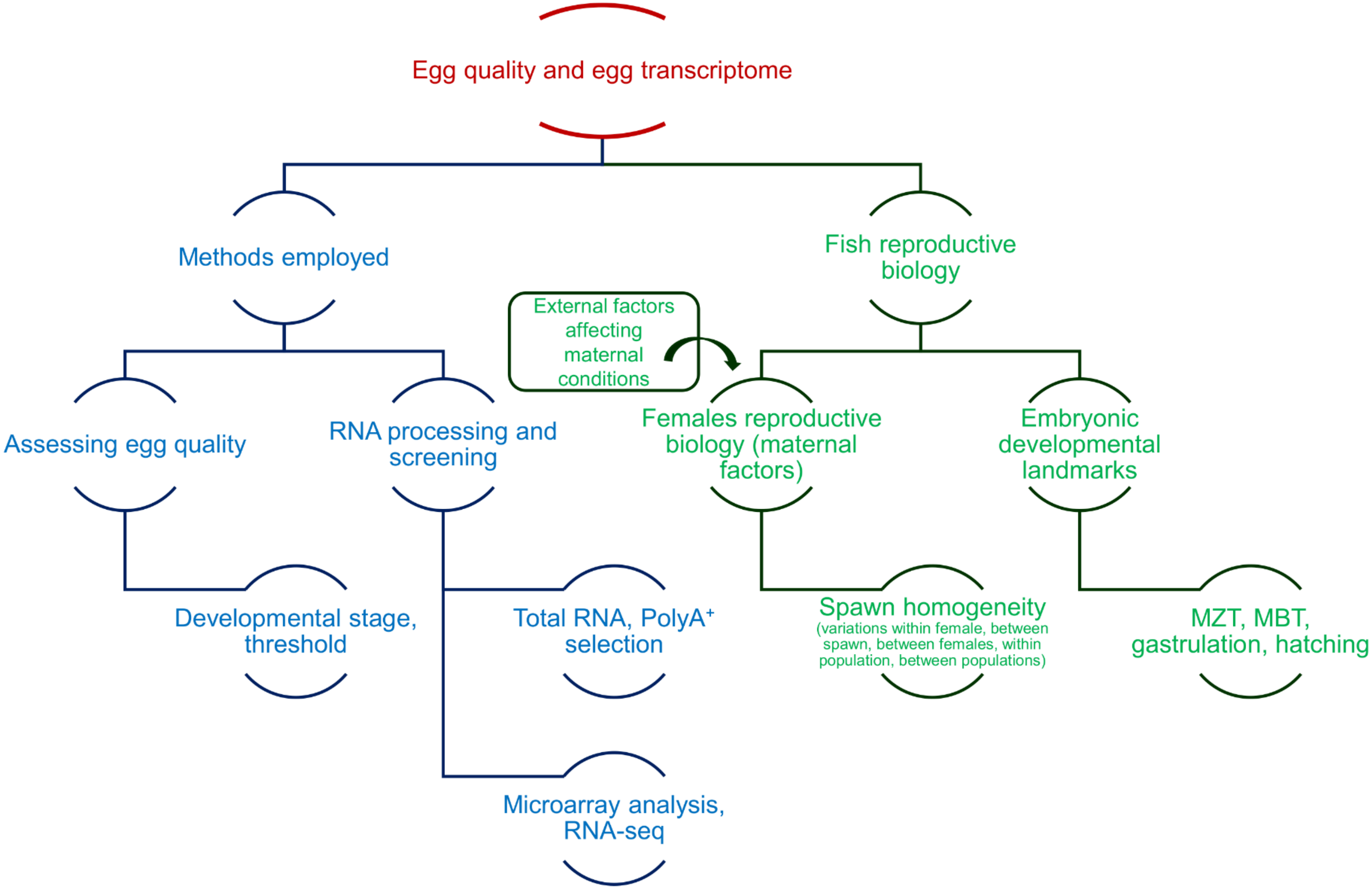


Figure 34. Scheme summarizing the main sources of variations in the acquisition and interpretation of results from studies aiming at correlate egg quality and eggs mRNA content. Green shaded branch lists some features lacking of more precise information, for many farmed species, while blue shaded one point to methods with potential to interfere in egg quality vs. transcriptomic studies. Additional knowledge on fish reproductive biology is necessary for better choose the methods to be employed.

Egg quality is a trick trait to assess and even more to predicted. Thus, researches on this topic contribute to improve the knowledge on the biology of embryos development and fish reproduction. In addition, it may constitute a first step on the identification of reliable traits that could be used in selective breeding programs in the future, as presented in the next section.

VIII. Conclusions and Perspectives

In the present study, the association between developmental phenotypes and different eggs' transcriptomic profiles provided new information about the reproductive biology in Eurasian perch (*Perca fluviatilis*). We gave a step forward in deciphering the molecular mechanisms involved in embryos early development because different gene expression profiles were identified on eggs from different quality groups, either when they were grouped using variable criteria or statistical analysis. We also pointed to an intrinsic factor, the domestication history, potentially impacting eggs transcriptome and their quality. Additionally, we provided the first results on the timing of Eurasian perch (*P. fluviatilis*) embryonic transcription, which should be continued in order to improve the information in the embryonic developmental landmarks and in molecular mechanisms that may be shared between species. Shared mechanisms are particularly important to understand the conservation or loss of some features through species evolution. To be able to identify similarities and differences between species, they should first be individually studied, since nowadays many basic information about fish reproductive biology are missing, which may lead to misinterpretation of results, as discussed in the last section.

Studying eggs' content is an interesting approach because it gives the possibility to evaluate females and offspring at the same time. Indeed, eggs correspond to an interface between mothers' investment to reproduction, and as such it informs about broodstocks' reproductive capacity; and embryos, informing about their potential to properly develop. In the aquaculture context, that targets increasing reproductive performance, egg quality corresponds to an important parameter to be considered. As discussed, egg quality is not an easy parameter to evaluate or predict. Thus, the most controlled the reproduction, the best the quality of the data available and as a consequence, it will be easier and faster to assess egg quality. Fish farmers could be an important source of information about fish reproductive biology due to the amount of spawning season followed and the number of fish populations they work with. A problem here is that many of them do not have implemented an efficient track system or even did not perform any kind of control. This makes difficult to have an overall perception of the variations patterns in fish reproductive biology and also to have a tight control of the production.

The first step toward increasing fish reproductive performance is better controlling the reproductive process, for so, it is necessary to keep traceability by collecting, storing and analyzing data from broodstock. To analyze these data, indexes allowing evaluate and classify broodstocks' reproductive performance should be fixed. Number of females spawning, females producing better quality eggs and number of larvae produced are examples of parameters that could be useful to follow. The absence of knowledge in the actual productive status in a fish farm, impede to make projections, reduce costs and increase productive efficiency. A proper reproductive control will allow for example, the elimination of females that did not spawn in two consecutive spawning seasons or those constantly producing bad quality eggs (depending on the species and indexes defined by the fish farm). Thinking in a long term, have information on the females' ability of produce better quality eggs may contribute to the reduction of the stock and increase of the efficiency of a fish farm because better breeders will be kept and spending food and time to manage infertile or unproductive females will be avoided. In farmed mammals, it is common to evaluate the reproductive efficiency of breeders considering their capacity of produce high quality descedants, which is closely monitored in both sexes, by following many traits. In cows, for example, productive life, calving intervals and production of stillbirth are traits usually included in genetic selective programs (Cole and VanRaden, 2018; Crowe et al., 2018). In fishes, it could also correspond to a manner to start better understanding and controlling fish reproductive dynamics.

There are two main possible explanations for the absence of a closest egg quality control in fish. The first one, is their prolificacy, incredibly high comparing with mammals, that in consequence may mask some economic impact in fish production. However, this apparent advantage should be pondered by the environmental impact of this lack of control. For example, the effect of throwing away thousands of litters of water, sometimes containing a huge concentration of organic material, every time a bad quality spawn is produced, should be considered in the perspective of the aquaculture sustainability. The second one, is that it is laborious to perform eggs quality control. Nowadays, considering the huge amount of work already existing in a fish farm, that considerably increases during the spawning season, the simplest monitoring is performed. An example of criteria used in Eurasian perch (*Perca fluviatilis*) is the ribbons' aspect, which means that the integrity of the ribbon is evaluated from the lowest to the highest quality: by the presence of individualized eggs, fragmented ribbon, ribbon in large pieces or intact ribbons. In disagreement with this criteria, good quality spawn has already been obtained in laboratory, under similar environmental conditions as in a fish farm, from fragmented ribbons, thus it would not be the most reliable phenotype to infer about egg quality. Because closer monitoring the reproductive process is hard to perform, it should be efficient, so some improvements are necessary and for so, investment in time, material and personal are needed.

Attempts to automatize egg quality evaluation are under development. For example, VisEgg is a high-throughput phenotyping tool developed to evaluate the developmental potential of rainbow trout (*Oncorhynchus mykiss*) eggs. It is used to count, measure and detect color changes in the eggs. Thus, white egg (usually incompatible with development) and dark spots (appearing at eyed stage) can be identified. It represents an advancement in performing these laborious tasks that are manually done so far. Developers believe that other parameters could be added to the tool, for example the ability of morphological evaluation of the oil droplet in eggs in species that have it, such as Eurasian perch (*P. fluviatilis*). While the technology is not available, other methods should be kept under investigation. In this concern, having a reliable developmental stage to assess egg quality may help in this task.

Once more extensive information about fish reproductive biology and most importantly about egg quality is available, other resources can be applied to improve reproduction and for its control. For example, it will be possible starting properly using it in selective programs that nowadays are done in a complete empirical way for most of farmed fish species. The introduction of females' ability to produce high quality eggs as parameter of selection could be helpful in projects such as FISHBOOST, a European project (2014-2019), that made researchers and fish farmers work together with the aim of improving the genetic background of the six major fish species produced in Europe (Atlantic salmon – *Salmo salar*, common carp – *Cyprinus carpio*, European seabass – *Dicentrarchus labrax*, gilthead seabream – *Sparus aurata*, rainbow trout – *Oncorhynchus mykiss* and turbot – *Scophthalmus maximus*), by applying a selective breeding program. Only few reproductive traits were used, such as sexual maturity age and fecundity, the other traits were related with growth performance, probably due to reasons above mentioned. Despite of egg quality do not be a trait used for selection nowadays, it is among the traits with potential to contribute in the improvement of fish production through improving fish reproductive performance. A prove of this potential is the implementation of European network, the AQUAGAMETE COST (European Cooperation in Science and Technology – 2012-2016) Action, that reunited scientists from 28 countries, including non-European ones, to better study and standardize methods to study fish gametes. Thus, researches on this field are to keep being developed.

IX. Annexes

1. Material and methods employed to characterize the maternal-to-zygotic transition (MZT) in Eurasian perch (*Perca fluviatilis*)

1.1. *Material and Methods*

Several exclusively maternal or zygotic transcripts have been identified in model species as zebrafish (Aanes et al., 2011; Harvey et al., 2013; Lee et al., 2013; Vesterlund et al., 2011), xenopus and drosophila [reviewed by (Lee et al., 2014; Tadros and Lipshitz, 2009)]. Information on the timing and dynamic of the ZGA in these species gives clues also for non-model species, such as Eurasian perch (*Perca fluviatilis*). Thus, we analyzed the expression pattern of some known-maternal and known-zygotic genes from other species on embryos of Eurasian perch at different stages of development.

1.1.1. Spawn origin, fertilization essay and transport to our facilities

Fertilized eggs of Eurasian perch were sampled at a partner fish-farm, Lucas Perches (Hampont, France), between October and November 2017. Broodstock came from Recirculating Aquaculture Systems (RAS). Broodstock and embryos were handled according to the European guidelines on the protection of animals used for scientific purposes (Directive 2010/63/UE).

The fertilization assays were done according to (Żarski et al., 2012c). Briefly, mature females were stripped on dry plastic baskets, where tank water was added. In the following a pool of sperm of three males was added onto the eggs for fertilization. The sperm of each male was checked for motility before fertilization. Right after fertilization, spawn were transferred to individual plastic bags for the transport to our facilities. To do so, we used thermal boxes containing recyclable ice in order to keep the optimal hatchery temperature (13°C).

1.1.2. Hatcheries management

In our facilities, each spawn was kept in an individual RAS hatchery. The hatcheries were kept at 13°C (water and room). A constant light/dark photoperiod (16:8) was used with two neon lamps (10% white, 2% blue and 2% purple lights) at the water surface.

Water temperature (13.32 ± 0.35), pH (8.20 ± 0.07) and dissolved oxygen (9.38 ± 0.33) were checked twice a week. Ammonium (0.24 ± 0) and nitrite (0.02 ± 0.01) were checked once during the experiment.

1.1.3. Study of developmental performance and embryos sampling

In total 6 spawn were studied to determine the early developmental performance. The following description was performed for each spawn. About one hour after fertilization (hpf), three samples of around 100 eggs were taken randomly from the spawn and kept apart, into individual bottom meshed boxes to determine the survival rate at 24, 48, 72 and 168/152hpf using the following formula: (number of alive embryos/total number of embryos)x100. This procedure was employed in order to avoid excess manipulation of the entire spawn.

About 8 embryos (~100mg) were sampled in duplicate every 2hpf for each spawn. We covered a large period of the embryos development, from 5 to 33 hours post-fertilization including mid-blastula transition (time of starting the asynchronous cell divisions during which the first stages of the ZGA occurs in other species), occurring at the 128 cells stage and the stage 50% epiboly corresponding to the midtime of the gastrulation period (also an important stage for the ZGA in many species).

Samples were collected from the entire spawn. They were conditioned in identified cryotubes and fast-frozen in liquid nitrogen, then they were transferred to a freezer and kept at -80°C until the molecular analysis. The sampling started at 5hpf (eight-cell stage) and ended at 33hpf (50% epiboly) or at 27hpf (beginning of gastrulation stage – Female 1). In total there were 15 or 12 (Female 1 and 3) sampling times.

To ensure that the embryos collected were developing properly according to (Alix et al., 2015), each sampling was done under a stereomicroscope (model M8 - Wild Heerbrugg, Switzerland) at 10x magnification.

1.1.4. Maternal or zygotic genes selection and primers design

As several exclusively maternal or zygotic transcripts have been identified in zebrafish in different studies (Aanes et al., 2011; Harvey et al., 2013; Lee et al., 2013; Vesterlund et al., 2011), we chose to test some of them that were common between studies (Table 15). Representing the maternal genes, we tested Serine/threonine-protein kinase PLK1-like *(plk1)*, Echinoderm microtubule-associated protein 1-like *(eml2)*, G2/mitotic-specific cyclin-B1 (*ccnb1)* and TATA-box-binding protein *(tbp)* and the zygotic genes tested were Inhibitor of DNA binding 1 (*id1)*, Krueppel-like factor 4 (*klf4)* and Fork head box protein A3 (*foxa3)*.

The Eurasian perch orthologs sequences for these genes were retrieved using Blast against the Phylofish databases (Pasquier et al., 2016). Specific primer for each sequence was designed using Primer3Plus or Primer Design Tool-NCBI software (Table 15).

Table 15. Primer sequences of the maternal and zygotic genes from zebrafish tested in RT-qPCR experiment and the reference genes used for data normalization.

Target gene	Abbreviated name	Phylofish/Gen Bank Gene ID	Forward sequence	Reverse sequence	Annealing temperature	Reference
Zebrafish maternal genes						
Serine/threonine-protein kinase PLK1-like	*plk1*	MPF_LOC101467664.1.2	ACCTGAAACTGGGCAACATC	CTTCGTAGCTGTGGCCTTTC	58°C	[1–3]
Echinoderm microtubule-associated protein 1-like	*eml2*	MPF_contig_045033	ATCTCTGCGATTCGTGGCTT	TGCATCGCCCCTTTCAGAAT	58°C	[1,3,4]
G2/mitotic-specific cyclin-B1	*ccnb1*	MPF_CCNB1.1.1	GCTTTCTTCAGGACCACCCA	GCGTGCGAAGAATGGTCATC	58°C	[1,3]
TATA-box-binding protein	*tbp*	MPF_LOC101470168.1.1	CAGGTGCCAAGGTGAGAGCA	ACAACAGCCCTTGCACAGCA	55°C	[1,3]
Zebrafish embryonic genes						
Inhibitor of DNA binding 1	*id1*	MPF_ID1.1.2	TATCTGGACACCACCGGTCT	CGCGAAGAACAAACAAGGCT	58°C	[1,2]
Fork head box protein A3	*foxa3*	MPF_FOXA3.1.1	CCCCACTACAACTTCAACCAC	TTGTATGCCATCACCTGGTC	58°C	[1–4]
Krueppel-like factor 4	*klf4*	MPF_LOC101073288.1.1	CCTCCAAATGACGTCGAGAT	GTTGGCACACTGGGTTTCTT	58°C	[1–3]
Reference genes						
Adenosine kinase-like	*adk*	MPF_LOC101464997.1.1	CTTCCTGACCGTCTCTTTGG	CCTTGGTCTCGAAGTCTTGC	55°C	*This study*
18S ribosomal RNA	-	FJ710875	CCTGCGGCTTAATTTGACTC	CTCAATCTCGTGTGGCTGAA	55°C	*This study*

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4. Harvey, S. A. *et al.* Identification of the zebrafish maternal and paternal transcriptomes. *Development* **140**, 2703-2710 (2013).

1.1.5. RNA extraction, DNase treatment and Reverse transcription

Thus, four spawn were kept for this analysis. Total RNA was extracted from 57 samples (mean weight of 100mg, about 8 embryos) using TRIzol reagent (Life Technologies) at a ratio of 100mg per mL of reagent and following the manufacturer's instructions with some modifications. Indeed, a milling step was added during the homogenization step to get rid more easily of the gelatinous envelope and the chorion surrounding the embryos. To do so, a bullet blender (Next Advance) and zirconium oxide beads 1.0 mm were used. In addition, a supplementary centrifugation (4°C, 30min. 13000 rpm) was performed before the addition of the chloroform to remove the lipids content. A NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies) was used to evaluate the quantity of total RNA. After total RNA extraction, DNase treatment (DNase I, RNase free - Thermo Scientific) was applied to 5 µg of all samples (n=57) following the manufacturer's protocol. Reverse transcription was performed in a final volume of 20 µl using a M-MLV Reverse Transcriptase (Sigma-Aldrich), 2 µg of RNA and random nonamers (2.5 µM - Sigma-Aldrich) and following the manufacturer's protocol.

1.1.6. RT-qPCR and statistical analyses

Reverse transcript products were diluted 1:45 and 5 µl were used for the RT-qPCR, using PerfeCTa SYBR Green SuperMix (Quanta Bioscience) and 5 pmol of each primer. The RT-qPCR was performed using a Step One Plus system (Applied Biosystems, Foster City, USA). The PCR program consists of a first step at 94°C for 2 min followed by 40 cycles consisting of a denaturation step at 94°C for 15s, an annealing step at 55 or 58°C depending on the primer pairs for 15s and an elongation step at 72°C for 30s. The amplification was followed by a melting curve stage, according to manufacturer's parameters in order to check the primers specificity. The abundance of the target cDNA in each sample was calculated using a serial dilution of a pool of all cDNA samples using StepOne Software (Applied Biosystems, version 2.1). This dilution curve was used to certify the reaction efficiency (80-120%). We only considered results presenting a Ct variation lower than 0.5 for further analysis. The selected genes were studied by RT-qPCR in all samples of embryos representing different stages of development. All samples were analyzed in duplicate and the geometric mean of the expression level data of the *adenosine kinase-like* and *rRNA18s* (Table 2) was used as reference to normalize the data obtained. These genes were found as stable in a preliminary RT-qPCR analysis in all samples. Data was log2 transformed before statistical analysis.

We used R (R Core Team (2017)) and *lme4* (Bates et al., 2015) to perform a linear mixed effects analysis of the relationship between gene expression levels and embryos development. As fixed effect, we entered time of sampling and as random effect, we had intercepts for the female effect. P-values were obtained through pairwise t-test comparisons between time points followed by a Bonferroni correction. The statistical probability significance was established at the $p<0.05$ level. Normality and homogeneity of variance were tested using Shapiro-Wilk and Levene's test, respectively. Data are represented as mean ± SEM. To present the results, statistical differences shown are always between the first time point evaluated and the others.

1.2. *Results*

1.1.1. Embryonic developmental performance

In order to avoid taking samples presenting some developmental impairment that could be reflected in the gene expression analysis, we used only the spawn presenting survival at 168/152h higher than 50%. From the 6 spawn followed, 4 presented survival rate at 168/152hpf higher than 50% (Table 16) and were thus used for the gene expression analysis. The 2 remaining spawn were excluded.

Table 16. Developmental performance of the six spawn evaluated. Percentages of survival rates are shown as mean±SD for each spawn on each developmental stage. Samples from females which results are gray shaded were excluded from the analysis.

	Survival rates (%)			
Female	24hpf	48hpf	72hpf	168/152hpf
1	84.26 ± 7.11	78.69 ± 7.51	73.81 ± 9.52	60.54 ± 15.46
2	96.13 ± 1.13	91.68 ± 2.87	91.4 ± 3.34	88.63 ± 4.56
3	44.72 ± 9.89	19.07 ± 7.47	17.17 ± 4.19	0
4	39.51 ± 17.92	32.61 ± 13.25	23.3 ± 10.28	19.35 ± 5.16
5	67.44 ± 6.62	64.36 ± 6.75	56.1 ± 10.97	54.68 ± 9.88
6	88.8 ± 3.32	80.99 ± 1.24	77.54 ± 2.01	77.26 ± 2.24

1.2.1. Gene expression pattern

No gene amplification was observed for the samples taken at 21hpf for three of the four females tested, consequently this timepoint was excluded from the analysis.

Four of the seven genes tested showed pattern of expression closer to maternal and zygotic profiles in perch, as in zebrafish (Figure 31, *in General Discussion section*).

2. Primers designed for Maternal Legacy experiments

Supplementary Table 15. Primer sequences of egg quality-related genes in zebrafish, tested by RT-qPCR experiment in Eurasian perch eggs. And reference genes used for data normalization.

Target gene	Abbreviated name	Phylofish/Gen Bank Gene ID	Forward sequence	Reverse sequence	Annealing temperature
Zebrafish maternal genes					
equilibrative nucleoside transporter 1-like	*slc29a1a*	MPF_LOC101478767.1.3	GCCGTCAACAGGAAAACCAC	CAATGTGATGACGCTCTGCG	50°C
ubiquitin thioesterase otulin	*otulin*	MPF_LOC101474680.1.1	AGTGCGGAGGAAAGAAGTGG	GCAACCTCAGGACTCTGCTT	50°C
inter-alpha-trypsin inhibitor heavy chain H2-like	*itih2*	MPF_LOC100693444.1.1	CCATTCTCATCGCGGCATTG	GGCGATAGCCAACCGGATAA	50°C
ribosome production factor 2 homolog	*rpf2*	MPF_LOC100699686.1.1	GGCCGTCGTTTGACTTGGTC	TGTGTACCCGGCCGAACTTT	50°C
Adenosine kinase-like	*adk*	MPF_LOC101464997.1.1	CTTCCTGACCGTCTCTTTGG	CCTTGGTCTCGAAGTCTTGC	50°C
40S ribosomal protein S27a	*rps27a*	MPF_LOC100697017.2.2	CGAGCTTTCAGCCCGTAGTA	AGCCACGTTCTGTCAAGAGG	50°C
ELAV-like protein 1-like	elavl1	MPF_LOC100695900.1.2	GATCGTGAACTACCTGCCCC	TTACCTGCCACTTTGTCCCG	50°C

X. References

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Supplementary Table 8**. Survival rates at 24, 48, 72 and 120 hours post-fertilization and at hatching in F1 and F7+ populations.** Columns 2 and 3 correspond to data presented in the Figure 28A when survival rates are estimated according to the total number of studied embryos. Columns 4 and 5 correspond to data presented in the Figure 28B when survival rates at 48hpf are estimated according to the total number of alive embryos at 24hpf. Different letters mean significant differences between populations or time of observation using an ANOVA two-way repeated measures followed by a TukeyHSD ($p \leq 0.05$; n= 19 and 13 for F1 and F7+, respectively). Concerning columns 4 and 5, exact p-values are 0.10 and 0.19 between populations at 24 and 48 hpf, respectively (n= 19 and 13 for F1 and F7+, respectively at 24 hpf and n= 16 and 12 for F1 and F7+, respectively at 48 hpf). Population means ± SEM are presented. 139

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Supplementary Table 10**. Differentially expressed genes list.** PhyloFish gene ID, gene description, False Discovery Rate (p-value) and log(2)FC of the 358 differentially expressed genes on eggs from the F7+ and F1 populations. 139

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Supplementary Table 15. Primer sequences of egg quality-related genes in zebrafish, tested by RT-qPCR experiment in Eurasian perch eggs. And reference genes used for data normalization. 205

XIII. Work valorization

1. Meetings and congresses

2019 Rocha de Almeida, T. ; Bobe, J. ; Le Cam, A. ; Klopp, C ; Montfort, J. ; Fontaine, P. ; Chardard, D. ; Schaerlinger, B. Difficulties to compare egg quality: insights from a transcriptomic analysis. [**Oral Presentation**]. 7th. International Workshop on the Biology of Fish Gametes. September 2nd - 6th, Rennes, France. Members of the scientific committee awarded this oral presentation as the **second best presentation** among the students' presentations in the workshop.

2018 Rocha de Almeida, T. ; Alix, M. ; Schaerlinger, B. ; Le Cam, A. ; Montfort, J. ; Toomey, L. ; Bobe, J. ; Chardard, D. ; Fontaine, P. A transcriptomic comparison suggests an influence of the domestication process on egg quality in Eurasian Perch (*Perca fluviatilis*) [**Poster and Oral Presentation**]. 11. International Symposium on Reproductive Physiology of Fish (2018-06-03-2018-06-08) Manaus (Brazil). In: New frontiers in reproductive diversity in a changing environment. 2018. 251 p.

2017 Rocha de Almeida, T. ; Schaerlinger, B. ; Le Cam, A. ; Alix, M. ; Montfort, J. ; Bobe, J. ; Chardard, D. ; Fontaine, P. Transcriptomic analysis of Eurasian perch (*Perca fluviatilis*) eggs assigned to distinct groups of quality [**Oral presentation**]. 6. International Workshop on the Biology of Fish Gametes (2017-09-04-2017-09-07) Vodnany (Czech Republic). In: 6. International Workshop on the Biology of Fish Gametes. Vodnany: University of South Bohemia in Ceske Budejovice; Faculty of Fisheries and Protection of Waters (1st), 2017. 156 p.

2017 Rocha de Almeida, T. ; Schaerlinger, B. ; Le Cam, A. ; Alix, M. ; Montfort, J. ; Bobe, J. ; Chardard, D. ; Fontaine, P. Transcriptomic analysis of Eurasian perch (*Perca fluviatilis*) eggs assigned to various groups of qualities according to a statistically based analysis [**Extended abstract and poster**]. 7th fish & shellfish larviculture symposium. (2017-09-04-2017-09-07) Ghent (Belgium). In: larvi 2017 - 7th fish & shellfish larviculture symposium. Ghent: Ghent University, 2017. pp. 370-373. The scientific committee of the symposium chose this work to also be **presented as teaser** for the plenary.

2017 Rocha de Almeida Tainá, Schaerlinger Bérénice, Chardard Dominique, Le-Cam Aurélie, Montfort Jérôme, Bobe Julien, Fontaine Pascal. Transcriptomic analysis of Eurasian perch (*Perca fluviatilis*) eggs according to embryo development [**Poster and abstract**]. Annual Seminary of the Doctoral School RP2E 2017 (2017-02-02) Nancy (France). In: Annual Seminary of the Doctoral School RP2E 2017. Nancy: Lorraine University, 2017.

2016 Rocha de Almeida Tainá, Schaerlinger Bérénice, Chardard Dominique, Fontaine Pascal. Study of the transcriptomic content of the Eurasian perch eggs: research of links with their quality **[Oral presentation]**. 5th Training School (2016-03-07-2017-03-11), Valencia (Spain). In: 5th Training School - Cryopreservation of fish germ cells. Valencia: Universitat Politècnica de València, 2016.

2. Paper accepted for publication

Rocha de Almeida, T., Alix, M., Le Cam, A., Klopp, C., Montfort, J., Toomey, L., Ledoré, Y., Bobe, J., Chardard, D., Schaerlinger, B., & Fontaine, P. (2019). **Domestication may affect the maternal mRNA profile in unfertilized eggs, potentially impacting the embryonic development of Eurasian perch (Perca fluviatilis)**. *PloS one*, *14*(12), e0226878. https://doi.org/10.1371/journal.pone.0226878

XIV. Long Supplementary Tables

1. Supplementary table 2

SR24_90+ vs SR24_45-				
Phylofish Gene ID	Gene description	p (Corr FDR)	Log FC	Regulation
MPF_CD99.1.1	CD99_HUMAN (sp|P14209) CD99 antigen OS=Homo sapiens GN=CD99 PE=1 SV=1	0.03799525	-1.8213806	down
MPF_CD68.2.2	NP_001158857.1 Macrosialin precursor [Salmo salar]	0.011256327	-3.321209	down
MPF_LOC100698998.2.7	XM_003439446.1 PREDICTED: Oreochromis niloticus myosin heavy chain, fast skeletal muscle-like (LOC100698998), mRNA	0.016491378	-2.7119951	down
MPF_LOC101157470.1.1	XM_004074516.1 PREDICTED: Oryzias latipes transportin-1-like (LOC101157470), mRNA	0.040899336	-1.480577	down
MPF_LOC101472355.1.1	XM_004556700.1 PREDICTED: Maylandia zebra peripheral myelin protein 22-like (LOC101472355), mRNA	0.010595669	-4.162342	down
MPF_contig_036757		0.04133058	1.012445	up
MPF_LOC100135188.1.5	NP_001107363.1 uncharacterized protein LOC100135188 [Xenopus (Silurana) tropicalis]	0.011256327	-2.9536827	down
MPF_LOC100702375.2.2	XM_003450215.1 PREDICTED: Oreochromis niloticus 6-phosphofructokinase type C-like (LOC100702375), mRNA	0.02261816	-1.6375858	down
MPF_LOC101473402.1.1	XM_004548338.1 PREDICTED: Maylandia zebra protein kinase C and casein kinase substrate in neurons protein 2-like (LOC101473402), transcript variant X3, mRNA	0.025232468	-1.1918286	down
MPF_LOC101472505.3.3	XM_004567307.1 PREDICTED: Maylandia zebra sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1-like (LOC101472505), transcript variant X4, mRNA	0.048345108	1.1558615	up
MPF_LOC101475041.3.3	XM_004549542.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 7-like (LOC101475041), transcript variant X2, mRNA	0.021017518	-3.2827473	down
MPF_contig_023930		0.016068961	-3.1160827	down
MPF_LOC100534427.1.1	XM_003440393.1 PREDICTED: Oreochromis niloticus lactate dehydrogenase, transcript variant 2 (LOC100534427), mRNA	0.043956067	-1.2258958	down
MPF_SRRM2.5.15	SRRM2_HUMAN (sp|Q9UQ35) Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	0.02018985	-2.6501107	down
MPF_contig_038379		0.027954783	-2.2329938	down
MPF_SSL-2.1.2	NP_001117194.1 serum lectin 2 precursor [Salmo salar]	0.029836256	-2.9240942	down
MPF_contig_013127	XM_004539189.1 PREDICTED: Maylandia zebra ATP-binding cassette sub-family A member 1-like (LOC101484083), transcript variant X1, mRNA	0.020932224	-1.8648944	down
MPF_LOC100693642.1.1	XM_003454966.1 PREDICTED: Oreochromis niloticus adenylate kinase isoenzyme 1-like, transcript variant 1 (LOC100693642), mRNA	0.021017518	-2.6898782	down
MPF_LOC101476572.2.2	XM_004541074.1 PREDICTED: Maylandia zebra tetraspanin-17-like (LOC101476572), mRNA	0.016177904	-3.2128332	down
MPF_LOC101469799.2.5	XM_004544977.1 PREDICTED: Maylandia zebra zinc finger protein Xfin-like (LOC101469799), transcript variant X17, mRNA	0.017280372	-1.3142335	down
MPF_contig_010177		0.024133291	1.0375129	up
MPF_contig_045323		0.0160005	-3.3135936	down
MPF_AHNAK.3.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]	0.010595669	-4.8153267	down
MPF_contig_020534		0.0145814	-2.993543	down

MPF_contig_005089		0.024618821	1.5060611	up
MPF_LOC101483521.1.1	XM_004540909.1 PREDICTED: Maylandia zebra early growth response protein 1-like (LOC101483521), mRNA	0.016177904	-3.7321649	down
MPF_LOC100690512.1.1	XP_003438469.1 PREDICTED: hypothetical protein LOC100690512 [Oreochromis niloticus]	0.014775532	-3.033624	down
MPF_LOC101169532.18.45	XP_004070110.1 PREDICTED: RNA-directed DNA polymerase from mobile element jockeylike [Oryzias latipes]	0.02741634	-1.3611172	down
MPF_LOC101476812.1.3	XM_004575484.1 PREDICTED: Maylandia zebra DNA-directed RNA polymerase III subunit RPC8-like (LOC101476812), mRNA	0.017280372	1.0785866	up
MPF_LOC101484448.2.3	XM_004540186.1 PREDICTED: Maylandia zebra lipid phosphate phosphatase-related protein type 3-like (LOC101484448), transcript variant X2, mRNA	0.024245406	1.0758889	up
MPF_LOC101464855.1.1	XM_004546244.1 PREDICTED: Maylandia zebra signal peptide, CUB and EGF-like domaincontaining protein 3-like (LOC101464855), transcript variant X1, mRNA	0.017280372	-3.3428488	down
MPF_LOC101485573.1.1	XM_004538383.1 PREDICTED: Maylandia zebra cystatin-S-like (LOC101485573), transcript variant X2, mRNA	0.018963305	-4.3025146	down
MPF_contig_016274		0.031615667	-1.5283008	down
MPF_contig_015023		0.023782896	-1.3455701	down
MPF_RPL22L1.1.1	NR_027625.1 Danio rerio ribosomal protein L22-like 1 (rpl22l1), transcript variant 2, noncoding RNA	0.026631793	-2.1297457	down
MPF_LOC101479407.1.1	XM_004547238.1 PREDICTED: Maylandia zebra macrophage-expressed gene 1 protein-like (LOC101479407), mRNA	0.017280372	-1.9760885	down
MPF_LOC100712028.1.5	XM_003450493.1 PREDICTED: Oreochromis niloticus apolipoprotein C-I-like (LOC100712028), mRNA	0.020559568	-3.2307248	down
MPF_contig_014892		0.02782313	-1.8847551	down
MPF_contig_017056	XM_004566361.1 PREDICTED: Maylandia zebra CREB-regulated transcription coactivator 3like (LOC101469041), transcript variant X2, mRNA	0.024133291	1.177855	up
MPF_SRRM2.13.15	SRRM2_HUMAN (sp|Q9UQ35) Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	0.020559568	-2.634757	down
MPF_LOC100708275.1.1	XM_003449495.1 PREDICTED: Oreochromis niloticus alpha-aspartyl dipeptidase-like (LOC100708275), mRNA	0.03943509	-2.1325788	down
MPF_LOC100701693.2.4	XM_003459252.1 PREDICTED: Oreochromis niloticus mamu class II histocompatibility antigen, DR alpha chain-like (LOC100701693), mRNA	0.04575675	-1.9141178	down
MPF_LOC100706528.6.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0.01596322	1.0857891	up
MPF_contig_005223	XM_004560039.1 PREDICTED: Maylandia zebra polyadenylate-binding protein 1-like (LOC101481678), transcript variant X1, mRNA	0.037587613	1.0058736	up
MPF_contig_022617		0.04518876	-3.1499617	down
MPF_contig_038427		0.032896757	1.1375332	up
MPF_LOC101485519.7.8	XM_004569613.1 PREDICTED: Maylandia zebra creatine kinase M-type-like (LOC101485519), mRNA	0.045433044	1.1047829	up
MPF_RL17.5.5	RL17_RAT (sp|P24049) 60S ribosomal protein L17 OS=Rattus norvegicus GN=Rpl17 PE=2 SV=3	0.027569868	-1.8104467	down
MPF_LOC100702817.2.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.01596322	-4.6568727	down
MPF_LECG.4.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.01708796	-5.0892143	down
MPF_LOC101156898.4.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	0.048983328	-3.2199414	down
MPF_LOC101172990.31.36	XP_004073946.1 PREDICTED: uncharacterized protein LOC101172990 [Oryzias latipes]	0.04835695	-2.3865173	down
MPF_LOC101469538.1.1	XM_004547384.1 PREDICTED: Maylandia zebra retinoblastoma-binding protein 5-like (LOC101469538), transcript variant X1, mRNA	0.030398514	1.7625693	up

MPF_contig_044938		0.037357267	-2.2539477	down
MPF_LOC100690258.1.1	XP_003440479.1 PREDICTED: annexin A2-A-like [Oreochromis niloticus]	0.02306824	-3.7015948	down
MPF_LOC101075367.4.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]	0.027706273	-1.8302488	down
MPF_LOC101477280.2.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.015841743	-3.410213	down
MPF_LOC100699178.1.1	XM_003438369.1 PREDICTED: Oreochromis niloticus inositol 1,4,5-triphosphate receptorinteracting protein-like (LOC100699178), mRNA	0.02710194	-2.524726	down
MPF_contig_014917		0.04630425	-1.302321	down
MPF_LOC101156898.1.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	0.031615667	-3.1431646	down
MPF_contig_035424		0.038819164	-1.169951	down
MPF_LOC101482372.2.4	XM_004542967.1 PREDICTED: Maylandia zebra macrophage mannose receptor 1-like (LOC101482372), mRNA	0.030398514	-3.7042985	down
MPF_RL7A.2.2	[BBH] RL7A_TAKRU (sp|O57592) 60S ribosomal protein L7a OS=Takifugu rubripes GN=rpl7a PE=3 SV=3	0.027706273	-1.5400019	down
MPF_LOC101463600.1.1	XM_004544939.1 PREDICTED: Maylandia zebra class E basic helix-loop-helix protein 40-like (LOC101463600), mRNA	0.031302825	-1.3047256	down
MPF_LOC101474121.17.17	XM_004575391.1 PREDICTED: Maylandia zebra stonustoxin subunit beta-like (LOC101474121), mRNA	0.049922515	-2.6756477	down
MPF_LOC101477399.1.1	XM_004538348.1 PREDICTED: Maylandia zebra uncharacterized LOC101477399 (LOC101477399), mRNA	0.016177904	-2.322365	down
MPF_LOC100933241.9.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.02741634	-2.9947305	down
MPF_LOC101162897.1.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]	0.016816037	-3.9189517	down
MPF_LOC101482220.3.3	XM_004571715.1 PREDICTED: Maylandia zebra h-2 class II histocompatibility antigen gamma chain-like (LOC101482220), mRNA	0.020052187	-4.002092	down
MPF_RS15A.1.5	[BBH] RS15A_RAT (sp|P62246) 40S ribosomal protein S15a OS=Rattus norvegicus GN=Rps15a PE=1 SV=2	0.049930144	-1.0061034	down
MPF_contig_016131		0.02018985	-2.3395472	down
MPF_RL37P.1.1	RL37P_RAT (sp|P61515) Putative 60S ribosomal protein L37a OS=Rattus norvegicus GN=Rpl37a-ps1 PE=5 SV=2	0.02069152	-2.7104921	down
MPF_contig_003939		0.026926706	-1.3570447	down
MPF_MIR142A.1.1	NR_030090.1 Danio rerio microRNA 142a (mir142a), microRNA	0.011679485	-3.584672	down
MPF_LOC101477280.5.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.01596322	-3.1822984	down
MPF_LOC101479551.1.1	XM_004555792.1 PREDICTED: Maylandia zebra SEC14-like protein 2-like (LOC101479551), mRNA	0.026884947	-1.3218994	down
MPF_AHNK.17.22	[BBH] AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.010595669	-4.665431	down
MPF_LOC101073984.1.2	XM_003972117.1 PREDICTED: Takifugu rubripes CREB-binding protein-like (LOC101073984), mRNA	0.02018985	1.0765052	up
MPF_LOC101474370.1.1	XM_004568239.1 PREDICTED: Maylandia zebra mitochondrial glutamate carrier 1-like (LOC101474370), transcript variant X3, mRNA	0.031615667	-1.8299801	down
MPF_LOC101479225.2.2	XM_004571532.1 PREDICTED: Maylandia zebra glucose-6-phosphate isomerase-like (LOC101479225), mRNA	0.043084357	1.0852712	up
MPF_LOC100704894.10.13	XM_003450635.1 PREDICTED: Oreochromis niloticus glyceraldehyde-3-phosphate dehydrogenase-like (LOC100704894), mRNA	0.02199939	-1.9439969	down
MPF_LOC100711796.2.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA	0.027706273	-2.1133456	down
MPF_contig_032146		0.019260636	-2.863822	down
MPF_LOC101485578.1.1	XM_004539623.1 PREDICTED: Maylandia zebra CD276 antigen-like (LOC101485578), mRNA	0.026884947	-1.9362664	down

MPF_contig_020082		0.029283023	-3.7698083	down
MPF_LOC101466143.5.18	XM_004574840.1 PREDICTED: Maylandia zebra 40S ribosomal protein S18-like (LOC101466143), mRNA	0.033782817	-1.6361094	down
MPF_contig_024224		0.016177904	-4.2613873	down
MPF_contig_029610		0.027453259	-1.0175009	down
MPF_LOC101061696.1.1	XM_003979541.1 PREDICTED: Takifugu rubripes zinc finger protein 467-like (LOC101061696), mRNA	0.024917157	1.1538844	up
MPF_LOC100933241.11.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.032603085	1.1172848	up
MPF_contig_028781		0.02741634	-1.7711796	down
MPF_LOC101477280.4.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.016254881	-3.1826806	down
MPF_LOC101171862.1.1	XM_004078612.1 PREDICTED: Oryzias latipes ras-related protein Rab-12-like (LOC101171862), mRNA	0.020620862	1.1435499	up

MPF_contig_000136		0.043856647	-2.6649742	down
MPF_HACE1.3.3	[BBH] HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2	0.04755172	-1.5680285	down
MPF_LOC101161674.1.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA	0.016254881	-2.7557812	down
MPF_EIF4A2.1.1	NM_001102893.1 Xenopus (Silurana) tropicalis eukaryotic translation initiation factor 4A2 (eif4a2), mRNA gb|BC135871.1| Xenopus tropicalis hypothetical protein LOC100124955, mRNA (cDNA clone MGC:121826 IMAGE:7637784), complete cds	0.04060607	-1.3138857	down
MPF_contig_035601		0.04140341	1.3696319	up
MPF_contig_018948	WP_006047458.1 hypothetical protein [Burkholderia graminis]	0.034148168	-2.1663942	down
MPF_contig_035116	XM_004567038.1 PREDICTED: Maylandia zebra transgelin-like (LOC101476292), transcript variant X1, mRNA	0.021553392	-4.205557	down
MPF_LECG.21.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.017680304	-4.315619	down
MPF_LOC101161574.14.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.016128596	-3.991218	down
MPF_contig_021317		0.041334953	-1.5516226	down
MPF_LECG.27.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.021617537	-3.6692095	down
MPF_LOC100702318.5.5	XP_003458375.1 PREDICTED: galectin-9-like [Oreochromis niloticus]	0.027632944	-2.383133	down
MPF_LOC101485836.2.2	XM_004559956.1 PREDICTED: Maylandia zebra muscle M-line assembly protein unc-89-like (LOC101485836), transcript variant X1, mRNA	0.040899336	2.2466402	up
MPF_CAL6303_1855.1.3	YP_007136861.1 hypothetical protein Cal6303_1855 [Calothrix sp. PCC 6303]	0.016254881	-2.6187553	down
MPF_LOC100704742.1.1	XP_003458221.1 PREDICTED: c-C motif chemokine 2-like [Oreochromis niloticus]	0.035424765	-1.8312569	down
MPF_LOC101466143.8.18	XM_004574840.1 PREDICTED: Maylandia zebra 40S ribosomal protein S18-like (LOC101466143), mRNA	0.04123251	-1.7863721	down
MPF_LOC101075367.1.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]	0.0279136	-1.9699564	down
MPF_LOC101159291.2.2	XM_004078003.1 PREDICTED: Oryzias latipes sodium/potassium-transporting ATPase subunit alpha-3-like (LOC101159291), mRNA	0.010595669	-3.7053943	down
MPF_contig_008714		0.010595669	-3.0373132	down
MPF_LOC101469709.1.2	XM_004569200.1 PREDICTED: Maylandia zebra eyes absent homolog 3-like (LOC101469709), transcript variant X2, mRNA	0.025986498	1.2698334	up
MPF_contig_023224		0.010595669	-3.2988439	down

MPF_LOC101475324.3.5	XM_004570832.1 PREDICTED: Maylandia zebra MOB kinase activator 2-like (LOC101475324), transcript variant X4, mRNA	0.019848077	-1.4473352	down
MPF_contig_040702		0.048345108	-3.0369475	down
MPF_POPTRDRAFT_794775.3.5	XP_002338344.1 predicted protein [Populus trichocarpa]	0.02589493	-1.2670592	down
MPF_LOC100698256.2.2	XM_003454320.1 PREDICTED: Oreochromis niloticus tubulin beta-6 chain-like (LOC100698256), mRNA	0.03196701	-1.5821128	down
MPF_contig_035342		0.038551345	-1.2822952	down
MPF_LOC100698082.2.2	XR_134880.1 PREDICTED: Oreochromis niloticus keratin, type I cytoskeletal 13-like (LOC100698082), miscRNA	0.01596322	-4.658929	down
MPF_LOC101155699.2.2	XM_004073699.1 PREDICTED: Oryzias latipes protein S100-A10-like (LOC101155699), mRNA	0.014915122	-4.3437076	down
MPF_LOC101077514.3.5	XP_003974477.1 PREDICTED: complement factor H-like [Takifugu rubripes]	0.024133291	-3.472116	down
MPF_contig_002780		0.046603955	1.0406847	up
MPF_LOC101474419.1.1	XM_004554493.1 PREDICTED: Maylandia zebra sperm-associated antigen 17-like (LOC101474419), mRNA	0.011256327	2.0044348	up
MPF_LOC100699721.2.2	XP_003460016.1 PREDICTED: bifunctional protein NCOAT-like, partial [Oreochromis niloticus]	0.016491378	-2.5345495	down
MPF_contig_038580		0.02030712	1.3546643	up
MPF_LOC101061679.1.1	XM_003975895.1 PREDICTED: Takifugu rubripes cAMP-responsive element modulator-like (LOC101061679), mRNA	0.02461522	-1.6132107	down
MPF_LOC100690401.2.3	XP_003454006.1 PREDICTED: hypothetical protein LOC100690401 [Oreochromis niloticus]	0.02741634	-3.13346	down
MPF_RL13.2.5	RL13_DANRE (sp|Q90Z10) 60S ribosomal protein L13 OS=Danio rerio GN=rpl13 PE=2 SV=3	0.039345793	-1.4088812	down
MPF_LOC101478586.2.2	XM_004550792.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 6-like (LOC101478586), transcript variant X2, mRNA	0.023772364	-2.6585898	down
MPF_contig_027404	XM_004568351.1 PREDICTED: Maylandia zebra protein kinase C beta type-like (LOC101478005), transcript variant X1, mRNA	0.02030712	-2.8329215	down
MPF_contig_019917		0.01596322	-2.8853035	down
MPF_LOC101156017.1.1	XP_004072239.1 PREDICTED: prostate stem cell antigen-like [Oryzias latipes]	0.024245406	-1.0245366	down
MPF_LOC101468983.2.2	XR_191999.1 PREDICTED: Maylandia zebra uncharacterized LOC101468983 (LOC101468983), misc_RNA	0.046603955	-1.4673553	down
MPF_AHNAK.4.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]	0.011679485	-4.641178	down
MPF_LOC100707140.3.4	XP_003458392.1 PREDICTED: hypothetical protein LOC100707140 [Oreochromis niloticus]	0.02030712	-1.9841537	down
MPF_LOC101476920.1.1	XM_004563122.1 PREDICTED: Maylandia zebra c-X-C chemokine receptor type 4-like (LOC101476920), mRNA	0.04883595	-1.6817117	down
MPF_contig_037980		0.023772364	-3.2302353	down
MPF_LOC101487021.1.1	XM_004540761.1 PREDICTED: Maylandia zebra thrombospondin-1-like (LOC101487021), transcript variant X2, mRNA	0.024917157	-3.6701276	down
MPF_AHNK.16.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.010595669	-4.857336	down
MPF_RSSA.9.9	RSSA_SPAAU (sp|Q4QY71) 40S ribosomal protein SA OS=Sparus aurata GN=rpsa PE=2 SV=2	0.04076093	-1.4135599	down
MPF_LOC101477831.3.3	XM_004548827.1 PREDICTED: Maylandia zebra complement C1q subcomponent subunit Blike (LOC101477831), mRNA	0.031615667	-3.2726812	down
MPF_LY9.3.3	LY9_HUMAN (sp|Q9HBG7) T-lymphocyte surface antigen Ly-9 OS=Homo sapiens GN=LY9 PE=1 SV=3	0.027954783	-2.2812166	down

MPF_contig_047695		0.04715796	1.6888715	up
MPF_LOC101070622.2.2	XM_003976449.1 PREDICTED: Takifugu rubripes glucose-6-phosphate isomerase-like, transcript variant 1 (LOC101070622), mRNA	0.046601474	1.0307854	up
MPF_SI_CH211-125E6.5.1.1	XP_001337601.1 PREDICTED: type-2 ice-structuring protein-like [Danio rerio]	0.034577772	-2.27775	down
MPF_contig_026633	XM_004549165.1 PREDICTED: Maylandia zebra neurocalcin-delta B-like (LOC101473406), transcript variant X2, mRNA	0.035424765	1.0537696	up
MPF_RL13.5.5	RL13_DANRE (sp|Q90Z10) 60S ribosomal protein L13 OS=Danio rerio GN=rpl13 PE=2 SV=3	0.04575675	-1.331337	down
MPF_LOC101475111.1.1	XM_004543683.1 PREDICTED: Maylandia zebra Down syndrome cell adhesion moleculelike protein 1 homolog (LOC101475111), transcript variant X1, mRNA	0.023065256	1.405611	up
MPF_MMP9.5.5	XM_003448139.1 PREDICTED: Oreochromis niloticus matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA	0.024133291	-1.338435	down
MPF_LOC101477415.1.3	XM_004565046.1 PREDICTED: Maylandia zebra leucine-rich repeat and fibronectin type III domain-containing protein 1-like protein-like (LOC101477415), mRNA	0.027954783	1.0070281	up
MPF_contig_042113	XM_004569199.1 PREDICTED: Maylandia zebra eyes absent homolog 3-like (LOC101469709), transcript variant X1, mRNA	0.025232468	1.2951955	up
MPF_contig_029437		0.034515023	1.4157809	up
MPF_LOC101156898.3.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	0.03156658	-3.4301386	down
MPF_LOC100707640.1.2	XP_003451524.1 PREDICTED: hypothetical protein LOC100707640 [Oreochromis niloticus]	0.035043854	-1.1387247	down
MPF_LOC100695691.2.2	XM_003455952.1 PREDICTED: Oreochromis niloticus actin-related protein 2/3 complex subunit 1B-like (LOC100695691), mRNA	0.01596322	-4.0656767	down
MPF_LOC101475950.3.3	XM_004553845.1 PREDICTED: Maylandia zebra cAMP-specific 3',5'-cyclic phosphodiesterase 4B-like (LOC101475950), transcript variant X3, mRNA	0.022510305	-3.3737621	down
MPF_contig_024077		0.025514856	-1.0611486	down
MPF_LOC100706937.4.4	XM_003449406.1 PREDICTED: Oreochromis niloticus myeloid protein 1-like (LOC100706937), mRNA	0.02018985	-1.4127293	down
MPF_LOC101483451.1.1	XM_004547058.1 PREDICTED: Maylandia zebra fumarylacetoacetate hydrolase domaincontaining protein 2-like (LOC101483451), transcript variant X2, mRNA	0.034577772	-1.8549228	down
MPF_C1QA.2.2	[BBH] C1QA_PIG (sp|Q69DL0) Complement C1q subcomponent subunit A OS=Sus scrofa GN=C1QA PE=2 SV=1	0.02461522	-3.8644705	down
MPF_contig_032442		0.031308513	-2.5490496	down
MPF_RL37A.1.1	RL37A_XENLA (sp|Q7SZB4) 60S ribosomal protein L37a OS=Xenopus laevis GN=rpl37a PE=3 SV=3	0.022020996	-2.6677408	down
MPF_LOC100708534.1.1	XM_003447507.1 PREDICTED: Oreochromis niloticus myeloid-associated differentiation marker homolog (LOC100708534), mRNA	0.01596322	-4.5034986	down
MPF_RPS18.2.2	XM_004267744.1 PREDICTED: Orcinus orca ribosomal protein S18 (RPS18), mRNA	0.045904655	-1.7601929	down
MPF_LOC100693926.1.1	XM_003438350.1 PREDICTED: Oreochromis niloticus protein FAM36A-like (LOC100693926), mRNA	0.048272904	1.1365247	up
MPF_LOC100705244.1.1	XM_003450063.1 PREDICTED: Oreochromis niloticus heme oxygenase 2-like (LOC100705244), mRNA	0.025232468	-2.0720901	down
MPF_contig_004075		0.033316415	-1.2522435	down
MPF_LOC100700248.2.5	XP_003459295.1 PREDICTED: butyrophilin-like protein 2-like [Oreochromis niloticus]	0.033044502	-1.699127	down
MPF_LOC100699383.1.6	XM_003445310.1 PREDICTED: Oreochromis niloticus translationally-controlled tumor protein homolog (LOC100699383), mRNA	0.02201327	1.1309195	up
MPF_contig_026335		0.04679448	-2.917039	down
MPF_contig_034209	XM_003198881.1 PREDICTED: Danio rerio retrotransposable element Tf2 155 kDa protein type 1-like (LOC100535308), mRNA	0.043856647	-1.7796706	down
MPF_LOC101482272.1.1	XM_004564790.1 PREDICTED: Maylandia zebra probable ATP-dependent RNA helicase DDX49-like (LOC101482272), mRNA	0.04883595	-1.7868649	down

MPF_LOC101474986.3.3	XM_004556522.1 PREDICTED: Maylandia zebra F-box/LRR-repeat protein 19-like (LOC101474986), mRNA	0.036671814	1.1087117	up
MPF_LOC101486559.2.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA	0.010595669	-4.148514	down
MPF_LOC100703996.2.2	XM_003450220.1 PREDICTED: Oreochromis niloticus armadillo repeat-containing protein 4like (LOC100703996), mRNA	0.021017518	1.1072116	up
MPF_LOC101486920.1.1	XM_004539290.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12-like (LOC101486920), mRNA	0.049979005	2.0353622	up
MPF_LOC101487453.1.2	XM_004548571.1 PREDICTED: Maylandia zebra aflatoxin B1 aldehyde reductase member 2like (LOC101487453), mRNA	0.041334953	1.0375476	up
MPF_contig_017069		0.04123251	1.0007534	up
MPF_LOC101469336.3.3	XM_004566007.1 PREDICTED: Maylandia zebra ras-related protein M-Ras-like (LOC101469336), mRNA	0.024245406	-1.48767	down
MPF_contig_028086		0.041281193	-2.933936	down
MPF_LOC101482754.1.1	XM_004564324.1 PREDICTED: Maylandia zebra serine-rich adhesin for platelets-like (LOC101482754), transcript variant X2, mRNA	0.03639751	1.0910387	up
MPF_contig_020945	XM_004542601.1 PREDICTED: Maylandia zebra muscleblind-like protein 1-like (LOC101483053), transcript variant X16, mRNA	0.023065256	-3.5618382	down
MPF_LOC101069688.1.1	XM_003973598.1 PREDICTED: Takifugu rubripes uncharacterized LOC101069688 (LOC101069688), mRNA	0.02482209	1.0437307	up
MPF_LOC101486124.4.4	XM_004575749.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12-like (LOC101486124), mRNA	0.04574575	-2.8384438	down
MPF_contig_023403		0.041281193	-1.0466113	down
MPF_LOC101482220.2.3	XM_004571715.1 PREDICTED: Maylandia zebra h-2 class II histocompatibility antigen gamma chain-like (LOC101482220), mRNA	0.02030712	-4.0491114	down
MPF_LOC100696784.1.1	XP_003441680.1 PREDICTED: HHIP-like protein 1-like [Oreochromis niloticus]	0.01596322	-2.8237202	down
MPF_contig_031843		0.02766524	1.197504	up
MPF_LOC101479225.1.2	XM_004571532.1 PREDICTED: Maylandia zebra glucose-6-phosphate isomerase-like (LOC101479225), mRNA	0.024917157	1.0550919	up
MPF_LOC101170487.4.4	XM_004085086.1 PREDICTED: Oryzias latipes low-density lipoprotein receptor 2-like (LOC101170487), mRNA	0.027569868	-2.0285325	down
MPF_contig_024095		0.027706273	-1.0366569	down
MPF_contig_017097		0.025415389	-2.6924741	down
MPF_contig_023411		0.04276229	-1.6748481	down
MPF_LOC100690793.2.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]	0.02199939	-4.0478826	down
MPF_contig_016299		0.037575997	1.0237049	up
MPF_contig_000405		0.048983328	-1.7235842	down
MPF_contig_018588	XM_004541787.1 PREDICTED: Maylandia zebra NHS-like protein 1-like (LOC101470763), transcript variant X7, mRNA	0.03861742	1.0770426	up
MPF_contig_015875		0.01914008	-2.9934645	down
MPF_contig_033424		0.0160005	-5.187712	down
MPF_LOC100706109.1.1	XM_003443229.1 PREDICTED: Oreochromis niloticus cyclic AMP-dependent transcription factor ATF-4-like (LOC100706109), mRNA	0.04755172	-1.2921615	down
MPF_contig_037687		0.031615667	1.7471713	up

MPF_contig_047204	XM_004553104.1 PREDICTED: Maylandia zebra immunoglobulin superfamily containing leucine-rich repeat protein 2-like (LOC101471771), transcript variant X1, mRNA	0.040625155	1.0847297	up
MPF_LOC101479214.1.1	XM_004545538.1 PREDICTED: Maylandia zebra sodium/potassium/calcium exchanger 3like (LOC101479214), mRNA	0.02899486	1.0143604	up
MPF_LOC101477532.1.1	XM_004569581.1 PREDICTED: Maylandia zebra claudin-4-like (LOC101477532), mRNA	0.025415389	1.0354319	up
MPF_LOC101468583.4.7	XM_004576296.1 PREDICTED: Maylandia zebra uncharacterized LOC101468583 (LOC101468583), mRNA	0.04813241	-1.5453242	down
MPF_LOC101485370.6.6	XM_004556380.1 PREDICTED: Maylandia zebra hepatic leukemia factor-like (LOC101485370), mRNA	0.02524851	1.2587881	up
MPF_LOC100710617.1.3	XP_003456137.1 PREDICTED: biogenesis of lysosome-related organelles complex 1 subunit 1-like [Oreochromis niloticus]	0.04123251	-3.6618443	down
MPF_LOC101471364.1.1	XM_004549927.1 PREDICTED: Maylandia zebra tenascin-like (LOC101471364), transcript variant X5, mRNA	0.037600752	-1.0299149	down
MPF_LOC101466239.3.3	XM_004550939.1 PREDICTED: Maylandia zebra apolipoprotein Eb-like (LOC101466239), mRNA	0.024245406	-3.4064746	down
MPF_LOC101484769.1.1	XM_004571907.1 PREDICTED: Maylandia zebra transcription factor MafB-like (LOC101484769), mRNA	0.032085758	-2.988831	down
MPF_LOC101481265.1.2	XM_004574593.1 PREDICTED: Maylandia zebra E3 ubiquitin/ISG15 ligase TRIM25-like (LOC101481265), mRNA	0.034446273	1.2290385	up
MPF_contig_009915		0.03944039	-1.8779895	down
MPF_LOC100304566.1.1	NM_001200148.1 Ictalurus punctatus 40S ribosomal protein S14 (LOC100304566), mRNA gb|GU589378.1| Ictalurus punctatus clone CBCZ11290 40S ribosomal protein s14 (RS14) mRNA, complete cds	0.046990186	-1.7274008	down
MPF_LOC101479573.1.2	XM_004565228.1 PREDICTED: Maylandia zebra lysosomal acid lipase/cholesteryl ester hydrolase-like (LOC101479573), mRNA	0.043084357	-1.4410739	down
MPF_LOC100711789.5.22	XP_003457783.1 PREDICTED: neural cell adhesion molecule 2-like [Oreochromis niloticus]	0.04883595	-2.1078715	down
MPF_LOC100691160.2.2	XP_003459991.1 PREDICTED: 5-hydroxytryptamine receptor 3A-like [Oreochromis niloticus]	0.01596322	-1.7100616	down
MPF_LOC101061379.1.2	XP_003976891.1 PREDICTED: sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1-like, partial [Takifugu rubripes]	0.038888626	-2.0479393	down
MPF_ANXA1.1.2	NP_001098295.1 annexin max3 [Oryzias latipes]	0.024917157	-1.5418577	down
MPF_LOC101484400.1.5	XM_004572910.1 PREDICTED: Maylandia zebra 60S ribosomal protein L22-like 1-like (LOC101484400), mRNA	0.024884876	-2.130396	down
MPF_LOC101477695.1.9	XM_004564867.1 PREDICTED: Maylandia zebra 60S ribosomal protein L18a-like (LOC101477695), transcript variant X2, mRNA	0.024133291	-1.3278389	down
MPF_LOC101169293.6.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.03331326	-1.1812339	down
MPF_LOC100929802.1.1	XP_003761948.1 PREDICTED: uncharacterized protein LOC100929802 [Sarcophilus harrisii]	0.027632944	-2.3838558	down
MPF_LOC569742.1.1	XP_698239.5 PREDICTED: hypothetical protein LOC569742 [Danio rerio]	0.02589493	-1.5339935	down
MPF_contig_008449	XM_004575192.1 PREDICTED: Maylandia zebra histone deacetylase 4-like (LOC101464986), transcript variant X2, mRNA	0.046821542	1.1777492	up
MPF_ENPP1.1.2	XM_003446358.1 PREDICTED: Oreochromis niloticus ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA	0.015058853	-3.1957436	down
MPF_contig_045727		0.024133291	1.3548486	up
MPF_LOC100690179.11.21	XM_003441609.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S25-like (LOC100690179), mRNA	0.048345108	-1.1964602	down
MPF_contig_034121		0.048983328	1.0508599	up
MPF_contig_030749		0.02018985	-2.7968354	down
MPF_contig_045587		0.04575675	1.1523936	up
MPF_LOC101465148.1.1	XM_004569455.1 PREDICTED: Maylandia zebra brain acid soluble protein 1-like (LOC101465148), transcript variant X1, mRNA	0.017680304	-4.0202026	down

MPF_LOC100692629.1.1	XM_003448362.1 PREDICTED: Oreochromis niloticus complement C1q subcomponent subunit C-like, transcript variant 2 (LOC100692629), mRNA	0.02461522	-3.7707224	down
MPF_contig_019847		0.04281289	-1.0091057	down
MPF_LOC101476819.3.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0.02018985	-1.669444	down
MPF_contig_043263		0.026633183	1.2844949	up

MPF_LOC101465079.2.2	XM_004551108.1 PREDICTED: Maylandia zebra basal cell adhesion molecule-like (LOC101465079), mRNA	0.017280372	-3.0683866	down
MPF_LOC101477400.4.4	XM_004538536.1 PREDICTED: Maylandia zebra cyclin-G2-like (LOC101477400), mRNA	0.010595669	1.0048876	up
MPF_LOC100697750.1.3	XM_003459604.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domainscontaining protein 14-like (LOC100697750), mRNA	0.019615307	-2.986568	down
MPF_LOC101469041.3.4	XM_004566363.1 PREDICTED: Maylandia zebra CREB-regulated transcription coactivator 3like (LOC101469041), transcript variant X4, mRNA	0.024245406	1.1367348	up
MPF_LOC101471553.1.1	XM_004572678.1 PREDICTED: Maylandia zebra protein capicua homolog (LOC101471553), transcript variant X4, mRNA	0.01596322	-1.4893522	down
MPF_LOC100691105.1.2	XP_003449231.1 PREDICTED: cytochrome c oxidase subunit 8B, mitochondrial-like [Oreochromis niloticus]	0.023065256	-2.9147549	down
MPF_LOC101480392.1.1	XM_004552287.1 PREDICTED: Maylandia zebra polymerase I and transcript release factorlike (LOC101480392), mRNA	0.039953947	1.713103	up
MPF_CFAH.8.15	CFAH_BOVIN (sp|Q28085) Complement factor H OS=Bos taurus GN=CFH PE=1 SV=3	0.024295906	-3.499118	down
MPF_LOC101484951.3.3	XM_004546887.1 PREDICTED: Maylandia zebra myosin regulatory light chain 2, smooth muscle minor isoform-like (LOC101484951), mRNA	0.02306824	-1.5125604	down
MPF_LOC100690212.1.1	XP_003452133.1 PREDICTED: protein NDRG1-like [Oreochromis niloticus]	0.024663433	1.7411314	up
MPF_LOC101472043.8.14	XM_004573789.1 PREDICTED: Maylandia zebra tight junction-associated protein 1-like (LOC101472043), transcript variant X4, mRNA	0.024917157	-2.3999493	down
MPF_LOC101465857.2.2	XM_004552698.1 PREDICTED: Maylandia zebra endophilin-A2-like (LOC101465857), transcript variant X1, mRNA	0.04755172	1.0572023	up
MPF_MXAN_5876.1.1	YP_634013.1 hypothetical protein MXAN_5876 [Myxococcus xanthus DK 1622]	0.010595669	-1.9627056	down
MPF_contig_011640		0.020052187	-3.8930922	down
MPF_LOC101473892.1.1	XM_004569569.1 PREDICTED: Maylandia zebra transforming growth factor beta-1-like (LOC101473892), transcript variant X2, mRNA	0.013443254	-3.313236	down
MPF_LOC101466169.1.1	XM_004558785.1 PREDICTED: Maylandia zebra formin-like protein 3-like (LOC101466169), transcript variant X2, mRNA	0.024917157	-2.2764766	down
MPF_LOC100706528.2.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0.010595669	1.128129	up
MPF_LOC101469041.2.4	XM_004566363.1 PREDICTED: Maylandia zebra CREB-regulated transcription coactivator 3like (LOC101469041), transcript variant X4, mRNA	0.010595669	1.0276914	up
MPF_LOC100703961.1.1	XM_003441739.1 PREDICTED: Oreochromis niloticus CDP-diacylglycerol--glycerol-3phosphate 3-phosphatidyltransferase, mitochondrial-like (LOC100703961), mRNA	0.040899336	1.0641356	up
MPF_LOC100710975.1.1	XP_003456782.1 PREDICTED: trimethylguanosine synthase-like [Oreochromis niloticus]	0.046641655	1.0143023	up
MPF_contig_018633		0.025232468	1.0503359	up
MPF_LOC101167345.32.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA	0.03909383	-2.3307319	down
MPF_LOC101470650.2.2	XM_004540130.1 PREDICTED: Maylandia zebra nesprin-1-like (LOC101470650), transcript variant X2, mRNA	0.039509952	-1.2295299	down
MPF_LOC101464586.2.2	XM_004571741.1 PREDICTED: Maylandia zebra tensin-3-like (LOC101464586), transcript variant X3, mRNA	0.031615667	-1.1382576	down
MPF_LOC101487230.3.3	XM_004568550.1 PREDICTED: Maylandia zebra pre-B-cell leukemia transcription factor 2like (LOC101487230), mRNA	0.021017518	-2.4174345	down
MPF_LOC101476997.1.2	XM_004552000.1 PREDICTED: Maylandia zebra microtubule-associated protein futsch-like (LOC101476997), mRNA	0.024133291	1.3181244	up

MPF_LOC101472858.1.1	XM_004538683.1 PREDICTED: Maylandia zebra protein PAT1 homolog 1-like (LOC101472858), transcript variant X2, mRNA	0.026778538	1.1495292	up
MPF_LOC101476475.1.1	XM_004562669.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 3-like (LOC101476475), mRNA	0.013250615	-5.194483	down
MPF_LECG.5.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.031792324	-2.3973546	down
MPF_LOC101487747.1.2	XM_004573537.1 PREDICTED: Maylandia zebra membrane-spanning 4-domains subfamily A member 15-like (LOC101487747), transcript variant X3, mRNA	0.019260636	-2.610291	down
MPF_LOC101472370.1.1	XM_004538428.1 PREDICTED: Maylandia zebra gelsolin-like (LOC101472370), transcript variant X2, mRNA	0.04575675	-2.7188964	down
MPF_contig_047566		0.02589493	-1.5879126	down
MPF_LOC100698899.1.1	XM_003457691.1 PREDICTED: Oreochromis niloticus protein PAT1 homolog 1-like (LOC100698899), mRNA	0.024917157	1.1972094	up
MPF_LOC101487706.1.1	XM_004565535.1 PREDICTED: Maylandia zebra cAMP-responsive element modulator-like (LOC101487706), transcript variant X2, mRNA	0.024245406	-1.5969191	down
MPF_LOC101171725.2.3	XP_004085595.1 PREDICTED: putative nuclease HARBI1-like [Oryzias latipes]	0.04755172	-1.0277174	down
MPF_contig_002650	XM_004079020.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 1 (LOC101161674), mRNA	0.016177904	-2.824422	down
MPF_LOC101481244.1.1	XM_004547901.1 PREDICTED: Maylandia zebra cytoplasmic dynein 1 intermediate chain 1like (LOC101481244), transcript variant X3, mRNA	0.04454718	1.0100985	up
MPF_LOC101466590.1.1	XM_004569012.1 PREDICTED: Maylandia zebra partner and localizer of BRCA2-like (LOC101466590), transcript variant X5, mRNA	0.02151995	-1.160481	down
MPF_LOC101163218.1.1	XP_004083710.1 PREDICTED: integrator complex subunit 9-like [Oryzias latipes]	0.034743514	-1.8777605	down
MPF_LOC101472227.1.1	XM_004549440.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase Topors-like (LOC101472227), mRNA	0.004379576	1.1332686	up
MPF_contig_030303		0.019260636	-1.0776538	down
MPF_contig_033809		0.024397738	1.3766232	up
MPF_LOC100696287.1.2	XP_003450735.1 PREDICTED: C-type lectin domain family 9 member A-like isoform 1 [Oreochromis niloticus]	0.014775532	-3.7527184	down
MPF_LOC101169293.1.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.026633183	-1.8194587	down
MPF_LOC100702771.1.1	XP_003459231.1 PREDICTED: WD repeat-containing protein 78-like [Oreochromis niloticus]	0.03466951	1.088139	up
MPF_LOC100703241.8.9	XM_003440649.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S29-like (LOC100703241), mRNA	0.04311773	-1.3653878	down
MPF_FZD6.5.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440 IMAGE:6971142), complete cds	0.037214924	-2.2545743	down
MPF_LOC100705063.1.1	XP_003446533.1 PREDICTED: cleavage stimulation factor subunit 1-like [Oreochromis niloticus]	0.020052187	1.6277424	up
MPF_contig_032831		0.011256327	-2.9913795	down
MPF_RT28.3.8	RT28_BOVIN (sp|P82928) 28S ribosomal protein S28, mitochondrial OS=Bos taurus GN=MRPS28 PE=1 SV=2	0.034446273	-1.5420966	down
MPF_contig_034792		0.02412605	-1.6092439	down
MPF_LOC100706528.1.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0.011256327	1.1620841	up
MPF_LOC100702519.1.1	XM_003441393.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702519), mRNA	0.026863318	-2.9105377	down
MPF_LOC101485221.2.2	XM_004541104.1 PREDICTED: Maylandia zebra disintegrin and metalloproteinase domaincontaining protein 19-like (LOC101485221), mRNA	0.02030712	-2.7221787	down
MPF_LOC100702817.1.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.011256327	-4.0485835	down

MPF_LOC101473182.1.3	XM_004566836.1 PREDICTED: Maylandia zebra sialoadhesin-like (LOC101473182), transcript variant X2, mRNA	0.010595669	-3.5355086	down
MPF_LOC100698726.1.1	XP_003460290.1 PREDICTED: hypothetical protein LOC100698726 [Oreochromis niloticus]	0.04833266	-3.8359604	down
MPF_LOC101479305.2.6	XM_004546110.1 PREDICTED: Maylandia zebra cytosolic sulfotransferase 3-like (LOC101479305), transcript variant X2, mRNA	0.024245406	-1.0280714	down
MPF_LOC101486209.1.4	XM_004551098.1 PREDICTED: Maylandia zebra uncharacterized LOC101486209 (LOC101486209), mRNA	0.011256327	-4.068742	down
MPF_LOC101468855.3.3	XM_004569017.1 PREDICTED: Maylandia zebra protein tweety homolog 3-like (LOC101468855), transcript variant X1, mRNA	0.031615667	-2.1600642	down
MPF_LOC101472936.1.2	XM_004553303.1 PREDICTED: Maylandia zebra FERM domain-containing protein 4A-like (LOC101472936), mRNA	0.025415389	-1.7362502	down
MPF_LOC101080012.1.1	XM_003977798.1 PREDICTED: Takifugu rubripes CDP-diacylglycerol--serine Ophosphatidyltransferase-like (LOC101080012), mRNA	0.037583128	-1.260733	down
MPF_TNR1B.1.1	[BBH] TNR1B_MOUSE (sp|P25119) Tumor necrosis factor receptor superfamily member 1B OS=Mus musculus GN=Tnfrsf1b PE=2 SV=1	0.010595669	-4.268846	down
MPF_LECE.1.1	LECE_HELCR (sp|P06027) Echinoidin OS=Heliocidaris crassispina PE=1 SV=1	0.0160005	-4.5240293	down
MPF_LOC101464596.2.2	XM_004551025.1 PREDICTED: Maylandia zebra sodium/hydrogen exchanger 1-like (LOC101464596), transcript variant X2, mRNA	0.019260636	-2.3810601	down
MPF_contig_009890	XM_003198881.1 PREDICTED: Danio rerio retrotransposable element Tf2 155 kDa protein type 1-like (LOC100535308), mRNA	0.025956307	1.3059599	up
MPF_LOC101465329.3.4	XM_004566526.1 PREDICTED: Maylandia zebra glutaminyl-peptide cyclotransferase-like (LOC101465329), mRNA	0.03639751	-1.470139	down
MPF_LOC101470763.1.1	XM_004541788.1 PREDICTED: Maylandia zebra NHS-like protein 1-like (LOC101470763), transcript variant X8, mRNA	0.03944039	1.1830983	up
MPF_LOC101479388.2.2	XM_004567238.1 PREDICTED: Maylandia zebra SH3-containing GRB2-like protein 3interacting protein 1-like (LOC101479388), mRNA	0.021017518	1.3401057	up
MPF_LOC101483284.1.1	XM_004550633.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase TRIM9-like (LOC101483284), transcript variant X2, mRNA	0.031615667	1.1622171	up
MPF_LOC101474179.2.3	XM_004568681.1 PREDICTED: Maylandia zebra nucleolin 2-like (LOC101474179), mRNA	0.01708796	-3.3519416	down
MPF_LOC101156352.1.1	XP_004077953.1 PREDICTED: ictacalcin-like [Oryzias latipes]	0.0145814	-3.2554822	down
MPF_FZD6.6.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440 IMAGE:6971142), complete cds	0.010595669	-3.3157957	down
MPF_LOC101480831.3.3	XM_004565417.1 PREDICTED: Maylandia zebra putative 60S ribosomal protein L37a-like (LOC101480831), mRNA	0.02018985	-2.764575	down
MPF_LOC101078462.1.1	XP_003965271.1 PREDICTED: lysosome membrane protein 2-like [Takifugu rubripes]	0.021017518	-3.7043552	down
MPF_LOC101484118.1.2	XM_004570768.1 PREDICTED: Maylandia zebra SLIT-ROBO Rho GTPase-activating protein 1-like (LOC101484118), transcript variant X4, mRNA	0.048983328	-1.1602435	down
MPF_LOC101074275.1.1	XP_003968653.1 PREDICTED: transforming growth factor beta-1-like [Takifugu rubripes]	0.017280372	-3.2558346	down
MPF_contig_027617		0.034148168	-1.3521528	down
MPF_contig_014802		0.024397738	-1.6706035	down
MPF_LOC101484400.2.5	XM_004572910.1 PREDICTED: Maylandia zebra 60S ribosomal protein L22-like 1-like (LOC101484400), mRNA	0.02782313	-1.9517006	down
MPF_LOC100711510.1.8	XM_003455849.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100711510), mRNA	0.016177904	-3.064332	down
MPF_LOC101486559.1.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA	0.011256327	-4.396509	down
MPF_LOC100689895.3.13	XP_003459184.1 PREDICTED: coxsackievirus and adenovirus receptor homolog [Oreochromis niloticus]	0.024245406	-1.6544156	down
MPF_contig_013338		0.031615667	-3.4652941	down
MPF_LOC100711484.2.8	XM_003448843.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100711484), mRNA	0.02407089	1.7795107	up

MPF_LOC100706330.1.1	XP_003457684.1 PREDICTED: hypothetical protein LOC100706330 [Oreochromis niloticus]	0.025415389	-2.3679423	down
MPF_contig_023699		0.017280372	-3.332151	down
MPF_LOC101464934.1.3	XM_004565357.1 PREDICTED: Maylandia zebra matrix metalloproteinase-14-like (LOC101464934), mRNA	0.02055744	-3.3865588	down
MPF_ZN226.1.1	ZN226_HUMAN (sp|Q9NYT6) Zinc finger protein 226 OS=Homo sapiens GN=ZNF226 PE=1 SV=2	0.025795393	1.5274768	up
MPF_LOC101469089.6.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA	0.04715796	-1.6154528	down
MPF_LOC101485244.1.1	XM_004568719.1 PREDICTED: Maylandia zebra zinc transporter 1-like (LOC101485244), mRNA	0.03284151	-1.9072232	down
MPF_contig_028808		0.024917157	-3.549377	down

MPF_LOC100701223.2.2	XM_003455894.1 PREDICTED: Oreochromis niloticus protein FAM165B-like (LOC100701223), mRNA	0.040899336	1.0933709	up
MPF_LOC101485628.1.3	XM_004574692.1 PREDICTED: Maylandia zebra beta-1,4-mannosyl-glycoprotein 4-beta-Nacetylglucosaminyltransferase-like (LOC101485628), transcript variant X5, mRNA	0.025795393	-2.5247326	down
MPF_contig_031758	XM_004550291.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1like (LOC101467183), transcript variant X2, mRNA	0.031615667	-2.202722	down
MPF_LOC101476648.1.1	XM_004538345.1 PREDICTED: Maylandia zebra chondroitin sulfate proteoglycan 4-like (LOC101476648), transcript variant X1, mRNA	0.046603955	2.3466945	up
MPF_contig_008230		0.01596322	-2.7904758	down
MPF_LOC101477091.1.3	XM_004574318.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1like (LOC101477091), transcript variant X5, mRNA	0.020559568	-1.2435699	down
MPF_LOC100690401.1.3	XP_003454006.1 PREDICTED: hypothetical protein LOC100690401 [Oreochromis niloticus]	0.03863755	-2.8901513	down
MPF_LOC101474833.1.3	XM_004570025.1 PREDICTED: Maylandia zebra bcl-2-like protein 11-like (LOC101474833), mRNA	0.010595669	-2.951158	down
MPF_LOC100703589.1.1	XM_003460117.1 PREDICTED: Oreochromis niloticus plasminogen activator inhibitor 1-like (LOC100703589), mRNA	0.01596322	-4.847616	down
MPF_LOC100697012.1.1	XP_003454202.1 PREDICTED: F-box only protein 21-like [Oreochromis niloticus]	0.04956417	1.0423331	up
MPF_AHNK.21.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.010595669	-4.3120737	down
MPF_contig_037191		0.049437914	1.4353426	up
MPF_contig_024444		0.023097917	1.1093855	up
MPF_LOC101475556.1.1	XM_004575798.1 PREDICTED: Maylandia zebra junction plakoglobin-like (LOC101475556), transcript variant X2, mRNA	0.0333852	1.844653	up
MPF_LOC101475584.3.5	XM_004561039.1 PREDICTED: Maylandia zebra thrombospondin type-1 domain-containing protein 7A-like (LOC101475584), mRNA	0.01596322	-3.7047977	down
MPF_LOC101075004.1.1	XM_003964966.1 PREDICTED: Takifugu rubripes uncharacterized LOC101075004 (LOC101075004), mRNA	0.018696768	-4.2383823	down
MPF_LOC101472438.1.4	XM_004575387.1 PREDICTED: Maylandia zebra collagen alpha-5(IV) chain-like (LOC101472438), mRNA	0.011256327	-2.7807279	down
MPF_LOC101482569.1.3	XM_004541189.1 PREDICTED: Maylandia zebra 60S ribosomal protein L18-like (LOC101482569), mRNA	0.048724335	-1.2786936	down
MPF_LOC100696821.2.2	XM_003452445.1 PREDICTED: Oreochromis niloticus ictacalcin-like (LOC100696821), mRNA	0.025232468	-3.0984662	down
MPF_DGCR2.2.2	NM_001002656.2 Danio rerio DiGeorge syndrome critical region gene 2 (dgcr2), mRNA	0.024245406	1.3022457	up
MPF_contig_029231		0.017680304	-2.1728873	down
MPF_contig_028541		0.027632944	-3.1658206	down

MPF_LOC101469089.2.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA	0.04575675	-1.64361	down
MPF_LOC100711789.8.22	XP_003457783.1 PREDICTED: neural cell adhesion molecule 2-like [Oreochromis niloticus]	0.04374933	-1.1040391	down
MPF_LOC100692490.4.4	XM_003457423.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L37a-like (LOC100692490), mRNA	0.024245406	2.5830426	up
MPF_HEPHL1.1.1	XM_003446729.1 PREDICTED: Oreochromis niloticus hephaestin-like 1 (HEPHL1), mRNA	0.026863318	-2.6594968	down
MPF_LOC100698649.6.10	XP_003460222.1 PREDICTED: complement C1q tumor necrosis factor-related protein 3-like [Oreochromis niloticus]	0.043577008	-3.9135785	down
MPF_contig_029570		0.025232468	-2.288113	down
MPF_LOC100689711.4.6	XP_003459483.1 PREDICTED: h-2 class I histocompatibility antigen, L-D alpha chain-like [Oreochromis niloticus]	0.02030712	-2.0101633	down
MPF_LOC101483580.1.1	XM_004556746.1 PREDICTED: Maylandia zebra leucine zipper putative tumor suppressor 2 homolog (LOC101483580), mRNA	0.019762442	1.2039222	up
MPF_LOC100692543.1.3	XM_003449439.1 PREDICTED: Oreochromis niloticus microfibril-associated glycoprotein 4like (LOC100692543), mRNA	0.031615667	-1.4166074	down
MPF_LOC100693537.6.6	XM_003449604.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L7a-like (LOC100693537), mRNA	0.037583128	-1.4482431	down
MPF_LOC101487444.1.1	XM_004547650.1 PREDICTED: Maylandia zebra alpha-1-syntrophin-like (LOC101487444), mRNA	0.038774587	-1.4392003	down
MPF_CRE_23222.1.2	XP_003089877.1 hypothetical protein CRE_23222 [Caenorhabditis remanei]	0.021169053	-1.2721657	down
MPF_LOC101465872.1.1	XM_004558783.1 PREDICTED: Maylandia zebra extended synaptotagmin-1-like (LOC101465872), mRNA	0.025791937	-4.071859	down
MPF_LOC100690727.1.1	XM_003443255.1 PREDICTED: Oreochromis niloticus ribosomal RNA processing protein 1 homolog B-like (LOC100690727), mRNA	0.031615667	-1.2835822	down
MPF_LOC101471935.1.1	XM_004545975.1 PREDICTED: Maylandia zebra transcription factor MafB-like (LOC101471935), mRNA	0.011256327	-3.128942	down
MPF_LOC100695240.1.2	XP_003452569.1 PREDICTED: calcium/calmodulin-dependent protein kinase type IV-like [Oreochromis niloticus]	0.028781192	-1.7649922	down
MPF_LOC101484703.2.2	XM_004555446.1 PREDICTED: Maylandia zebra transmembrane protein 41A-A-like (LOC101484703), mRNA	0.010595669	-2.8758922	down
MPF_LOC100705985.4.5	XP_003459382.1 PREDICTED: butyrophilin subfamily 1 member A1-like [Oreochromis niloticus]	0.02909936	-1.4501709	down
MPF_contig_012534		0.025488323	-1.3942175	down
MPF_LOC100564008.1.1	XM_003223200.1 PREDICTED: Anolis carolinensis 40S ribosomal protein S26-like (LOC100564008), mRNA	0.047392525	-1.6102171	down
MPF_LOC100709741.1.1	XM_003456979.1 PREDICTED: Oreochromis niloticus macrophage colony-stimulating factor 1 receptor 2-like (LOC100709741), mRNA	0.024917157	-3.0958855	down
MPF_LOC100690793.1.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]	0.016491378	-4.4672933	down
MPF_LOC101485836.1.2	XM_004559956.1 PREDICTED: Maylandia zebra muscle M-line assembly protein unc-89-like (LOC101485836), transcript variant X1, mRNA	0.03639751	2.3555799	up
MPF_LOC101479312.2.2	XM_004548084.1 PREDICTED: Maylandia zebra tribbles homolog 1-like (LOC101479312), mRNA	0.004379576	-2.9845574	down
MPF_LOC100534480.2.2	XM_003447448.1 PREDICTED: Oreochromis niloticus inducible cAMP early repressor (LOC100534480), mRNA	0.027954783	-1.3292804	down
MPF_LOC100712420.1.5	XP_003456711.1 PREDICTED: adenine phosphoribosyltransferase-like [Oreochromis niloticus]	0.024245406	-1.3789053	down
MPF_contig_024080		0.033782817	1.171976	up
MPF_LOC100695994.33.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.025791937	-1.4337177	down
MPF_LOC101473612.4.5	XM_004550873.1 PREDICTED: Maylandia zebra sodium/potassium-transporting ATPase subunit alpha-3-like (LOC101473612), transcript variant X2, mRNA	0.010595669	-3.3400989	down

MPF_LOC101464956.1.1	XM_004545486.1 PREDICTED: Maylandia zebra large neutral amino acids transporter small subunit 3-like (LOC101464956), mRNA	0.01596322	-2.7428212	down
MPF_LOC100701242.9.9	XM_003459250.1 PREDICTED: Oreochromis niloticus h-2 class II histocompatibility antigen, I-A beta chain-like, transcript variant 1 (LOC100701242), mRNA	0.031308513	-2.4666405	down
MPF_contig_047601		0.024917157	-2.4137897	down
MPF_LOC100693091.2.2	XM_003450261.1 PREDICTED: Oreochromis niloticus fucolectin-7-like (LOC100693091), mRNA	0.025795393	-3.5274916	down
MPF_LOC101477479.1.1	XM_004555047.1 PREDICTED: Maylandia zebra MOB kinase activator 3C-like (LOC101477479), transcript variant X2, mRNA	0.031199234	-1.3837525	down
MPF_LOC100691260.2.6	XM_003443681.1 PREDICTED: Oreochromis niloticus glyceraldehyde 3-phosphate dehydrogenase, testis-specific-like (LOC100691260), mRNA	0.04318178	-1.5216298	down
MPF_LOC100703754.1.1	XM_003456632.1 PREDICTED: Oreochromis niloticus mannosyl-oligosaccharide 1,2-alphamannosidase IA-like (LOC100703754), mRNA	0.026810538	-2.1203525	down
MPF_COX3.3.3	[BBH] COX3_GADMO (sp|P55777) Cytochrome c oxidase subunit 3 OS=Gadus morhua GN=mt-co3 PE=3 SV=1	0.0333852	1.1613779	up
MPF_LOC100697415.3.3	XP_003444759.1 PREDICTED: neuroblast differentiation-associated protein AHNAK-like [Oreochromis niloticus]	0.011256327	-4.645359	down
MPF_contig_011672	XM_004550791.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 6-like (LOC101478586), transcript variant X1, mRNA	0.031615667	-2.4549994	down
MPF_LOC101068359.1.1	XP_003962600.1 PREDICTED: gap junction beta-4 protein-like [Takifugu rubripes]	0.004379576	1.0755043	up
MPF_LOC101472402.1.1	XM_004568494.1 PREDICTED: Maylandia zebra 6-phosphofructokinase type C-like (LOC101472402), transcript variant X1, mRNA	0.025415389	-1.509861	down
MPF_LOC101465264.1.5	XM_004573930.1 PREDICTED: Maylandia zebra tripartite motif-containing protein 16-like (LOC101465264), mRNA	0.024295906	1.1411715	up
MPF_K1C18.1.2	K1C18_DANRE (sp|Q7ZTS4) Keratin, type I cytoskeletal 18 OS=Danio rerio GN=krt18 PE=1 SV=2	0.011963667	-4.1830926	down
MPF_LOC100694868.1.2	XM_003446700.1 PREDICTED: Oreochromis niloticus c-C chemokine receptor type 6-like (LOC100694868), mRNA	0.016236318	-1.6108193	down
MPF_contig_046558	XM_003198881.1 PREDICTED: Danio rerio retrotransposable element Tf2 155 kDa protein type 1-like (LOC100535308), mRNA	0.038888626	-1.3654056	down
MPF_LOC101476819.5.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0.018963305	-2.896152	down
MPF_contig_018142		0.043393664	-1.6482916	down
MPF_POL.2.6	POL_FENV1 (sp|P31792) Pol polyprotein (Fragment) OS=Feline endogenous virus ECE1 GN=pol PE=3 SV=1	0.039509952	-2.9771976	down
MPF_contig_037954		0.016254881	-1.2740625	down
MPF_LOC101463819.1.1	XM_004549502.1 PREDICTED: Maylandia zebra tetraspanin-5-like (LOC101463819), transcript variant X2, mRNA	0.012417686	-3.5372417	down
MPF_LOC101471157.1.1	XM_004569028.1 PREDICTED: Maylandia zebra protein ELFN1-like (LOC101471157), transcript variant X2, mRNA	0.02899486	1.5173787	up
MPF_LOC101472090.4.4	XM_004541980.1 PREDICTED: Maylandia zebra vascular endothelial growth factor A-A-like (LOC101472090), mRNA	0.025232468	-1.7986681	down
MPF_LOC100693203.3.4	XM_003457748.1 PREDICTED: Oreochromis niloticus tetraspanin-5-like (LOC100693203), mRNA	0.032997966	-1.0784069	down
MPF_LOC101465015.1.1	XM_004562273.1 PREDICTED: Maylandia zebra MKL/myocardin-like protein 2-like (LOC101465015), transcript variant X4, mRNA	0.018963305	-1.3837552	down
MPF_contig_036789		0.018963305	-2.2169573	down
MPF_LOC100710548.3.4	XP_003459320.1 PREDICTED: major histocompatibility complex class I-related gene proteinlike [Oreochromis niloticus]	0.016177904	-3.6201165	down
MPF_LOC101072249.3.3	XP_003966663.1 PREDICTED: target of Nesh-SH3-like [Takifugu rubripes]	0.010595669	-3.315271	down
MPF_CFAH.14.15	CFAH_MOUSE (sp|P06909) Complement factor H OS=Mus musculus GN=Cfh PE=1 SV=2	0.030517532	-2.8360748	down
MPF_contig_017105		0.04835695	1.0885496	up

MPF_SRRM2.14.15	SRRM2_MOUSE (sp|Q8BTI8) Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3	0.027341519	-2.3297834	down
MPF_contig_006239		0.042182866	1.0486202	up
MPF_LOC101481869.4.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA	0.017280372	-1.4340129	down
MPF_LOC100711796.1.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA	0.024133291	-2.090314	down
MPF_LOC100705145.1.1	XM_003445077.1 PREDICTED: Oreochromis niloticus phenylserine dehydratase-like (LOC100705145), mRNA	0.025791937	1.761182	up
MPF_contig_043875		0.030366093	1.7597752	up
MPF_LOC101487842.1.1	XM_004575185.1 PREDICTED: Maylandia zebra intermediate filament protein ON3-like (LOC101487842), transcript variant X2, mRNA	0.031615667	1.0311089	up
MPF_RBBP5.1.1	XP_003447710.1 PREDICTED: retinoblastoma-binding protein 5 [Oreochromis niloticus]	0.025232468	1.2975492	up
MPF_LOC101479192.1.1	XM_004541915.1 PREDICTED: Maylandia zebra lebercilin-like (LOC101479192), transcript variant X1, mRNA	0.024295906	-2.810941	down
MPF_AHNK.22.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.010595669	-2.630941	down
MPF_TNF6B.1.1	TNF6B_HUMAN (sp|O95407) Tumor necrosis factor receptor superfamily member 6B OS=Homo sapiens GN=TNFRSF6B PE=1 SV=1	0.01596322	-5.2254944	down
MPF_LOC100705618.1.1	XP_003453815.1 PREDICTED: protogenin-like [Oreochromis niloticus]	0.04386513	-1.9594603	down
MPF_LOC101063750.2.2	XM_003973181.1 PREDICTED: Takifugu rubripes 40S ribosomal protein S26-like (LOC101063750), mRNA	0.04883595	-1.6482177	down
MPF_LOC100708333.1.1	XP_003442142.1 PREDICTED: hypothetical protein LOC100708333 [Oreochromis niloticus]	0.01596322	1.5172303	up
MPF_LOC101487137.1.1	XM_004545126.1 PREDICTED: Maylandia zebra calcium/calmodulin-dependent protein kinase II inhibitor 2-like (LOC101487137), mRNA	0.028370207	-1.1382861	down
MPF_contig_044606		0.02018985	-3.4600048	down
MPF_contig_039525		0.04833266	1.0244673	up
MPF_contig_049016		0.031615667	1.1403773	up
MPF_LOC101486434.1.2	XM_004560149.1 PREDICTED: Maylandia zebra cathepsin K-like (LOC101486434), mRNA	0.017280372	-4.0683236	down
MPF_contig_015596		0.032085758	-1.8626649	down
MPF_LOC100694681.1.1	XM_003444619.1 PREDICTED: Oreochromis niloticus 39S ribosomal protein L11, mitochondrial-like (LOC100694681), mRNA	0.034446273	1.4204539	up
MPF_contig_039397		0.020356022	-1.1347256	down
MPF_LOC101061752.1.1	XM_003975168.1 PREDICTED: Takifugu rubripes SEC14-like protein 2-like (LOC101061752), mRNA	0.024245406	-2.8108723	down
MPF_LOC100702817.3.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.015957259	-4.739643	down
MPF_LOC100488485.5.10	XP_002941723.1 PREDICTED: hypothetical protein LOC100488485 [Xenopus (Silurana) tropicalis]	0.026872601	-3.3443508	down
MPF_LOC101064862.1.1	XP_003969643.1 PREDICTED: src substrate protein p85-like [Takifugu rubripes]	0.046603955	1.1271209	up
MPF_LOC101472640.3.4	XM_004574391.1 PREDICTED: Maylandia zebra microtubule-associated serine/threonineprotein kinase 3-like (LOC101472640), transcript variant X2, mRNA	0.024663433	-1.5285324	down
MPF_LOC101076756.1.1	XM_003972767.1 PREDICTED: Takifugu rubripes histone-lysine N-methyltransferase MLL5like (LOC101076756), mRNA	0.022665633	-2.4891822	down
MPF_LOC101482128.1.2	XM_004574739.1 PREDICTED: Maylandia zebra MARCKS-related protein-like (LOC101482128), mRNA	0.0160005	2.603372	up

MPF_LOC101483311.1.1	XM_004561531.1 PREDICTED: Maylandia zebra small glutamine-rich tetratricopeptide repeat-containing protein alpha-like (LOC101483311), transcript variant X2, mRNA	0.03863755	1.1324868	up
MPF_LOC100712517.2.2	XM_003459650.1 PREDICTED: Oreochromis niloticus RNA (guanine-9-)-methyltransferase domain-containing protein 2-like (LOC100712517), mRNA	0.024245406	-1.5584445	down
MPF_FCGR1.1.1	FCGR1_MOUSE (sp|P26151) High affinity immunoglobulin gamma Fc receptor I OS=Mus musculus GN=Fcgr1 PE=1 SV=1	0.040596336	-3.295848	down
MPF_LOC101480609.1.2	XM_004539422.1 PREDICTED: Maylandia zebra homeodomain-interacting protein kinase 3like (LOC101480609), transcript variant X2, mRNA	0.011256327	-3.7073135	down
MPF_LOC100708213.1.1	XP_003457845.1 PREDICTED: hypothetical protein LOC100708213 [Oreochromis niloticus]	0.027621096	-3.3992271	down
MPF_LOC101483514.1.1	XM_004539709.1 PREDICTED: Maylandia zebra glucose-6-phosphate isomerase-like (LOC101483514), mRNA	0.027195308	1.0234938	up
MPF_LOC101465129.6.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA	0.024245406	-1.7518611	down
MPF_LOC100709671.1.2	XM_003460204.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100709671 (LOC100709671), mRNA	0.04651519	-1.5356984	down
MPF_contig_016004		0.025415389	1.3919675	up
MPF_LOC101479518.3.5	XM_004570668.1 PREDICTED: Maylandia zebra alpha-actinin-3-like (LOC101479518), mRNA	0.037357267	-1.838881	down
MPF_LOC100705343.3.3	XM_003450141.1 PREDICTED: Oreochromis niloticus claudin-8-like (LOC100705343), mRNA	0.020052187	-3.559311	down
MPF_LOC101167345.13.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA	0.021017518	-2.6693132	down
MPF_contig_017955		0.0333852	-1.5508757	down
MPF_contig_009977		0.016254881	-1.6990118	down
MPF_LOC101487936.1.3	XM_004552317.1 PREDICTED: Maylandia zebra F-box/LRR-repeat protein 20-like (LOC101487936), transcript variant X2, mRNA	0.020070592	1.1085677	up
MPF_LOC101484083.3.3	XM_004539190.1 PREDICTED: Maylandia zebra ATP-binding cassette sub-family A member 1-like (LOC101484083), transcript variant X2, mRNA	0.020052187	-1.7684431	down
MPF_contig_026589		0.024397738	1.212418	up
MPF_contig_004003		0.047462545	-1.9918838	down
MPF_LOC100692490.2.4	XM_003457423.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L37a-like (LOC100692490), mRNA	0.01914008	-2.7250333	down
MPF_LOC101485480.1.2	XM_004538914.1 PREDICTED: Maylandia zebra uncharacterized LOC101485480 (LOC101485480), mRNA	0.023065256	1.147633	up
MPF_LOC100706186.1.2	XM_003460059.1 PREDICTED: Oreochromis niloticus calpain-2 catalytic subunit-like (LOC100706186), mRNA	0.04076093	-2.1024613	down
MPF_NEMVEDRAFT_V1G118504.1.1	XP_001628905.1 predicted protein [Nematostella vectensis]	0.02306824	-2.3300695	down
MPF_LOC101481489.4.6	XM_004564502.1 PREDICTED: Maylandia zebra 40S ribosomal protein S13-like (LOC101481489), mRNA	0.016254881	-1.425678	down
MPF_LOC100706211.1.2	XM_003445662.1 PREDICTED: Oreochromis niloticus piwi-like protein 2-like (LOC100706211), mRNA	0.025791937	-1.4906545	down
MPF_NPEPL1.1.1	XP_003441551.1 PREDICTED: probable aminopeptidase NPEPL1 [Oreochromis niloticus]	0.029044243	1.1803025	up
MPF_HACE1.1.3	HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2	0.01596322	-4.9470143	down
MPF_LOC101482220.1.3	XM_004571715.1 PREDICTED: Maylandia zebra h-2 class II histocompatibility antigen gamma chain-like (LOC101482220), mRNA	0.023334052	-4.0526233	down
MPF_LOC100696180.1.1	XR_134816.1 PREDICTED: Oreochromis niloticus fibronectin-like (LOC100696180), miscRNA	0.016254881	-5.177691	down
MPF_LOC101162897.2.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]	0.019260636	-3.5891538	down
MPF_LOC100700407.1.1	XM_003454414.1 PREDICTED: Oreochromis niloticus IGF-like family receptor 1-like (LOC100700407), mRNA	0.01596322	-3.688717	down

MPF_SRRM2.3.15	XP_002926593.1 PREDICTED: serine/arginine repetitive matrix protein 2-like [Ailuropoda melanoleuca]	0.02261816	-2.5855703	down
MPF_LOC101466143.14.18	XM_004574840.1 PREDICTED: Maylandia zebra 40S ribosomal protein S18-like (LOC101466143), mRNA	0.042575497	-1.7659731	down
MPF_LOC101466143.1.18	XM_004574840.1 PREDICTED: Maylandia zebra 40S ribosomal protein S18-like (LOC101466143), mRNA	0.025232468	-1.8828791	down
MPF_LOC101473055.1.4	XM_004560375.1 PREDICTED: Maylandia zebra basement membrane-specific heparan sulfate proteoglycan core protein-like (LOC101473055), transcript variant X2, mRNA	0.030009525	-1.5802891	down
MPF_LOC100634711.1.2	XP_003391247.1 PREDICTED: hypothetical protein LOC100634711 [Amphimedon queenslandica]	0.031615667	-1.9156833	down
MPF_LOC101473855.11.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA	0.02306824	-1.0141399	down
MPF_LOC101171771.1.2	XM_004077345.1 PREDICTED: Oryzias latipes uncharacterized LOC101171771 (LOC101171771), mRNA	0.024745662	-1.919445	down
MPF_LOC100705819.1.1	XP_003438527.1 PREDICTED: hypothetical protein LOC100705819 [Oreochromis niloticus]	0.04755172	-1.5310855	down
MPF_PSV.1.1	PSV_DICDI (sp|P08798) Prespore vesicle protein OS=Dictyostelium discoideum GN=psvA PE=2 SV=3	0.04883595	-1.9409347	down
MPF_LOC101161574.4.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.024605608	-2.5909438	down
MPF_contig_032895		0.02306824	-1.538939	down
MPF_LOC100708211.3.3	XM_003457561.1 PREDICTED: Oreochromis niloticus GON-4-like protein-like (LOC100708211), mRNA	0.016491378	1.3963279	up
MPF_LOC100535356.1.1	XP_003199172.1 PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Danio rerio]	0.037575997	-1.9069052	down
MPF_LOC101467796.9.9	XM_004554825.1 PREDICTED: Maylandia zebra nesprin-2-like (LOC101467796), mRNA	0.016254881	-1.8041668	down
MPF_contig_015699		0.043499112	-1.0049787	down
MPF_LOC101488070.1.1	XM_004543546.1 PREDICTED: Maylandia zebra neprilysin-like (LOC101488070), transcript variant X1, mRNA	0.0160005	-5.7708745	down
MPF_LOC100690179.5.21	XM_003441609.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S25-like (LOC100690179), mRNA	0.03466951	-1.4151206	down
MPF_C1QC.1.1	NP_001135251.1 complement C1q subcomponent subunit C precursor [Salmo salar]	0.031615667	-1.8852663	down
MPF_LOC100690282.1.1	XP_003445069.1 PREDICTED: tripartite motif-containing protein 39-like [Oreochromis niloticus]	0.026926706	-1.0750973	down
MPF_contig_003837		0.02018985	-3.4762945	down
MPF_LOC101472300.1.1	XM_004568586.1 PREDICTED: Maylandia zebra uncharacterized LOC101472300 (LOC101472300), mRNA	0.012505665	-3.9324875	down
MPF_LOC101161574.3.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.026633183	-1.0871806	down
MPF_contig_020110		0.024133291	-1.0874157	down
MPF_contig_044670		0.034807544	1.2903948	up
MPF_contig_015500		0.016236318	-3.4079287	down
MPF_LOC100710690.1.1	XM_003452159.1 PREDICTED: Oreochromis niloticus UPF0609 protein C4orf27 homolog (LOC100710690), mRNA	0.047697406	1.3477736	up
MPF_LOC101470197.1.1	XM_004546369.1 PREDICTED: Maylandia zebra IQ motif and SEC7 domain-containing protein 2-like (LOC101470197), transcript variant X3, mRNA	0.032365307	1.7631123	up
MPF_LOC101477280.6.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.016254881	-3.2996397	down
MPF_contig_028860		0.019260636	-3.548831	down

MPF_CXXC1.1.1	XM_003457633.1 PREDICTED: Oreochromis niloticus CXXC finger protein 1 (CXXC1), mRNA	0.02261816	1.2109551	up
MPF_LOC100703120.2.3	XP_003458215.1 PREDICTED: hypothetical protein LOC100703120 [Oreochromis niloticus]	0.028370207	-1.9276052	down
MPF_LOC100698625.10.22	XM_003456694.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100698625), mRNA	0.032603085	-1.2450104	down
MPF_PCGF1.2.2	PCGF1_DANRE (sp|Q7ZYZ7) Polycomb group RING finger protein 1 OS=Danio rerio GN=pcgf1 PE=3 SV=1	0.04140341	-1.9615095	down
MPF_LOC100695830.1.2	XM_003445456.1 PREDICTED: Oreochromis niloticus serine/arginine-rich splicing factor 4like, transcript variant 1 (LOC100695830), mRNA	0.011256327	-3.3374023	down
MPF_LOC100693306.12.13	XP_003458501.1 PREDICTED: protein NLRC3-like [Oreochromis niloticus]	0.046603955	1.2916889	up
MPF_RPS7.1.12	XM_003971400.1 PREDICTED: Takifugu rubripes 40S ribosomal protein S7-like (LOC101073757), mRNA	0.031615667	-1.6624565	down
MPF_LOC100695326.1.1	XM_003453338.1 PREDICTED: Oreochromis niloticus uncharacterized protein C7orf26 homolog (LOC100695326), mRNA	0.041837275	1.109663	up
MPF_NEMVEDRAFT_V1G131035.1.1	XP_001625099.1 predicted protein [Nematostella vectensis]	0.032603085	-3.1303933	down
MPF_contig_028605		0.01596322	-3.491006	down
MPF_LOC101464712.2.5	XM_004554817.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2B-like (LOC101464712), transcript variant X2, mRNA	0.024884876	-1.4808869	down
MPF_contig_015464		0.010595669	-3.612388	down
MPF_LOC100703239.1.1	XP_003440200.1 PREDICTED: hypothetical protein LOC100703239 [Oreochromis niloticus]	0.016254881	-3.3549976	down
MPF_contig_022962		0.011256327	-2.8408003	down
MPF_LOC101488089.1.1	XM_004570084.1 PREDICTED: Maylandia zebra uncharacterized LOC101488089 (LOC101488089), transcript variant X3, mRNA	0.01743274	-3.3076253	down
MPF_LOC100704547.1.2	XM_003453764.1 PREDICTED: Oreochromis niloticus tether containing UBX domain for GLUT4-like (LOC100704547), mRNA	0.04715796	1.2003336	up
MPF_contig_027052		0.019762442	-2.2848	down
MPF_LOC101063580.1.1	XP_003966085.1 PREDICTED: syndecan-2-like [Takifugu rubripes]	0.024917157	-1.9259586	down
MPF_contig_016527	XM_004566361.1 PREDICTED: Maylandia zebra CREB-regulated transcription coactivator 3like (LOC101469041), transcript variant X2, mRNA	0.024605608	1.1746492	up
MPF_LOC100702906.1.1	XP_003448860.1 PREDICTED: putative transporter SVOPL-like [Oreochromis niloticus]	0.01614976	1.2068768	up
MPF_LOC101464848.5.5	XM_004545232.1 PREDICTED: Maylandia zebra bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]-like (LOC101464848), transcript variant X2, mRNA	0.04575675	-1.4119978	down
MPF_contig_007919		0.04883595	-1.53059	down
MPF_LOC100707046.6.12	XM_003454686.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100707046), mRNA	0.04123251	-2.0200858	down
MPF_LOC101468563.1.2	XM_004572588.1 PREDICTED: Maylandia zebra alkaline nuclease-like (LOC101468563), transcript variant X6, mRNA	0.016177904	-1.8465991	down
MPF_LOC101471834.1.4	XM_004546921.1 PREDICTED: Maylandia zebra titin-like (LOC101471834), transcript variant X2, mRNA	0.024605608	-1.826319	down
MPF_LOC101068301.2.3	XM_003966217.1 PREDICTED: Takifugu rubripes protein S100-A11-like (LOC101068301), mRNA	0.019273274	-3.2843232	down
MPF_FZD6.11.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440 IMAGE:6971142), complete cds	0.01596322	1.9487073	up
MPF_contig_022315		0.040511526	-1.3974522	down
MPF_contig_042931		0.023771022	-1.9602199	down

MPF_LOC101470306.1.1	XM_004574119.1 PREDICTED: Maylandia zebra uncharacterized LOC101470306 (LOC101470306), mRNA	0.024245406	-2.7600884	down
MPF_LOC101467779.3.5	XM_004552436.1 PREDICTED: Maylandia zebra LIM domain-containing protein 2-like (LOC101467779), mRNA	0.030809928	1.1468053	up
MPF_LOC101473855.10.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA	0.02730229	-1.8285446	down
MPF_LOC100700605.16.27	XM_003458555.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100700605), mRNA	0.016254881	-2.064304	down
MPF_contig_034282	XM_004546150.1 PREDICTED: Maylandia zebra FYVE, RhoGEF and PH domain-containing protein 3-like (LOC101464674), transcript variant X1, mRNA	0.028438346	1.0933075	up
MPF_contig_005681	XM_004546367.1 PREDICTED: Maylandia zebra IQ motif and SEC7 domain-containing protein 2-like (LOC101470197), transcript variant X1, mRNA	0.03710956	1.0099173	up
MPF_SRRM2.9.15	SRRM2_HUMAN (sp|Q9UQ35) Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	0.026872601	-2.277401	down
MPF_LOC100696821.1.2	XP_003452493.1 PREDICTED: ictacalcin-like [Oreochromis niloticus]	0.027706273	-3.5099387	down
MPF_LOC100699007.2.2	XM_003442225.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100699007, transcript variant 2 (LOC100699007), mRNA	0.017280372	-4.368744	down
MPF_contig_019808		0.0410502	1.0125577	up
MPF_LOC100706983.1.11	XP_003460110.1 PREDICTED: 28S ribosomal protein S28, mitochondrial-like [Oreochromis niloticus]	0.031494927	-1.4996195	down
MPF_contig_026907		0.02018985	-3.6795385	down
MPF_contig_032259		0.015188972	-3.2838554	down
MPF_contig_031639		0.023120647	-2.966292	down
MPF_LOC100709552.1.1	XP_003456537.1 PREDICTED: cysteine-rich protein 2-binding protein-like [Oreochromis niloticus]	0.024745662	1.1030941	up
MPF_LOC101160141.1.1	XR_177319.1 PREDICTED: Oryzias latipes keratin, type I cytoskeletal 13-like (LOC101160141), misc_RNA	0.01596322	-3.707899	down
MPF_LOC101467183.1.2	XM_004550296.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1like (LOC101467183), transcript variant X7, mRNA	0.026197506	-2.4339585	down
MPF_LOC100709634.2.3	XM_003455185.1 PREDICTED: Oreochromis niloticus h-2 class II histocompatibility antigen gamma chain-like (LOC100709634), mRNA	0.025791937	-4.0011735	down
MPF_contig_048319		0.046955165	-1.411562	down
MPF_contig_012573		0.024745662	-3.337438	down
MPF_contig_021708		0.010595669	-2.079267	down
MPF_LOC100694351.1.1	XM_003450430.1 PREDICTED: Oreochromis niloticus aryl hydrocarbon receptor nuclear translocator 2-like, transcript variant 1 (LOC100694351), mRNA	0.03639751	-2.3495898	down
MPF_LOC101465192.1.6	XM_004554818.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2B-like (LOC101465192), mRNA	0.036283772	-2.0736427	down
MPF_C1QT3.4.4	C1QT3_MOUSE (sp|Q9ES30) Complement C1q tumor necrosis factor-related protein 3 OS=Mus musculus GN=C1qtnf3 PE=2 SV=1	0.04884551	-3.1361113	down
MPF_LOC100698649.3.10	XP_003460222.1 PREDICTED: complement C1q tumor necrosis factor-related protein 3-like [Oreochromis niloticus]	0.039246835	-3.5811212	down
MPF_LOC101481376.3.4	XM_004557456.1 PREDICTED: Maylandia zebra heat shock protein beta-1-like (LOC101481376), mRNA	0.019615307	-3.1922731	down
MPF_LOC101470299.3.3	XM_004549153.1 PREDICTED: Maylandia zebra synaptic vesicle glycoprotein 2A-like (LOC101470299), transcript variant X2, mRNA	0.013443254	1.0331571	up
MPF_contig_043078		0.034491166	1.0520495	up
MPF_LOC100697579.1.2	XP_003439236.1 PREDICTED: cystatin-A1-like [Oreochromis niloticus]	0.031615667	-4.054066	down
MPF_LOC101482632.1.1	XM_004560784.1 PREDICTED: Maylandia zebra myocardin-related transcription factor B-like (LOC101482632), transcript variant X2, mRNA	0.0448195	1.4166093	up

MPF_LOC100695137.3.3	XP_003447509.1 PREDICTED: high affinity immunoglobulin epsilon receptor subunit gammalike [Oreochromis niloticus]	0.01370748	-4.583019	down
MPF_LOC101476292.1.1	XM_004567039.1 PREDICTED: Maylandia zebra transgelin-like (LOC101476292), transcript variant X2, mRNA	0.020070592	-5.0425615	down
MPF_contig_026973	XM_004553863.1 PREDICTED: Maylandia zebra poly [ADP-ribose] polymerase 12-like (LOC101480887), transcript variant X1, mRNA	0.040299594	-1.9920801	down
MPF_LOC100693156.1.1	XM_003444114.1 PREDICTED: Oreochromis niloticus hyccin-like (LOC100693156), mRNA	0.044233333	1.5979174	up
MPF_RPS7.11.12	XM_003971400.1 PREDICTED: Takifugu rubripes 40S ribosomal protein S7-like (LOC101073757), mRNA	0.04833266	-1.4287987	down
MPF_contig_011996		0.027746603	-1.3443584	down
MPF_LOC101478373.2.2	XM_004545374.1 PREDICTED: Maylandia zebra neurofilament heavy polypeptide-like (LOC101478373), mRNA	0.02199939	1.1712455	up

MPF_LOC101166773.1.1	XP_004085184.1 PREDICTED: uncharacterized protein LOC101166773, partial [Oryzias latipes]	0.040899336	-1.0720295	down
MPF_LOC100697337.2.4	XP_003446015.1 PREDICTED: hypothetical protein LOC100697337 [Oreochromis niloticus]	0.020052187	-1.5352874	down
MPF_LOC101464732.1.3	XM_004538651.1 PREDICTED: Maylandia zebra F-box only protein 48-like (LOC101464732), mRNA	0.031615667	1.2856655	up
MPF_BHWA1_01395.1.1	YP_002721575.1 hypothetical protein BHWA1_01395 [Brachyspira hyodysenteriae WA1]	0.014572915	-2.6439376	down
MPF_contig_023611		0.024730926	-2.5028439	down
MPF_LOC101483197.2.8	XM_004575580.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12-like (LOC101483197), mRNA	0.04575675	1.485095	up
MPF_contig_031891		0.030398514	-3.1910133	down
MPF_CD48.2.4	CD48_MOUSE (sp|P18181) CD48 antigen OS=Mus musculus GN=Cd48 PE=1 SV=1	0.01596322	-3.301118	down
MPF_LOC100706287.1.1	XP_003448039.1 PREDICTED: CD209 antigen-like [Oreochromis niloticus]	0.024618821	-3.259573	down
MPF_LOC101466928.1.1	XM_004563455.1 PREDICTED: Maylandia zebra inositol 1,4,5-trisphosphate receptor type 2like (LOC101466928), mRNA	0.039345793	1.0233582	up
MPF_contig_023735		0.025232468	-1.343194	down
MPF_contig_043323		0.04575675	-1.1916666	down
MPF_contig_042687		0.021017518	-2.7049985	down
MPF_contig_044163	XM_004540054.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2-like (LOC101476846), transcript variant X1, mRNA	0.02782313	1.2421198	up
MPF_LOC101479570.1.2	XM_004564494.1 PREDICTED: Maylandia zebra transcription factor SOX-6-like (LOC101479570), mRNA	0.043084357	1.1032143	up
MPF_LOC100706573.1.1	XP_003452280.1 PREDICTED: arachidonate 15-lipoxygenase B-like [Oreochromis niloticus]	0.040625155	-1.2937279	down
MPF_LOC101485929.1.2	XM_004560148.1 PREDICTED: Maylandia zebra cathepsin S-like (LOC101485929), transcript variant X2, mRNA	0.049359675	-2.6047397	down
MPF_LOC101168710.1.1	XP_004070984.1 PREDICTED: CD27 antigen-like [Oryzias latipes]	0.024133291	-3.160152	down
MPF_LOC101486414.1.1	XM_004575832.1 PREDICTED: Maylandia zebra disintegrin and metalloproteinase domaincontaining protein 19-like (LOC101486414), mRNA	0.039509952	-1.3786392	down
MPF_LOC101473901.1.2	XM_004572233.1 PREDICTED: Maylandia zebra CDC42 small effector protein 1-like (LOC101473901), transcript variant X2, mRNA	0.02199939	-3.650536	down
MPF_contig_005114		0.043551203	1.0229445	up
MPF_LOC101478250.3.3	XM_004538353.1 PREDICTED: Maylandia zebra flocculation protein FLO11-like (LOC101478250), transcript variant X3, mRNA	0.017280372	-4.2951403	down
MPF_LOC100692406.1.1	XP_003439388.1 PREDICTED: nucleolar MIF4G domain-containing protein 1-like [Oreochromis niloticus]	0.024245406	1.14363	up

MPF_LOC100707640.2.2	XP_003451524.1 PREDICTED: hypothetical protein LOC100707640 [Oreochromis niloticus]	0.026158115	-1.3424053	down
MPF_LECG.42.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.019273274	-4.5053263	down
MPF_contig_020212		0.024133291	-3.903839	down
MPF_LOC101470011.1.1	XM_004572767.1 PREDICTED: Maylandia zebra agrin-like (LOC101470011), transcript variant X5, mRNA	0.043084357	-2.08213	down
MPF_LOC100710874.10.12	XP_003453997.1 PREDICTED: hypothetical protein LOC100710874 [Oreochromis niloticus]	0.024917157	-1.8726687	down
MPF_LOC100698701.1.2	XM_003455230.1 PREDICTED: Oreochromis niloticus protein S100-A13-like (LOC100698701), mRNA	0.037767183	-2.699461	down
MPF_RL23.2.9	RL23_RAT (sp|P62832) 60S ribosomal protein L23 OS=Rattus norvegicus GN=Rpl23 PE=2 SV=1	0.02782313	-1.9049797	down
MPF_LOC445921.1.1	XP_003979513.1 PREDICTED: Ig mu chain C region membrane-bound form [Takifugu rubripes]	0.031615667	-2.8055425	down
MPF_LOC101477280.1.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.020052187	-2.992015	down
MPF_LOC101160373.1.1	XP_004083232.1 PREDICTED: DNA damage-regulated autophagy modulator protein 1-like [Oryzias latipes]	0.025109002	-1.8668714	down
MPF_LOC101470738.2.20	XM_004560737.1 PREDICTED: Maylandia zebra actin, cytoplasmic 1-like (LOC101470738), mRNA	0.043956067	1.0049543	up
MPF_contig_009872		0.04575675	-1.1330495	down
MPF_contig_009643		0.018841967	-1.1600814	down
MPF_APOC1.1.1	NP_001134834.1 Apolipoprotein C-I precursor [Salmo salar]	0.021106303	-2.9775424	down
MPF_LOC101475513.1.1	XM_004545621.1 PREDICTED: Maylandia zebra EGF-containing fibulin-like extracellular matrix protein 2-like (LOC101475513), mRNA	0.016491378	-3.3294582	down
MPF_LOC100694733.1.1	XP_003438312.1 PREDICTED: pleckstrin-like [Oreochromis niloticus]	0.03466951	-2.220442	down
MPF_RS7.7.10	RS7_TAKRU (sp|P50894) 40S ribosomal protein S7 OS=Takifugu rubripes GN=rps7 PE=3 SV=1	0.017280372	-2.0883665	down
MPF_contig_035547		0.025232468	-2.4044933	down
MPF_LOC101061096.1.1	XM_003962598.1 PREDICTED: Takifugu rubripes ryanodine receptor 3-like (LOC101061096), mRNA	0.026799427	1.0975475	up
MPF_LOC100691990.2.2	XM_003445526.1 PREDICTED: Oreochromis niloticus annexin A1-like (LOC100691990), mRNA	0.024618821	-1.5349331	down
MPF_contig_032267		0.021017518	-3.717348	down
MPF_LOC101156880.1.1	XM_004067635.1 PREDICTED: Oryzias latipes small glutamine-rich tetratricopeptide repeatcontaining protein alpha-like (LOC101156880), mRNA	0.021608736	1.2928014	up
MPF_LOC101155558.1.1	XM_004082371.1 PREDICTED: Oryzias latipes interferon alpha-inducible protein 27-like protein 2-like (LOC101155558), mRNA	0.016491378	-3.1699286	down
MPF_contig_019882		0.027706273	1.0030539	up
MPF_LOC101486169.4.4	XM_004566076.1 PREDICTED: Maylandia zebra cyclin-T2-like (LOC101486169), mRNA	0.011679485	-5.7212486	down
MPF_LOC101169293.7.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.0376549	-1.2112422	down
MPF_contig_014120		0.046641655	-3.578203	down
MPF_LOC100689966.1.1	XP_003456465.1 PREDICTED: C-type lectin domain family 4 member M-like [Oreochromis niloticus]	0.037575997	-1.9160312	down
MPF_LOC101484929.1.3	XM_004542976.1 PREDICTED: Maylandia zebra CMP-N-acetylneuraminate-beta-1,4galactoside alpha-2,3-sialyltransferase-like (LOC101484929), mRNA	0.024113597	-1.5163012	down
MPF_contig_043487		0.026158115	-1.4180932	down

MPF_contig_016882		0.010595669	-1.9792147	down
MPF_ACBD5.1.1	ACBD5_PONAB (sp|Q5R7V3) Acyl-CoA-binding domain-containing protein 5 OS=Pongo abelii GN=ACBD5 PE=2 SV=1	0.025415389	-1.7248206	down
MPF_contig_020194		0.011256327	-3.936284	down
MPF_LOC101478318.1.1	XM_004555702.1 PREDICTED: Maylandia zebra nucleoporin GLE1-like (LOC101478318), transcript variant X2, mRNA	0.04281289	1.355016	up
MPF_LOC100692501.1.2	XM_003459223.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100692501 (LOC100692501), mRNA	0.025415389	-1.720602	down
MPF_LOC101465099.1.1	XM_004557394.1 PREDICTED: Maylandia zebra moesin-like (LOC101465099), mRNA	0.020746412	-3.8708696	down
MPF_LOC101482523.2.10	XM_004574334.1 PREDICTED: Maylandia zebra 60S ribosomal protein L14-like (LOC101482523), mRNA	0.04076093	1.0425748	up
MPF_AHNK.11.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.020746412	-4.0576634	down
MPF_LOC101466459.9.29	XM_004554283.1 PREDICTED: Maylandia zebra semaphorin-3G-like (LOC101466459), mRNA	0.032603085	-1.6620169	down
MPF_LOC101476415.1.1	XM_004548724.1 PREDICTED: Maylandia zebra prostacyclin synthase-like (LOC101476415), mRNA	0.02461522	-1.1067233	down
MPF_LOC101487074.1.1	XM_004574997.1 PREDICTED: Maylandia zebra cGMP-specific 3',5'-cyclic phosphodiesterase-like (LOC101487074), transcript variant X3, mRNA	0.04575675	-1.0492091	down
MPF_LOC100692104.3.7	XP_003454922.1 PREDICTED: nebulin-like [Oreochromis niloticus]	0.040899336	1.3213668	up
MPF_LOC101485781.2.4	XM_004542132.1 PREDICTED: Maylandia zebra bromo adjacent homology domaincontaining 1 protein-like (LOC101485781), mRNA	0.04780585	1.2335614	up
MPF_LOC100709397.2.2	XM_003438901.1 PREDICTED: Oreochromis niloticus diacylglycerol kinase alpha-like (LOC100709397), mRNA	0.033782817	1.382873	up
MPF_NU5M.1.5	NU5M_SALSA (sp|Q9ZZM3) NADH-ubiquinone oxidoreductase chain 5 OS=Salmo salar GN=MT-ND5 PE=3 SV=1	0.046601474	1.0895476	up
MPF_LOC101467829.1.2	XM_004565458.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase pim-1-like (LOC101467829), mRNA	0.02018985	-2.5612807	down
MPF_LOC101173666.1.1	XP_004082016.1 PREDICTED: poliovirus receptor-related protein 2-like [Oryzias latipes]	0.02069152	-2.0110073	down
MPF_LOC101487208.1.1	XM_004564346.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase ZFP91-like (LOC101487208), transcript variant X3, mRNA	0.024618821	-2.887187	down
MPF_LOC101165175.3.3	XM_004078345.1 PREDICTED: Oryzias latipes cathepsin S-like (LOC101165175), mRNA	0.020559568	-2.6578965	down
MPF_LOC100699797.1.1	XP_003438745.1 PREDICTED: transcription factor VBP-like [Oreochromis niloticus]	0.025795393	1.1786134	up
MPF_contig_041682	XM_004538959.1 PREDICTED: Maylandia zebra metal transporter CNNM2-like (LOC101472577), transcript variant X1, mRNA	0.026926706	-1.7432976	down
MPF_LOC101478710.1.1	XM_004562050.1 PREDICTED: Maylandia zebra DEP domain-containing protein 1A-like (LOC101478710), transcript variant X2, mRNA	0.043084357	1.0783341	up
MPF_LOC101484400.4.5	XM_004572910.1 PREDICTED: Maylandia zebra 60S ribosomal protein L22-like 1-like (LOC101484400), mRNA	0.03944039	-1.7190657	down
MPF_LOC101479628.3.3	XM_004554593.1 PREDICTED: Maylandia zebra proto-oncogene c-Rel-like (LOC101479628), mRNA	0.024884876	-1.7029309	down
MPF_LOC100699721.1.2	XP_003460016.1 PREDICTED: bifunctional protein NCOAT-like, partial [Oreochromis niloticus]	0.030657958	-3.337429	down
MPF_LOC101481500.3.3	XM_004542966.1 PREDICTED: Maylandia zebra macrophage mannose receptor 1-like (LOC101481500), transcript variant X4, mRNA	0.017280372	-3.4614296	down
MPF_contig_011981		0.011256327	-4.329427	down
MPF_LOC101156484.2.2	XM_004067491.1 PREDICTED: Oryzias latipes CD81 antigen-like (LOC101156484), mRNA	0.025232468	-2.357687	down
MPF_contig_021826		0.043084357	-1.5142074	down
MPF_LOC101482619.1.3	XM_004556458.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase TAO2-like (LOC101482619), transcript variant X2, mRNA	0.045513906	1.0576901	up

MPF_LOC101473855.2.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA	0.027632944	-2.0027323	down
MPF_contig_023618		0.040596336	1.1536689	up
MPF_LOC101469207.1.1	XM_004560645.1 PREDICTED: Maylandia zebra c-Jun-amino-terminal kinase-interacting protein 3-like (LOC101469207), transcript variant X10, mRNA	0.02461522	-2.0914433	down
MPF_contig_018921		0.04495405	-1.7426769	down
MPF_LOC101473090.1.1	XM_004545716.1 PREDICTED: Maylandia zebra centromere protein I-like (LOC101473090), transcript variant X1, mRNA	0.043052386	1.293503	up
MPF_LOC100708357.1.1	XP_003448298.1 PREDICTED: formin-like protein 2-like [Oreochromis niloticus]	0.018963305	-2.1460574	down
MPF_LOC101159641.5.35	XM_004085298.1 PREDICTED: Oryzias latipes tenascin-like (LOC101159641), mRNA	0.026458893	-1.7983904	down
MPF_LOC100701242.3.9	XM_003459250.1 PREDICTED: Oreochromis niloticus h-2 class II histocompatibility antigen, I-A beta chain-like, transcript variant 1 (LOC100701242), mRNA	0.027706273	-3.5768833	down
MPF_LOC100701266.1.1	XM_003442151.1 PREDICTED: Oreochromis niloticus peptidyl-prolyl cis-trans isomerase FKBP10-like (LOC100701266), mRNA	0.025232468	1.1319926	up
MPF_LOC100707166.2.2	XM_003442172.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100707166 (LOC100707166), mRNA	0.032049805	-1.9013982	down
MPF_contig_043823		0.04140341	-2.056399	down
MPF_contig_028990		0.031199234	-2.2123022	down

MPF_LOC101470884.1.1	XM_004546372.1 PREDICTED: Maylandia zebra membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2-like (LOC101470884), transcript variant X3, mRNA	0.02067234	1.1113135	up
MPF_LOC101466731.1.2	XM_004553632.1 PREDICTED: Maylandia zebra glutamate receptor 2-like (LOC101466731), transcript variant X2, mRNA	0.021017518	-1.9687953	down
MPF_LOC101161674.2.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA	0.019260636	-2.6914024	down
MPF_LOC101483532.1.2	XM_004543245.1 PREDICTED: Maylandia zebra transcription factor PU.1-like (LOC101483532), transcript variant X2, mRNA	0.045957807	-1.856924	down
MPF_RS6.6.11	RS6_PROMA (sp|Q7V9F9) 30S ribosomal protein S6 OS=Prochlorococcus marinus (strain SARG / CCMP1375 / SS120) GN=rpsF PE=3 SV=1	0.011256327	-3.7015076	down
MPF_LOC101479639.1.1	XM_004558834.1 PREDICTED: Maylandia zebra neuron navigator 1-like (LOC101479639), transcript variant X2, mRNA	0.027706273	1.1348324	up
MPF_LOC101484929.2.3	XM_004542976.1 PREDICTED: Maylandia zebra CMP-N-acetylneuraminate-beta-1,4galactoside alpha-2,3-sialyltransferase-like (LOC101484929), mRNA	0.016254881	-2.654807	down
MPF_LOC101071928.1.1	XP_003978669.1 PREDICTED: uncharacterized protein LOC101071928 [Takifugu rubripes]	0.010595669	-3.0604315	down
MPF_LOC101472403.3.3	XM_004569122.1 PREDICTED: Maylandia zebra G1/S-specific cyclin-D2-like (LOC101472403), transcript variant X2, mRNA	0.049979005	1.1793659	up
MPF_LOC100690998.1.1	XM_003444519.1 PREDICTED: Oreochromis niloticus probable peptidyl-tRNA hydrolase-like (LOC100690998), mRNA	0.010595669	1.2354898	up
MPF_LOC100697793.2.2	XM_003447553.1 PREDICTED: Oreochromis niloticus DNA polymerase III polC-type-like (LOC100697793), mRNA	0.026799427	-3.291571	down
MPF_LOC101484945.1.1	XM_004546029.1 PREDICTED: Maylandia zebra metabotropic glutamate receptor 7-like (LOC101484945), mRNA	0.03639751	1.1611099	up
MPF_LOC101482434.3.5	XM_004575658.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101482434), mRNA	0.037575997	1.2675642	up
SR24_80+ vs SR24_45-				
Phylofish Gene ID	Gene description	p (Corr FDR)	Log FC	Regulation
MPF_LOC101477684.3.4	XM_004539594.1 PREDICTED: Maylandia zebra small EDRK-rich factor 2-like (LOC101477684), mRNA	0.03753504	-0.699483	down
MPF_LOC101474419.1.1	XM_004554493.1 PREDICTED: Maylandia zebra sperm-associated antigen 17-like (LOC101474419), mRNA	0.03753504	-1.709513	down
MPF_contig_008230		0.049496774	2.622416	up

MPF_LOC101072249.3.3	XP_003966663.1 PREDICTED: target of Nesh-SH3-like [Takifugu rubripes]	0.03753504	3.1074996	up
MPF_LOC100708211.3.3	XM_003457561.1 PREDICTED: Oreochromis niloticus GON-4-like protein-like (LOC100708211), mRNA	0.03753504	-1.342235	down
MPF_contig_015464		0.03753504	3.1383443	up
MPF_CD4.1.1	NP_001072091.1 T-cell surface glycoprotein CD4 [Takifugu rubripes]	0.03753504	-0.72464657	down
MPF_LOC101477684.2.4	XM_004539594.1 PREDICTED: Maylandia zebra small EDRK-rich factor 2-like (LOC101477684), mRNA	0.03753504	-0.6989889	down
MPF_contig_016882		0.03753504	1.7897282	up
MPF_LOC100710715.3.3	XM_003458665.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100710715 (LOC100710715), mRNA	0.03753504	-0.55364895	down
MPF_LOC101156189.1.1	XM_004076645.1 PREDICTED: Oryzias latipes tetratricopeptide repeat protein 1-like (LOC101156189), mRNA	0.03753504	-0.7078228	down
SR48_80+ vs SR48_30-				
Phylofish Gene ID	Gene description	p (Corr FDR)	Log FC	Regulation
MPF_contig_034181		0.024555614	-2.208012	down
MPF_CD68.2.2	NP_001158857.1 Macrosialin precursor [Salmo salar]	0.016467266	-3.3046575	down
MPF_LOC100696676.4.4	XP_003459127.1 PREDICTED: zinc finger protein 235-like [Oreochromis niloticus]	0.01718951	0.49012753	up
MPF_LOC100698998.2.7	XM_003439446.1 PREDICTED: Oreochromis niloticus myosin heavy chain, fast skeletal muscle-like (LOC100698998), mRNA	0.024555614	-3.3230085	down
MPF_LOC100706528.4.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0.01658866	1.1160135	up
MPF_LOC101157594.1.1	XP_004065840.1 PREDICTED: uncharacterized protein LOC101157594 [Oryzias latipes]	0.019181546	-2.8401918	down
MPF_LOC101472355.1.1	XM_004556700.1 PREDICTED: Maylandia zebra peripheral myelin protein 22-like (LOC101472355), mRNA	0.016467266	-4.793164	down
MPF_contig_045041		0.045131866	0.85603005	up
MPF_LOC100135188.1.5	NP_001107363.1 uncharacterized protein LOC100135188 [Xenopus (Silurana) tropicalis]	0.036926053	-3.285157	down
MPF_LOC100702375.2.2	XM_003450215.1 PREDICTED: Oreochromis niloticus 6-phosphofructokinase type C-like (LOC100702375), mRNA	0.024614157	-2.0942378	down
MPF_contig_003522	XM_004551014.1 PREDICTED: Maylandia zebra akirin-1-like (LOC101486208), transcript variant X1, mRNA	0.011534123	-3.459177	down
MPF_LOC101473402.1.1	XM_004548338.1 PREDICTED: Maylandia zebra protein kinase C and casein kinase substrate in neurons protein 2-like (LOC101473402), transcript variant X3, mRNA	0.02901613	-1.5629458	down
MPF_contig_045446		0.011534123	0.6028523	up
MPF_LOC101472043.4.14	XM_004573789.1 PREDICTED: Maylandia zebra tight junction-associated protein 1-like (LOC101472043), transcript variant X4, mRNA	0.016467266	-2.1496713	down
MPF_contig_044599		0.02789708	1.0658985	up
MPF_contig_023930		0.018083682	-3.988323	down
MPF_contig_040368		0.017283726	-3.2419217	down
MPF_contig_038379		0.040895488	-3.0042713	down
MPF_SSL-2.1.2	NP_001117194.1 serum lectin 2 precursor [Salmo salar]	0.010127341	-3.7260528	down
MPF_LOC101470583.3.3	XM_004571226.1 PREDICTED: Maylandia zebra TSC22 domain family protein 1-like (LOC101470583), mRNA	0.031947624	1.2773285	up
MPF_TTC9B.1.1	NM_001078791.2 Xenopus (Silurana) tropicalis tetratricopeptide repeat domain 9B (ttc9b), mRNA	0.012938407	-2.8359723	down

MPF_LOC101172154.1.1	XP_004068682.1 PREDICTED: epithelial membrane protein 3-like [Oryzias latipes]	0.012606664	-3.9188113	down
MPF_LOC100700496.3.3	XM_003453022.1 PREDICTED: Oreochromis niloticus probable ribonuclease ZC3H12D-like (LOC100700496), mRNA	0.011534123	-3.2287974	down
MPF_LOC101476572.2.2	XM_004541074.1 PREDICTED: Maylandia zebra tetraspanin-17-like (LOC101476572), mRNA	0.003644191	-4.5288997	down
MPF_LOC101155471.2.2	XM_004080809.1 PREDICTED: Oryzias latipes cullin-1-like (LOC101155471), mRNA	0.019817997	1.0317163	up
MPF_contig_045323		0.01658866	-4.157819	down
MPF_LOC101474911.1.1	XM_004566844.1 PREDICTED: Maylandia zebra B-cell receptor CD22-like (LOC101474911), transcript variant X3, mRNA	0.035200294	-3.8317897	down
MPF_AHNAK.3.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]	0.019181546	-5.5105305	down
MPF_LOC101472002.1.2	XM_004541243.1 PREDICTED: Maylandia zebra histone-lysine N-methyltransferase ASH1Llike (LOC101472002), transcript variant X1, mRNA	0.017750166	-2.8137345	down
MPF_THAP9.1.1	[BBH] THAP9_HUMAN (sp|Q9H5L6) DNA transposase THAP9 OS=Homo sapiens GN=THAP9 PE=1 SV=2	0.010997458	-3.460091	down
MPF_LOC101470829.1.1	XM_004557598.1 PREDICTED: Maylandia zebra desumoylating isopeptidase 1-like (LOC101470829), mRNA	0.005932611	-3.8159094	down
MPF_contig_026757		0.02173044	-2.77009	down
MPF_LOC101483521.1.1	XM_004540909.1 PREDICTED: Maylandia zebra early growth response protein 1-like (LOC101483521), mRNA	0.006872254	-4.804389	down
MPF_LOC100690512.1.1	XP_003438469.1 PREDICTED: hypothetical protein LOC100690512 [Oreochromis niloticus]	0.026164155	-3.5749276	down
MPF_LOC101170712.1.1	XM_004080140.1 PREDICTED: Oryzias latipes hemoglobin subunit beta-1-like (LOC101170712), mRNA	0.03887031	-2.4964442	down
MPF_LOC101476936.1.1	XM_004565493.1 PREDICTED: Maylandia zebra peptidyl-prolyl cis-trans isomerase FKBP1Alike (LOC101476936), mRNA	0.017880041	-2.706188	down
MPF_LOC101464855.1.1	XM_004546244.1 PREDICTED: Maylandia zebra signal peptide, CUB and EGF-like domaincontaining protein 3-like (LOC101464855), transcript variant X1, mRNA	0.045961503	-4.1123295	down
MPF_LOC100711025.1.1	XP_003444057.1 PREDICTED: putative helicase Mov10l1-like [Oreochromis niloticus]	0.048807908	0.7101298	up
MPF_LOC100693993.1.1	XM_003453809.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693993 (LOC100693993), mRNA	0.044288024	-2.74786	down
MPF_LOC101479407.1.1	XM_004547238.1 PREDICTED: Maylandia zebra macrophage-expressed gene 1 protein-like (LOC101479407), mRNA	0.016467266	-2.7296147	down
MPF_LOC101487734.2.2	XM_004571292.1 PREDICTED: Maylandia zebra cytohesin-4-like (LOC101487734), mRNA	0.031770308	-3.110243	down
MPF_RNASEL2.2.3	NP_001093575.1 ribonuclease like 2 precursor [Danio rerio]	0.04817274	1.0061493	up
MPF_contig_038012		0.022291025	-3.0046782	down
MPF_LOC100708275.1.1	XM_003449495.1 PREDICTED: Oreochromis niloticus alpha-aspartyl dipeptidase-like (LOC100708275), mRNA	0.010373932	-2.868022	down
MPF_LOC101464789.7.10	XM_004574915.1 PREDICTED: Maylandia zebra heat shock cognate 71 kDa protein-like (LOC101464789), mRNA	0.04464448	0.42760274	up
MPF_LOC101486244.2.2	XM_004539011.1 PREDICTED: Maylandia zebra transcription factor MafG-like (LOC101486244), transcript variant X3, mRNA	0.010780305	-2.80055	down
MPF_LOC100706528.6.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0.0391763	1.2180676	up
MPF_contig_022617		0.038277525	-4.14954	down
MPF_RL17.5.5	RL17_RAT (sp|P24049) 60S ribosomal protein L17 OS=Rattus norvegicus GN=Rpl17 PE=2 SV=3	0.045032855	-2.2327862	down
MPF_LOC100702817.2.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.017283726	-6.184757	down
MPF_LOC101486439.1.1	XM_004561632.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 21-like (LOC101486439), mRNA	0.011534123	-2.685773	down
MPF_LOC101156898.4.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	0.047253896	-4.497014	down

MPF_LOC100690258.1.1	XP_003440479.1 PREDICTED: annexin A2-A-like [Oreochromis niloticus]	0.038277525	-5.061736	down
MPF_LOC101075367.4.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]	0.048438825	-2.3135471	down
MPF_ZG57.7.12	ZG57_XENLA (sp|P18729) Gastrula zinc finger protein XlCGF57.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.041503254	1.1482701	up
MPF_LOC101477280.2.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.029462842	-3.9611187	down
MPF_contig_044194		0.02613457	-3.1849	down
MPF_MOR1A.1.1	[BBH] MOR1A_CHICK (sp|Q2YHT7) Cell surface glycoprotein CD200 receptor 1-A OS=Gallus gallus GN=CD200R1A PE=1 SV=1	0.011534123	-3.5841885	down
MPF_LOC101156898.1.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	0.045032855	-3.8364968	down
MPF_contig_036689		0.04602931	0.9231662	up
MPF_contig_035424		0.033274923	-1.7494087	down
MPF_LOC101466332.2.2	XM_004574102.1 PREDICTED: Maylandia zebra heterogeneous nuclear ribonucleoprotein Llike (LOC101466332), mRNA	0.04634622	0.7679558	up
MPF_contig_013399		0.02379514	0.78261477	up
MPF_LOC101474121.17.17	XM_004575391.1 PREDICTED: Maylandia zebra stonustoxin subunit beta-like (LOC101474121), mRNA	0.0179574	-4.072511	down
MPF_LOC101477399.1.1	XM_004538348.1 PREDICTED: Maylandia zebra uncharacterized LOC101477399 (LOC101477399), mRNA	0.012938407	-2.2151923	down
MPF_LOC100933241.9.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.041411318	-3.6757205	down
MPF_LOC101472694.2.4	XM_004542457.1 PREDICTED: Maylandia zebra ephrin type-A receptor 3-like (LOC101472694), transcript variant X2, mRNA	0.02808027	0.58886236	up

MPF_contig_015342		0.0205103	-2.5281837	down
MPF_LOC101162897.1.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]	0.029333163	-4.2892413	down
MPF_LOC100706983.6.11	XM_003460062.1 PREDICTED: Oreochromis niloticus 28S ribosomal protein S28, mitochondrial-like (LOC100706983), mRNA	0.04602931	-2.5326335	down
MPF_LOC101485932.1.1	XM_004538480.1 PREDICTED: Maylandia zebra phosphatidylinositol 4-phosphate 5-kinase type-1 beta-like (LOC101485932), transcript variant X2, mRNA	0.0340328	-2.520379	down
MPF_LOC100698096.4.4	XM_003457021.1 PREDICTED: Oreochromis niloticus H/ACA ribonucleoprotein complex subunit 2-like protein-like (LOC100698096), mRNA	0.022055771	1.2679127	up
MPF_contig_016131		0.02901613	-3.2127054	down
MPF_RL37P.1.1	RL37P_RAT (sp|P61515) Putative 60S ribosomal protein L37a OS=Rattus norvegicus GN=Rpl37a-ps1 PE=5 SV=2	0.04602931	-3.3253713	down
MPF_MIR142A.1.1	NR_030090.1 Danio rerio microRNA 142a (mir142a), microRNA	0.04420101	-3.9406464	down
MPF_LOC101477280.5.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.017283726	-3.9779596	down
MPF_AHNK.17.22	[BBH] AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.016999198	-5.083932	down
MPF_LOC101062855.1.1	XM_003970797.1 PREDICTED: Takifugu rubripes polyubiquitin-B-like, transcript variant 2 (LOC101062855), mRNA	0.016467266	0.39608955	up
MPF_LOC101474370.1.1	XM_004568239.1 PREDICTED: Maylandia zebra mitochondrial glutamate carrier 1-like (LOC101474370), transcript variant X3, mRNA	0.0336634	-2.5654607	down
MPF_LOC100706657.3.3	XP_003447550.1 PREDICTED: CD48 antigen-like [Oreochromis niloticus]	0.035200294	-3.4839568	down
MPF_LOC100711796.2.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA	0.04249592	-2.8511186	down
MPF_contig_032146		0.03701327	-3.418663	down

MPF_LOC101485578.1.1	XM_004539623.1 PREDICTED: Maylandia zebra CD276 antigen-like (LOC101485578), mRNA	0.044288024	-2.524374	down
MPF_contig_020082		0.0391763	-4.425737	down
MPF_contig_024224		0.02119597	-5.5015974	down
MPF_MYHM2126-2.1.3	XP_003975582.1 PREDICTED: myosin-7 [Takifugu rubripes]	0.010780305	-3.47406	down
MPF_LOC101480826.9.9	XM_004564784.1 PREDICTED: Maylandia zebra ubiquitin-60S ribosomal protein L40-like (LOC101480826), mRNA	0.029485393	0.8199434	up
MPF_LOC101164237.1.2	XP_004073974.1 PREDICTED: uncharacterized protein LOC101164237 [Oryzias latipes]	0.04249592	1.1720858	up
MPF_LOC100933241.11.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.03382377	1.7213216	up
MPF_B2MG.3.10	B2MG_CYPCA (sp|Q03422) Beta-2-microglobulin OS=Cyprinus carpio GN=b2m PE=3 SV=1	0.024553591	-3.8648863	down
MPF_LOC101069906.1.1	XP_003969359.1 PREDICTED: tissue factor pathway inhibitor-like [Takifugu rubripes]	0.03995285	-2.6749568	down
MPF_LOC101477280.4.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.025042892	-3.8922653	down
MPF_LOC101161674.1.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA	0.0205103	-3.3742743	down
MPF_contig_018948	WP_006047458.1 hypothetical protein [Burkholderia graminis]	0.03450962	-2.9533095	down
MPF_LOC101161574.14.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.0336634	-4.749422	down
MPF_LOC101481543.7.7	XM_004550249.1 PREDICTED: Maylandia zebra zinc finger BED domain-containing protein 1-like (LOC101481543), mRNA	0.012938407	-4.2284837	down
MPF_contig_021317		0.014306544	-2.484542	down
MPF_LOC101481234.4.12	XM_004569866.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2B-like (LOC101481234), mRNA	0.035200294	-2.5206244	down
MPF_LOC101478567.1.1	XM_004547038.1 PREDICTED: Maylandia zebra claudin-5-like (LOC101478567), mRNA	0.029391069	0.5954271	up
MPF_contig_029207		0.024555614	-3.0672965	down
MPF_LOC100702318.5.5	XP_003458375.1 PREDICTED: galectin-9-like [Oreochromis niloticus]	0.031468377	-3.2399106	down
MPF_CAL6303_1855.1.3	YP_007136861.1 hypothetical protein Cal6303_1855 [Calothrix sp. PCC 6303]	0.028703447	-2.6452274	down
MPF_LOC101065219.3.3	XM_003969289.1 PREDICTED: Takifugu rubripes protein S100-A1-like (LOC101065219), mRNA	3.64E-04	-3.180781	down
MPF_LOC101075367.1.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]	0.033274923	-2.5176792	down
MPF_LOC101159291.2.2	XM_004078003.1 PREDICTED: Oryzias latipes sodium/potassium-transporting ATPase subunit alpha-3-like (LOC101159291), mRNA	0.010780305	-4.301447	down
MPF_contig_008714		0.02173044	-3.1445966	down
MPF_LOC101173086.4.5	XP_004077318.1 PREDICTED: G-protein coupled receptor 4-like [Oryzias latipes]	0.01718951	-1.0362281	down
MPF_contig_023224		0.011534123	-3.9507804	down
MPF_contig_045616		0.01658866	-4.1847696	down
MPF_contig_028716		0.041210905	-2.7046127	down
MPF_contig_043137		0.045032855	1.1586177	up
MPF_LOC100698082.2.2	XR_134880.1 PREDICTED: Oreochromis niloticus keratin, type I cytoskeletal 13-like (LOC100698082), miscRNA	0.019096334	-6.062546	down
MPF_LOC101155699.2.2	XM_004073699.1 PREDICTED: Oryzias latipes protein S100-A10-like (LOC101155699), mRNA	0.022055771	-5.59369	down
MPF_LOC101077514.3.5	XP_003974477.1 PREDICTED: complement factor H-like [Takifugu rubripes]	0.0336634	-4.018136	down

MPF_LOC100693648.1.1	XM_003456513.1 PREDICTED: Oreochromis niloticus probable methyltransferase C20orf7 homolog, mitochondrial-like (LOC100693648), mRNA	0.017813347	0.8557653	up
MPF_LOC100699721.2.2	XP_003460016.1 PREDICTED: bifunctional protein NCOAT-like, partial [Oreochromis niloticus]	0.04464448	-2.9598246	down
MPF_LOC100700605.10.27	XM_003458555.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100700605), mRNA	0.044288024	-2.0437462	down

MPF_LOC100712299.1.1	XM_003451996.1 PREDICTED: Oreochromis niloticus myoferlin-like (LOC100712299), mRNA	0.019096334	-4.136894	down
MPF_LOC101478586.2.2	XM_004550792.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 6-like (LOC101478586), transcript variant X2, mRNA	0.029391069	-2.973082	down
MPF_AHNAK.4.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]	0.016732054	-5.605562	down
MPF_LOC100707140.3.4	XP_003458392.1 PREDICTED: hypothetical protein LOC100707140 [Oreochromis niloticus]	0.043257233	-2.15938	down
MPF_LOC101465129.15.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA	0.0336634	0.6235771	up
MPF_contig_027340		0.046119817	-1.643864	down
MPF_LOC101487021.1.1	XM_004540761.1 PREDICTED: Maylandia zebra thrombospondin-1-like (LOC101487021), transcript variant X2, mRNA	0.029391069	-5.1666517	down
MPF_AHNK.16.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.021297889	-5.2289743	down
MPF_LOC101485716.5.12	XM_004572825.1 PREDICTED: Maylandia zebra multivesicular body subunit 12B-like (LOC101485716), mRNA	0.03984605	-3.2809684	down
MPF_RS13.9.9	RS13_GILMI (sp|Q9DFR6) 40S ribosomal protein S13 OS=Gillichthys mirabilis GN=rps13 PE=2 SV=3	0.044269044	-1.5966523	down
MPF_LOC101477831.3.3	XM_004548827.1 PREDICTED: Maylandia zebra complement C1q subcomponent subunit Blike (LOC101477831), mRNA	0.0336634	-4.0111036	down
MPF_ZKSC3.1.1	ZKSC3_HUMAN (sp|Q9BRR0) Zinc finger protein with KRAB and SCAN domains 3 OS=Homo sapiens GN=ZKSCAN3 PE=1 SV=2	0.039892565	0.64685386	up
MPF_LY9.3.3	LY9_HUMAN (sp|Q9HBG7) T-lymphocyte surface antigen Ly-9 OS=Homo sapiens GN=LY9 PE=1 SV=3	0.014710586	-3.9309247	down
MPF_SI_CH211-125E6.5.1.1	XP_001337601.1 PREDICTED: type-2 ice-structuring protein-like [Danio rerio]	0.010780305	-2.8505912	down
MPF_LOC100707411.2.2	XM_003458503.1 PREDICTED: Oreochromis niloticus E3 ubiquitin-protein ligase ZNRF2-like (LOC100707411), mRNA	0.036637183	-3.8818245	down
MPF_LOC101469126.1.1	XM_004562729.1 PREDICTED: Maylandia zebra monocarboxylate transporter 13-like (LOC101469126), transcript variant X5, mRNA	0.02051149	-3.1670947	down
MPF_contig_009677		0.033640783	-2.434509	down
MPF_LOC101484994.1.2	XM_004555447.1 PREDICTED: Maylandia zebra UPF0524 protein C3orf70 homolog A-like (LOC101484994), mRNA	0.013800118	-3.2237916	down
MPF_LOC101156898.3.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	0.044109177	-3.9288363	down
MPF_LOC100695691.2.2	XM_003455952.1 PREDICTED: Oreochromis niloticus actin-related protein 2/3 complex subunit 1B-like (LOC100695691), mRNA	0.01658866	-5.1340437	down
MPF_contig_024249		0.037894323	0.65432453	up
MPF_LOC101475950.3.3	XM_004553845.1 PREDICTED: Maylandia zebra cAMP-specific 3',5'-cyclic phosphodiesterase 4B-like (LOC101475950), transcript variant X3, mRNA	0.029370636	-4.152605	down
MPF_C1QA.2.2	[BBH] C1QA_PIG (sp|Q69DL0) Complement C1q subcomponent subunit A OS=Sus scrofa GN=C1QA PE=2 SV=1	0.045032855	-4.2355886	down
MPF_contig_032442		0.03791587	-3.6254883	down
MPF_LOC100691043.5.5	XM_003457742.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domainscontaining protein 12-like (LOC100691043), mRNA	0.02051149	-2.69343	down
MPF_LOC100710259.1.2	XM_003450909.1 PREDICTED: Oreochromis niloticus NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3-like (LOC100710259), mRNA	0.032686193	0.91041565	up

MPF_RL37A.1.1	RL37A_XENLA (sp|Q7SZB4) 60S ribosomal protein L37a OS=Xenopus laevis GN=rpl37a PE=3 SV=3	0.04759332	-3.2742057	down
MPF_LOC100708534.1.1	XM_003447507.1 PREDICTED: Oreochromis niloticus myeloid-associated differentiation marker homolog (LOC100708534), mRNA	0.037147112	-5.1417637	down
MPF_MAG.1.4	MAG_RAT (sp|P07722) Myelin-associated glycoprotein OS=Rattus norvegicus GN=Mag PE=1 SV=1	0.011941686	-3.3353944	down
MPF_contig_020726		0.049676374	0.87106895	up
MPF_contig_026335		0.022140114	-3.7552328	down
MPF_LOC101486559.2.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA	0.031947624	-4.991473	down
MPF_LOC101469336.3.3	XM_004566007.1 PREDICTED: Maylandia zebra ras-related protein M-Ras-like (LOC101469336), mRNA	0.03658253	-1.7355586	down
MPF_LOC101475205.1.2	XM_004543789.1 PREDICTED: Maylandia zebra lissencephaly-1 homolog (LOC101475205), transcript variant X4, mRNA	0.040270757	1.2157001	up
MPF_contig_020945	XM_004542601.1 PREDICTED: Maylandia zebra muscleblind-like protein 1-like (LOC101483053), transcript variant X16, mRNA	0.029145047	-4.4312696	down
MPF_LOC101477243.1.1	XM_004544896.1 PREDICTED: Maylandia zebra rho guanine nucleotide exchange factor 25like (LOC101477243), transcript variant X3, mRNA	0.019679412	-2.9551437	down
MPF_LOC100696784.1.1	XP_003441680.1 PREDICTED: HHIP-like protein 1-like [Oreochromis niloticus]	0.02073058	-3.6721122	down
MPF_LOC101170487.4.4	XM_004085086.1 PREDICTED: Oryzias latipes low-density lipoprotein receptor 2-like (LOC101170487), mRNA	0.017283726	-2.7955842	down
MPF_contig_032239		0.020352319	-3.5580268	down
MPF_contig_017097		0.016467266	-3.9683652	down
MPF_LOC101479522.1.2	XM_004547622.1 PREDICTED: Maylandia zebra acid-sensing ion channel 1-like (LOC101479522), transcript variant X5, mRNA	0.033203978	-3.7437873	down
MPF_LOC100690793.2.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]	0.01718951	-5.4777117	down
MPF_LOC101480396.1.1	XM_004552665.1 PREDICTED: Maylandia zebra 5'-AMP-activated protein kinase subunit gamma-2-like (LOC101480396), transcript variant X2, mRNA	0.006872254	-2.7171645	down
MPF_LOC101468488.3.7	XM_004552241.1 PREDICTED: Maylandia zebra 40S ribosomal protein S11-like (LOC101468488), mRNA	0.04195998	0.9143142	up
MPF_contig_006069		0.037378278	-2.6452212	down
MPF_contig_015875		0.041411318	-3.7543616	down
MPF_contig_007959		0.04634622	-2.5570042	down
MPF_contig_033424		0.016467266	-6.0161214	down
MPF_contig_035511	XM_004558926.1 PREDICTED: Maylandia zebra ketohexokinase-like (LOC101480218), transcript variant X3, mRNA	0.033203978	-3.0828593	down
MPF_LOC100697541.1.1	XP_003452659.1 PREDICTED: ADP-ribosylation factor GTPase-activating protein 2-like [Oreochromis niloticus]	0.038797848	0.5600209	up
MPF_CD63.1.2	NM_001124496.1 Oncorhynchus mykiss Cd63 antigen (cd63), mRNA gb|AY593998.1| Oncorhynchus mykiss CD63 (CD63) mRNA, complete cds	0.014456297	-3.4368472	down
MPF_contig_035918		0.017925398	-2.8533647	down
MPF_LOC101481611.1.2	XM_004544911.1 PREDICTED: Maylandia zebra elongation factor Ts, mitochondrial-like (LOC101481611), mRNA	0.03995285	0.594883	up
MPF_LOC100709074.1.1	XM_003448084.1 PREDICTED: Oreochromis niloticus T-complex protein 1 subunit beta-like (LOC100709074), mRNA	0.01658866	-3.620543	down
MPF_ANXA1.1.2	NP_001098295.1 annexin max3 [Oryzias latipes]	0.016467266	-2.2217398	down

MPF_LOC101477695.1.9	XM_004564867.1 PREDICTED: Maylandia zebra 60S ribosomal protein L18a-like (LOC101477695), transcript variant X2, mRNA	0.01718951	-1.8340724	down
MPF_LOC101169293.6.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.02023051	-1.843051	down
MPF_ENPP1.1.2	XM_003446358.1 PREDICTED: Oreochromis niloticus ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA	0.012938407	-4.2954836	down
MPF_LOC101468606.1.3	XM_004561834.1 PREDICTED: Maylandia zebra protein PBDC1-like (LOC101468606), transcript variant X2, mRNA	0.020789223	0.5475893	up
MPF_contig_030749		0.035200294	-3.368052	down
MPF_UBC.1.5	UBC_RAT (sp|Q63429) Polyubiquitin-C OS=Rattus norvegicus GN=Ubc PE=1 SV=1	0.021832021	0.43740273	up
MPF_LOC101465148.1.1	XM_004569455.1 PREDICTED: Maylandia zebra brain acid soluble protein 1-like (LOC101465148), transcript variant X1, mRNA	0.035200294	-4.732541	down
MPF_LOC100692629.1.1	XM_003448362.1 PREDICTED: Oreochromis niloticus complement C1q subcomponent subunit C-like, transcript variant 2 (LOC100692629), mRNA	0.045032855	-4.1207304	down
MPF_UBR4.2.2	XM_003444861.1 PREDICTED: Oreochromis niloticus ubiquitin protein ligase E3 component n-recognin 4 (UBR4), mRNA	0.021755263	0.70450073	up
MPF_LOC101465079.2.2	XM_004551108.1 PREDICTED: Maylandia zebra basal cell adhesion molecule-like (LOC101465079), mRNA	0.010997458	-4.112129	down
MPF_LOC101477400.4.4	XM_004538536.1 PREDICTED: Maylandia zebra cyclin-G2-like (LOC101477400), mRNA	0.027233807	1.0395459	up
MPF_CD276.3.9	CD276_XENLA (sp|Q68EV1) CD276 antigen homolog OS=Xenopus laevis GN=cd276 PE=2 SV=1	0.035200294	-2.2619116	down
MPF_LOC100697750.1.3	XM_003459604.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domainscontaining protein 14-like (LOC100697750), mRNA	0.02462294	-3.9108622	down
MPF_LOC101471553.1.1	XM_004572678.1 PREDICTED: Maylandia zebra protein capicua homolog (LOC101471553), transcript variant X4, mRNA	0.020943312	-1.733942	down
MPF_LOC100691105.1.2	XP_003449231.1 PREDICTED: cytochrome c oxidase subunit 8B, mitochondrial-like [Oreochromis niloticus]	0.027085958	-3.7343688	down
MPF_CFAH.8.15	CFAH_BOVIN (sp|Q28085) Complement factor H OS=Bos taurus GN=CFH PE=1 SV=3	0.037378278	-4.0461335	down
MPF_contig_025452		0.011534123	-2.4543848	down
MPF_LOC101472043.8.14	XM_004573789.1 PREDICTED: Maylandia zebra tight junction-associated protein 1-like (LOC101472043), transcript variant X4, mRNA	0.04057241	-3.2937627	down
MPF_contig_037474		0.035200294	-0.93533856	down
MPF_MXAN_5876.1.1	YP_634013.1 hypothetical protein MXAN_5876 [Myxococcus xanthus DK 1622]	0.016467266	-2.160039	down
MPF_contig_011640		0.026535317	-4.786183	down
MPF_LOC101473892.1.1	XM_004569569.1 PREDICTED: Maylandia zebra transforming growth factor beta-1-like (LOC101473892), transcript variant X2, mRNA	0.0336634	-3.770307	down
MPF_LOC101062526.1.1	XP_003962815.1 PREDICTED: d-2-hydroxyglutarate dehydrogenase, mitochondrial-like [Takifugu rubripes]	0.03995285	0.8067665	up
MPF_LOC100706528.2.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0.029333163	1.1781286	up
MPF_LOC100696360.1.3	XP_003446837.1 PREDICTED: signal-induced proliferation-associated 1-like protein 2-like [Oreochromis niloticus]	0.019096334	-2.7642064	down
MPF_contig_027915	XM_004568424.1 PREDICTED: Maylandia zebra cytochrome P450 2K3-like (LOC101476301), transcript variant X1, mRNA	0.017880041	-2.3787112	down
MPF_LOC101167345.32.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA	0.0486452	-3.0719995	down
MPF_contig_019843		0.03525393	-1.083786	down
MPF_LOC101478535.2.2	XM_004540728.1 PREDICTED: Maylandia zebra latent-transforming growth factor betabinding protein 2-like (LOC101478535), mRNA	0.039211888	-3.0102153	down
MPF_LOC101464586.2.2	XM_004571741.1 PREDICTED: Maylandia zebra tensin-3-like (LOC101464586), transcript variant X3, mRNA	0.017813347	-1.7465286	down

MPF_LOC101476475.1.1	XM_004562669.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 3-like (LOC101476475), mRNA	0.017283726	-6.4161205	down
MPF_LECG.5.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne natteri PE=1 SV=1	0.016467266	-2.8849673	down
MPF_LOC101472370.1.1	XM_004538428.1 PREDICTED: Maylandia zebra gelsolin-like (LOC101472370), transcript variant X2, mRNA	0.035200294	-4.2165513	down
MPF_contig_028429		0.029333163	-3.309226	down
MPF_LOC101158287.1.1	XP_004073601.1 PREDICTED: iduronate 2-sulfatase-like [Oryzias latipes]	0.01718951	0.81904167	up
MPF_HSD17B8.1.1	XM_003457993.1 PREDICTED: Oreochromis niloticus 17-beta hydroxysteroid dehydrogenase type 8 (HSD17B8), mRNA	0.02226714	0.6505623	up
MPF_contig_002650	XM_004079020.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 1 (LOC101161674), mRNA	0.019096334	-3.443843	down
MPF_contig_022248		0.01658866	0.8012557	up
MPF_LOC100696287.1.2	XP_003450735.1 PREDICTED: C-type lectin domain family 9 member A-like isoform 1 [Oreochromis niloticus]	0.03658253	-4.4891844	down
MPF_LOC101169293.1.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.028703447	-2.552433	down

MPF_LOC101482059.1.3	XM_004563140.1 PREDICTED: Maylandia zebra mitogen-activated protein kinase kinase kinase kinase 4-like (LOC101482059), transcript variant X2, mRNA	0.036436506	-2.653882	down
MPF_LOC100705069.1.1	XP_003447626.1 PREDICTED: shootin-1-like [Oreochromis niloticus]	0.029391069	-3.265813	down
MPF_contig_034792		0.03871176	-2.202486	down
MPF_LOC101483357.1.1	XM_004573344.1 PREDICTED: Maylandia zebra transgelin-like (LOC101483357), mRNA	0.02023051	-3.5255861	down
MPF_LOC100700712.2.3	XP_003440431.1 PREDICTED: hypothetical protein LOC100700712 [Oreochromis niloticus]	0.036637183	-3.640725	down
MPF_LOC100706528.1.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0.0179574	1.2539749	up
MPF_LOC100702519.1.1	XM_003441393.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702519), mRNA	0.032686193	-4.077055	down
MPF_LOC100555635.1.1	XP_003229374.1 PREDICTED: uncharacterized protein C14orf93-like [Anolis carolinensis]	0.04305904	-1.921798	down
MPF_LOC101473755.3.3	XM_004564853.1 PREDICTED: Maylandia zebra CCR4-NOT transcription complex subuni 2like (LOC101473755), transcript variant X2, mRNA	0.022140114	-2.5650768	down
MPF_LOC100702817.1.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.013120863	-5.2874446	down
MPF_LOC100693237.1.1	XM_003442623.1 PREDICTED: Oreochromis niloticus catechol O-methyltransferase-like (LOC100693237), mRNA	0.022055771	-3.0632172	down
MPF_LOC101473182.1.3	XM_004566836.1 PREDICTED: Maylandia zebra sialoadhesin-like (LOC101473182), transcript variant X2, mRNA	0.011534123	-4.0141706	down
MPF_LOC101479305.2.6	XM_004546110.1 PREDICTED: Maylandia zebra cytosolic sulfotransferase 3-like (LOC101479305), transcript variant X2, mRNA	0.046552062	-1.4171538	down
MPF_contig_020368	XM_004550291.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1like (LOC101467183), transcript variant X2, mRNA	0.0223594	-3.0003872	down
MPF_LOC101486209.1.4	XM_004551098.1 PREDICTED: Maylandia zebra uncharacterized LOC101486209 (LOC101486209), mRNA	0.034183595	-4.469425	down
MPF_LOC101464936.1.1	XM_004541956.1 PREDICTED: Maylandia zebra sex comb on midleg-like protein 4-like (LOC101464936), transcript variant X3, mRNA	0.0179574	-2.183691	down
MPF_LOC101468855.3.3	XM_004569017.1 PREDICTED: Maylandia zebra protein tweety homolog 3-like (LOC101468855), transcript variant X1, mRNA	0.029333163	-2.89724	down
MPF_LOC101080012.1.1	XM_003977798.1 PREDICTED: Takifugu rubripes CDP-diacylglycerol--serine Ophosphatidyltransferase-like (LOC101080012), mRNA	0.0457797	-1.9963374	down
MPF_TNR1B.1.1	[BBH] TNR1B_MOUSE (sp|P25119) Tumor necrosis factor receptor superfamily member 1B OS=Mus musculus GN=Tnfrsf1b PE=2 SV=1	0.033203978	-4.4387045	down

MPF_LOC101487243.1.3	XM_004570967.1 PREDICTED: Maylandia zebra pleckstrin homology domain-containing family M member 2-like (LOC101487243), transcript variant X2, mRNA	0.033203978	-1.7325034	down
MPF_contig_036091		0.016467266	-2.3952851	down
MPF_LOC101484749.1.1	XM_004544925.1 PREDICTED: Maylandia zebra methyltransferase-like protein 7A-like (LOC101484749), transcript variant X2, mRNA	0.049604226	0.698648	up
MPF_LOC101070379.1.1	XP_003974368.1 PREDICTED: uncharacterized protein LOC101070379 [Takifugu rubripes]	0.04817274	-2.847787	down
MPF_contig_045322		0.021521684	-3.4096985	down
MPF_LOC100698399.1.1	XM_003444297.1 PREDICTED: Oreochromis niloticus non-specific lipid-transfer protein-like (LOC100698399), mRNA	0.03887031	0.8448467	up
MPF_LOC101474179.2.3	XM_004568681.1 PREDICTED: Maylandia zebra nucleolin 2-like (LOC101474179), mRNA	0.007458308	-4.5272923	down
MPF_LOC101156352.1.1	XP_004077953.1 PREDICTED: ictacalcin-like [Oryzias latipes]	0.043061953	-3.777919	down
MPF_FZD6.6.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440 IMAGE:6971142), complete cds	0.01589579	-3.9071875	down
MPF_LOC101480831.3.3	XM_004565417.1 PREDICTED: Maylandia zebra putative 60S ribosomal protein L37a-like (LOC101480831), mRNA	0.046321355	-3.2902799	down
MPF_LOC101078462.1.1	XP_003965271.1 PREDICTED: lysosome membrane protein 2-like [Takifugu rubripes]	0.024942003	-4.8912163	down
MPF_LOC101074275.1.1	XP_003968653.1 PREDICTED: transforming growth factor beta-1-like [Takifugu rubripes]	0.034183595	-3.8481593	down
MPF_LOC100711510.1.8	XM_003455849.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100711510), mRNA	0.02051149	-3.7975883	down
MPF_LOC101486559.1.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA	0.010997458	-5.709249	down
MPF_LOC101464886.1.1	XM_004575104.1 PREDICTED: Maylandia zebra anoctamin-5-like (LOC101464886), transcript variant X2, mRNA	0.02051149	-3.1011481	down
MPF_LOC101466654.1.2	XM_004538580.1 PREDICTED: Maylandia zebra sodium-dependent phosphate transporter 1B-like (LOC101466654), partial mRNA	0.016467266	-3.1636596	down
MPF_LOC100706330.1.1	XP_003457684.1 PREDICTED: hypothetical protein LOC100706330 [Oreochromis niloticus]	0.011534123	-3.0755062	down
MPF_LOC101464934.1.3	XM_004565357.1 PREDICTED: Maylandia zebra matrix metalloproteinase-14-like (LOC101464934), mRNA	0.0336634	-4.35816	down
MPF_LOC101466346.1.1	XM_004553806.1 PREDICTED: Maylandia zebra tyrosine-protein kinase ZAP-70-like (LOC101466346), transcript variant X4, mRNA	0.02023051	-2.8718162	down
MPF_LOC101485244.1.1	XM_004568719.1 PREDICTED: Maylandia zebra zinc transporter 1-like (LOC101485244), mRNA	0.03880414	-2.5931106	down
MPF_LOC100692921.1.1	XM_003454794.1 PREDICTED: Oreochromis niloticus P2Y purinoceptor 12-like (LOC100692921), mRNA	0.02023051	-2.3567216	down
MPF_contig_028808		0.01658866	-4.8180804	down
MPF_contig_031758	XM_004550291.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1like (LOC101467183), transcript variant X2, mRNA	0.041210905	-2.738479	down
MPF_LOC101469549.1.2	XM_004573028.1 PREDICTED: Maylandia zebra interleukin-1 receptor-like 1-like (LOC101469549), mRNA	0.035200294	-2.8226101	down
MPF_contig_008230		0.03424468	-3.2160742	down
MPF_LOC101477091.1.3	XM_004574318.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1like (LOC101477091), transcript variant X5, mRNA	0.012606664	-1.9721106	down
MPF_LOC100690401.1.3	XP_003454006.1 PREDICTED: hypothetical protein LOC100690401 [Oreochromis niloticus]	0.01658866	-4.615611	down
MPF_LOC100703589.1.1	XM_003460117.1 PREDICTED: Oreochromis niloticus plasminogen activator inhibitor 1-like (LOC100703589), mRNA	0.010997458	-6.372183	down
MPF_LOC101168933.2.2	XP_004086950.1 PREDICTED: macrophage receptor MARCO-like [Oryzias latipes]	0.03416801	-2.3144531	down
MPF_AHNK.21.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.01658866	-4.8892703	down

MPF_contig_023757		0.017880041	-3.6241274	down
MPF_LOC101475584.3.5	XM_004561039.1 PREDICTED: Maylandia zebra thrombospondin type-1 domain-containing protein 7A-like (LOC101475584), mRNA	0.029462842	-4.273311	down
MPF_LOC101075004.1.1	XM_003964966.1 PREDICTED: Takifugu rubripes uncharacterized LOC101075004 (LOC101075004), mRNA	0.019797137	-5.0822744	down
MPF_LOC100710693.1.3	XP_003453586.1 PREDICTED: complement factor H-like [Oreochromis niloticus]	0.01718951	-3.4714317	down
MPF_contig_048789		0.032686193	1.0406504	up
MPF_LOC100180429.3.7	XM_002120912.1 PREDICTED: Ciona intestinalis uncharacterized LOC100180429 (LOC100180429), mRNA	0.035200294	-2.3136392	down
MPF_LOC101485262.1.1	XM_004572362.1 PREDICTED: Maylandia zebra membrane-spanning 4-domains subfamily A member 12-like (LOC101485262), mRNA	0.024555614	-3.2704911	down
MPF_LOC100696821.2.2	XM_003452445.1 PREDICTED: Oreochromis niloticus ictacalcin-like (LOC100696821), mRNA	0.04759332	-4.4984236	down
MPF_LOC101469726.1.2	XM_004572396.1 PREDICTED: Maylandia zebra pre-mRNA 3' end processing protein WDR33-like (LOC101469726), transcript variant X2, mRNA	0.024631001	1.0081863	up
MPF_contig_047891		0.016467266	-3.740108	down
MPF_LOC100712302.1.1	XP_003452302.1 PREDICTED: aminoacyl tRNA synthase complex-interacting multifunctional protein 1-like [Oreochromis niloticus]	0.016467266	-3.5456767	down
MPF_LOC100706878.5.6	XP_003458391.1 PREDICTED: hypothetical protein LOC100706878 [Oreochromis niloticus]	0.011534123	-3.2936835	down
MPF_contig_028541		0.026766373	-4.0811315	down
MPF_HEPHL1.1.1	XM_003446729.1 PREDICTED: Oreochromis niloticus hephaestin-like 1 (HEPHL1), mRNA	0.019181546	-3.364187	down
MPF_contig_014987		0.04634622	0.6739378	up
MPF_LOC100689711.4.6	XP_003459483.1 PREDICTED: h-2 class I histocompatibility antigen, L-D alpha chain-like [Oreochromis niloticus]	0.02211233	-2.578095	down
MPF_LOC100692258.2.2	XM_003445695.1 PREDICTED: Oreochromis niloticus ferritin, heavy subunit-like (LOC100692258), mRNA	0.04057241	0.47276446	up
MPF_contig_020580		0.035200294	-3.2553067	down
MPF_CRE_07824.1.1	XP_003093184.1 hypothetical protein CRE_07824 [Caenorhabditis remanei]	0.04895499	-3.3095322	down
MPF_LOC101471521.1.3	XM_004543486.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF128-like (LOC101471521), mRNA	0.01658866	-3.8107615	down
MPF_LOC101480440.1.1	XM_004541919.1 PREDICTED: Maylandia zebra deleted in malignant brain tumors 1 proteinlike (LOC101480440), mRNA	0.04634622	-0.9954924	down
MPF_CRE_23222.1.2	XP_003089877.1 hypothetical protein CRE_23222 [Caenorhabditis remanei]	0.022702836	-1.5666894	down
MPF_LOC101465872.1.1	XM_004558783.1 PREDICTED: Maylandia zebra extended synaptotagmin-1-like (LOC101465872), mRNA	0.03223174	-5.15211	down
MPF_LOC101478190.2.2	XM_004571703.1 PREDICTED: Maylandia zebra platelet basic protein-like (LOC101478190), mRNA	0.03887031	-3.3270772	down
MPF_LOC101471935.1.1	XM_004545975.1 PREDICTED: Maylandia zebra transcription factor MafB-like (LOC101471935), mRNA	0.021521684	-3.8034105	down
MPF_LOC100559296.1.1	XP_003228542.1 PREDICTED: zinc finger protein 229-like [Anolis carolinensis]	0.04639371	0.5891728	up
MPF_LOC100700016.1.1	XM_003447883.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100700016 (LOC100700016), mRNA	0.019181546	-2.064024	down
MPF_LOC100708084.3.4	XM_003447339.1 PREDICTED: Oreochromis niloticus uridine phosphorylase 2-like (LOC100708084), mRNA	0.029485393	-2.298925	down
MPF_LOC101467232.1.1	XM_004541226.1 PREDICTED: Maylandia zebra ceramide synthase 2-like (LOC101467232), mRNA	0.009101946	-3.8973403	down
MPF_LOC101484703.2.2	XM_004555446.1 PREDICTED: Maylandia zebra transmembrane protein 41A-A-like (LOC101484703), mRNA	0.003644191	-3.8322272	down
MPF_LOC100690793.1.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]	0.030492596	-5.398214	down

MPF_contig_037007		0.018690573	-3.4099998	down
MPF_LOC101473612.4.5	XM_004550873.1 PREDICTED: Maylandia zebra sodium/potassium-transporting ATPase subunit alpha-3-like (LOC101473612), transcript variant X2, mRNA	0.016467266	-4.1912994	down
MPF_LOC101464956.1.1	XM_004545486.1 PREDICTED: Maylandia zebra large neutral amino acids transporter small subunit 3-like (LOC101464956), mRNA	0.025189415	-3.7939618	down
MPF_LOC101481309.1.1	XM_004541558.1 PREDICTED: Maylandia zebra histone-lysine N-methyltransferase MLLlike (LOC101481309), transcript variant X1, mRNA	0.04744662	0.95622873	up
MPF_LOC101464117.1.1	XM_004572292.1 PREDICTED: Maylandia zebra solute carrier family 12 member 7-like (LOC101464117), transcript variant X3, mRNA	0.038729865	-2.3019452	down
MPF_contig_005656		0.021521684	0.9926729	up
MPF_LOC100697415.3.3	XP_003444759.1 PREDICTED: neuroblast differentiation-associated protein AHNAK-like [Oreochromis niloticus]	0.017880041	-5.3717175	down
MPF_contig_011672	XM_004550791.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 6-like (LOC101478586), transcript variant X1, mRNA	0.036863893	-2.5919318	down
MPF_LOC100706922.1.1	XP_003446211.1 PREDICTED: transcription initiation factor TFIID subunit 2-like [Oreochromis niloticus]	0.045889337	1.3943138	up
MPF_K1C18.1.2	K1C18_DANRE (sp|Q7ZTS4) Keratin, type I cytoskeletal 18 OS=Danio rerio GN=krt18 PE=1 SV=2	0.01718951	-5.535241	down
MPF_LOC101483054.1.2	XM_004542678.1 PREDICTED: Maylandia zebra serotransferrin-like (LOC101483054), mRNA	0.04095554	-3.254096	down
MPF_LOC101158485.1.2	XM_004080739.1 PREDICTED: Oryzias latipes nucleoside diphosphate kinase A-like, transcript variant 3 (LOC101158485), mRNA	0.01658866	1.1543868	up
MPF_LOC100694868.1.2	XM_003446700.1 PREDICTED: Oreochromis niloticus c-C chemokine receptor type 6-like (LOC100694868), mRNA	0.04357966	-2.003394	down
MPF_LOC101471731.1.2	XM_004544422.1 PREDICTED: Maylandia zebra myocyte-specific enhancer factor 2C-like (LOC101471731), transcript variant X6, mRNA	0.010780305	-4.27655	down
MPF_LOC101476819.5.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0.031066773	-3.5695772	down
MPF_GP91PHOX.2.2	NM_001032732.1 Takifugu rubripes gp91phox protein (gp91phox), mRNA	0.036637183	-3.1427975	down
MPF_contig_023804		0.017880041	-1.3299804	down
MPF_contig_036789		0.029333163	-3.1842804	down
MPF_LOC101486284.2.3	XM_004546431.1 PREDICTED: Maylandia zebra transmembrane protein 189-like (LOC101486284), mRNA	0.012938407	0.7705421	up
MPF_LOC101482854.4.4	XM_004540267.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(q) subunit alpha-like (LOC101482854), transcript variant X3, mRNA	0.035200294	0.80447096	up
MPF_LOC100710548.3.4	XP_003459320.1 PREDICTED: major histocompatibility complex class I-related gene proteinlike [Oreochromis niloticus]	0.038277525	-3.9958427	down
MPF_LOC101072249.3.3	XP_003966663.1 PREDICTED: target of Nesh-SH3-like [Takifugu rubripes]	0.013120863	-3.7893085	down
MPF_LOC101169293.5.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.02051149	-2.5026085	down
MPF_LOC100706800.1.1	XM_003439818.1 PREDICTED: Oreochromis niloticus retinoic acid receptor RXR-gamma-Blike, transcript variant 1 (LOC100706800), mRNA	0.044288024	-2.8539815	down
MPF_CFAH.14.15	CFAH_MOUSE (sp|P06909) Complement factor H OS=Mus musculus GN=Cfh PE=1 SV=2	0.031947624	-3.0861006	down
MPF_LOC101067754.3.3	XM_003961265.1 PREDICTED: Takifugu rubripes NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4-like (LOC101067754), mRNA	0.0336634	-3.3519347	down
MPF_LOC100704396.2.3	XP_003459961.1 PREDICTED: neoverrucotoxin subunit alpha-like [Oreochromis niloticus]	0.01658866	-4.277787	down
MPF_contig_044005		0.016467266	-3.2948842	down
MPF_LOC101481869.4.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA	0.0179574	-1.7481651	down
MPF_LOC100711796.1.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA	0.035200294	-2.725048	down

MPF_contig_004128		0.02710801	-3.1293972	down
MPF_contig_004261		0.017880041	-3.2745376	down
MPF_PFL1445W.1.1	XP_001350695.2 conserved Plasmodium protein [Plasmodium falciparum 3D7]	0.014502768	-3.099511	down
MPF_CD28.1.1	[BBH] CD28_HUMAN (sp|P10747) T-cell-specific surface glycoprotein CD28 OS=Homo sapiens GN=CD28 PE=1 SV=1	0.019096334	-3.0359974	down
MPF_LOC101479192.1.1	XM_004541915.1 PREDICTED: Maylandia zebra lebercilin-like (LOC101479192), transcript variant X1, mRNA	0.016467266	-3.7575555	down
MPF_AHNK.22.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.023719203	-2.344696	down
MPF_contig_032455		0.025501568	-1.4902575	down
MPF_contig_023721		0.035200294	-1.9995906	down
MPF_TNF6B.1.1	TNF6B_HUMAN (sp|O95407) Tumor necrosis factor receptor superfamily member 6B OS=Homo sapiens GN=TNFRSF6B PE=1 SV=1	0.016999198	-6.1991434	down
MPF_LOC100705618.1.1	XP_003453815.1 PREDICTED: protogenin-like [Oreochromis niloticus]	0.028703447	-3.3657746	down
MPF_contig_044606		0.036863893	-4.0316005	down
MPF_contig_033640	XM_004548336.1 PREDICTED: Maylandia zebra protein kinase C and casein kinase substrate in neurons protein 2-like (LOC101473402), transcript variant X1, mRNA	0.0391763	-1.4933586	down
MPF_LOC101173086.5.5	XP_004077318.1 PREDICTED: G-protein coupled receptor 4-like [Oryzias latipes]	0.04602931	-0.9710913	down
MPF_LOC101486434.1.2	XM_004560149.1 PREDICTED: Maylandia zebra cathepsin K-like (LOC101486434), mRNA	0.028703447	-4.773645	down
MPF_LOC101061752.1.1	XM_003975168.1 PREDICTED: Takifugu rubripes SEC14-like protein 2-like (LOC101061752), mRNA	0.035200294	-3.651393	down
MPF_LOC100702817.3.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.01658866	-6.319756	down
MPF_LOC101076756.1.1	XM_003972767.1 PREDICTED: Takifugu rubripes histone-lysine N-methyltransferase MLL5like (LOC101076756), mRNA	0.011534123	-3.3957186	down
MPF_LOC101482128.1.2	XM_004574739.1 PREDICTED: Maylandia zebra MARCKS-related protein-like (LOC101482128), mRNA	0.009729241	3.1571312	up
MPF_LOC100712517.2.2	XM_003459650.1 PREDICTED: Oreochromis niloticus RNA (guanine-9-)-methyltransferase domain-containing protein 2-like (LOC100712517), mRNA	0.044109177	-2.1131709	down
MPF_contig_004326		0.016467266	-2.5846448	down
MPF_LOC101480609.1.2	XM_004539422.1 PREDICTED: Maylandia zebra homeodomain-interacting protein kinase 3like (LOC101480609), transcript variant X2, mRNA	0.011534123	-4.7348213	down
MPF_LOC101465129.6.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA	0.04634622	-2.3891044	down
MPF_contig_029673		0.01718951	-2.4196236	down
MPF_LOC101487373.23.24	XM_004576282.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101487373), mRNA	0.019679412	-1.2816243	down
MPF_LOC100704053.3.12	XM_003440652.1 PREDICTED: Oreochromis niloticus ubiquitin-like protein FUBI-like (LOC100704053), mRNA	0.04634622	-1.5901041	down
MPF_contig_043890		0.027233807	-2.1212025	down
MPF_LOC100699618.1.3	XM_003458706.1 PREDICTED: Oreochromis niloticus macrophage-capping protein-like (LOC100699618), mRNA	0.045742314	-3.6982234	down
MPF_contig_025370	XM_004558558.1 PREDICTED: Maylandia zebra autism susceptibility gene 2 protein-like (LOC101480020), transcript variant X7, mRNA	0.016467266	-3.3792162	down
MPF_LOC101077329.1.1	XP_003965511.1 PREDICTED: glycerol-3-phosphate acyltransferase 3-like [Takifugu rubripes]	0.035200294	0.5391473	up
MPF_LOC101479518.3.5	XM_004570668.1 PREDICTED: Maylandia zebra alpha-actinin-3-like (LOC101479518), mRNA	0.049676374	-2.581444	down

MPF_LOC100705343.3.3	XM_003450141.1 PREDICTED: Oreochromis niloticus claudin-8-like (LOC100705343), mRNA	0.029462842	-4.581944	down
MPF_LOC101167345.13.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA	0.011534123	-3.5083098	down

MPF_contig_017955		0.035200294	-1.9654016	down
MPF_LOC101475629.1.1	XM_004570493.1 PREDICTED: Maylandia zebra lactosylceramide 1,3-N-acetyl-beta-Dglucosaminyltransferase A-like (LOC101475629), transcript variant X2, mRNA	0.01658866	-2.8269672	down
MPF_LOC101487936.1.3	XM_004552317.1 PREDICTED: Maylandia zebra F-box/LRR-repeat protein 20-like (LOC101487936), transcript variant X2, mRNA	0.034505185	1.5108747	up
MPF_LOC101466772.1.2	XM_004542617.1 PREDICTED: Maylandia zebra glypican-5-like (LOC101466772), transcript variant X2, mRNA	0.027812004	0.5292578	up
MPF_contig_026589		0.038729865	1.699933	up
MPF_LOC101480505.1.1	XM_004557175.1 PREDICTED: Maylandia zebra ankyrin repeat domain-containing protein 29-like (LOC101480505), transcript variant X3, mRNA	0.0412985	0.61424166	up
MPF_LOC101161574.12.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.024553591	-3.5222292	down
MPF_contig_013979	XM_004551640.1 PREDICTED: Maylandia zebra 40S ribosomal protein S24-like (LOC101482129), transcript variant X1, mRNA	0.012606664	-4.1645794	down
MPF_LOC100692490.2.4	XM_003457423.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L37a-like (LOC100692490), mRNA	0.032686193	-3.361215	down
MPF_LOC100706186.1.2	XM_003460059.1 PREDICTED: Oreochromis niloticus calpain-2 catalytic subunit-like (LOC100706186), mRNA	0.017760739	-2.9407153	down
MPF_LOC101466612.1.2	XM_004549597.1 PREDICTED: Maylandia zebra zinc finger protein 462-like (LOC101466612), transcript variant X1, mRNA	0.0336634	-2.7982302	down
MPF_LOC101473441.1.1	XM_004558810.1 PREDICTED: Maylandia zebra transcription factor NF-E2 45 kDa subunitlike (LOC101473441), transcript variant X2, mRNA	0.035200294	-1.5510898	down
MPF_NEMVEDRAFT_V1G118504.1.1	XP_001628905.1 predicted protein [Nematostella vectensis]	0.036637183	-2.9561744	down
MPF_contig_024386		0.036637183	-3.4335861	down
MPF_HACE1.1.3	HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2	0.017283726	-5.591163	down
MPF_OSTC.2.3	OSTC_DANRE (sp|Q7ZWJ3) Oligosaccharyltransferase complex subunit ostc OS=Danio rerio GN=ostc PE=2 SV=1	0.032686193	-2.2333627	down
MPF_contig_032849		0.03658253	-2.1423798	down
MPF_LOC101162897.2.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]	0.028703447	-3.8258722	down
MPF_LOC100700407.1.1	XM_003454414.1 PREDICTED: Oreochromis niloticus IGF-like family receptor 1-like (LOC100700407), mRNA	0.022055771	-4.197659	down
MPF_LOC101168228.1.1	XP_004076087.1 PREDICTED: T-cell immunoglobulin and mucin domain-containing protein 4-like [Oryzias latipes]	0.043779302	-3.9079735	down
MPF_ZC2HC1C.1.1	XP_003924603.1 PREDICTED: zinc finger C2HC domain-containing protein 1C homolog isoform 1 [Saimiri boliviensis boliviensis]	0.04602931	0.70156485	up
MPF_contig_009740		0.036637183	-1.2067595	down
MPF_LOC101161574.4.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.02901613	-3.4249637	down
MPF_contig_032895		0.037746806	-1.7164011	down
MPF_contig_015435		0.01658866	-3.5280433	down
MPF_LOC101488070.1.1	XM_004543546.1 PREDICTED: Maylandia zebra neprilysin-like (LOC101488070), transcript variant X1, mRNA	0.021755263	-6.783157	down
MPF_LOC101166970.1.1	XP_004073985.1 PREDICTED: uncharacterized protein LOC101166970 [Oryzias latipes]	0.00963008	-4.8677406	down

MPF_C1QC.1.1	NP_001135251.1 complement C1q subcomponent subunit C precursor [Salmo salar]	0.04817274	-2.218679	down
MPF_contig_003837		0.04057241	-4.2820606	down
MPF_LOC101472300.1.1	XM_004568586.1 PREDICTED: Maylandia zebra uncharacterized LOC101472300 (LOC101472300), mRNA	0.011534123	-4.7800303	down
MPF_LOC100709648.6.13	XM_003457730.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S4-like (LOC100709648), mRNA	0.027233807	0.9656844	up
MPF_contig_037247		0.024553591	-2.9003642	down
MPF_contig_015500		0.021521684	-4.2258654	down
MPF_LOC100488659.3.10	XP_002933173.1 PREDICTED: hypothetical protein LOC100488659 [Xenopus (Silurana) tropicalis]	0.037056934	-3.0092409	down
MPF_LOC101477280.6.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.02901613	-3.9323344	down
MPF_contig_028860		0.035901163	-4.3202024	down
MPF_LOC101076460.1.1	XP_003978301.1 PREDICTED: homeobox protein CDX-1-like [Takifugu rubripes]	0.03677341	0.56748194	up
MPF_RTBS.12.36	RTBS_DROME (sp|Q95SX7) Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1	0.03701327	-4.0767307	down
MPF_LOC100695830.1.2	XM_003445456.1 PREDICTED: Oreochromis niloticus serine/arginine-rich splicing factor 4like, transcript variant 1 (LOC100695830), mRNA	0.010997458	-4.2166977	down
MPF_LOC101486993.1.1	XM_004554270.1 PREDICTED: Maylandia zebra sodium-dependent neutral amino acid transporter SLC6A17-like (LOC101486993), mRNA	0.044109177	-2.5425951	down
MPF_contig_028605		0.012938407	-4.4360275	down
MPF_contig_015464		0.018193826	-4.2576523	down
MPF_LOC101165232.1.1	XP_004070172.1 PREDICTED: N-terminal EF-hand calcium-binding protein 2-like [Oryzias latipes]	0.031770308	0.63300127	up
MPF_LOC101076840.1.1	XM_003974902.1 PREDICTED: Takifugu rubripes chemokine-like receptor 1-like (LOC101076840), mRNA	0.048568904	-3.3169065	down
MPF_contig_022962		0.0205103	-3.0219526	down
MPF_LOC101488089.1.1	XM_004570084.1 PREDICTED: Maylandia zebra uncharacterized LOC101488089 (LOC101488089), transcript variant X3, mRNA	0.03701327	-3.5587573	down
MPF_contig_027052		0.035901163	-2.8941858	down
MPF_LOC101063580.1.1	XP_003966085.1 PREDICTED: syndecan-2-like [Takifugu rubripes]	0.045131866	-2.2198372	down
MPF_LOC100703560.1.2	XM_003453596.1 PREDICTED: Oreochromis niloticus BRCA1-A complex subunit Abraxaslike (LOC100703560), mRNA	0.04249592	0.56530327	up

MPF_LOC101468563.1.2	XM_004572588.1 PREDICTED: Maylandia zebra alkaline nuclease-like (LOC101468563), transcript variant X6, mRNA	0.005053798	-2.2771358	down
MPF_contig_014816		0.03313761	-2.9133687	down
MPF_LOC101068301.2.3	XM_003966217.1 PREDICTED: Takifugu rubripes protein S100-A11-like (LOC101068301), mRNA	0.01658866	-4.4930587	down
MPF_contig_037637		0.032411985	-0.834548	down
MPF_LOC100005864.2.2	XP_001921726.1 PREDICTED: GTPase IMAP family member 8-like [Danio rerio]	0.022882693	-3.1070514	down
MPF_LOC101481185.2.2	XM_004538074.1 PREDICTED: Maylandia zebra mothers against decapentaplegic homolog 4-like (LOC101481185), mRNA	0.017283726	-3.101789	down
MPF_LOC101487734.1.2	XM_004571292.1 PREDICTED: Maylandia zebra cytohesin-4-like (LOC101487734), mRNA	0.0181206	-3.737102	down
MPF_LOC101473855.10.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA	0.03877526	-2.289383	down

MPF_LOC101481486.1.2	XM_004563678.1 PREDICTED: Maylandia zebra MARCKS-related protein-like (LOC101481486), mRNA	0.032970488	3.0900688	up
MPF_contig_019388		0.02173044	-2.792027	down
MPF_LOC101471890.1.1	XM_004559351.1 PREDICTED: Maylandia zebra nuclear GTPase SLIP-GC-like (LOC101471890), mRNA	0.011534123	-3.3832982	down
MPF_RTXE.3.6	RTXE_DROME (sp|Q9NBX4) Probable RNA-directed DNA polymerase from transposon Xelement OS=Drosophila melanogaster GN=X-elementORF2 PE=3 SV=1	0.010780305	-2.7212143	down
MPF_LOC101156534.1.3	XR_177556.1 PREDICTED: Oryzias latipes synaptotagmin-1-like (LOC101156534), misc_RNA	0.013800118	-2.29247	down
MPF_LOC100699007.2.2	XM_003442225.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100699007, transcript variant 2 (LOC100699007), mRNA	0.045742314	-4.869918	down
MPF_contig_025924	XM_004574349.1 PREDICTED: Maylandia zebra protein FAM49A-like (LOC101486310), transcript variant X2, mRNA	0.031770308	-3.337266	down
MPF_BLCAP.2.2	[BBH] BLCAP_DANRE (sp|Q9IB61) Bladder cancer-associated protein OS=Danio rerio GN=blcap PE=3 SV=1	0.027308725	0.69747114	up
MPF_contig_026907		0.04607347	-4.2599473	down
MPF_contig_032259		0.01718951	-4.1290197	down
MPF_contig_023989		0.04377358	-2.7955265	down
MPF_contig_031639		0.04607347	-3.6487596	down
MPF_contig_021432		0.029485393	-2.8012986	down
MPF_LOC101160141.1.1	XR_177319.1 PREDICTED: Oryzias latipes keratin, type I cytoskeletal 13-like (LOC101160141), misc_RNA	0.02901613	-4.8655033	down
MPF_LOC101467183.1.2	XM_004550296.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1like (LOC101467183), transcript variant X7, mRNA	0.01658866	-3.1663272	down
MPF_LOC101468196.2.2	XM_004575285.1 PREDICTED: Maylandia zebra caspase-12-like (LOC101468196), mRNA	0.003030338	-4.456868	down
MPF_contig_012573		0.03223174	-3.873251	down
MPF_contig_021708		0.016732054	-2.2786732	down
MPF_LOC101481376.3.4	XM_004557456.1 PREDICTED: Maylandia zebra heat shock protein beta-1-like (LOC101481376), mRNA	0.036637183	-4.4203863	down
MPF_LOC101476137.1.1	XM_004574406.1 PREDICTED: Maylandia zebra baculoviral IAP repeat-containing protein 6like (LOC101476137), transcript variant X5, mRNA	0.028614575	0.5179467	up
MPF_LOC101477938.4.9	XM_004574058.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101477938), mRNA	0.013120863	-3.556346	down
MPF_LOC101477850.6.10	XM_004575562.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12-like (LOC101477850), mRNA	0.016467266	-4.2474785	down
MPF_LOC101064338.1.1	XM_003970413.1 PREDICTED: Takifugu rubripes putative monooxygenase p33MONOX-like (LOC101064338), mRNA	0.04634622	0.76701885	up
MPF_LOC100695137.3.3	XP_003447509.1 PREDICTED: high affinity immunoglobulin epsilon receptor subunit gammalike [Oreochromis niloticus]	0.035200294	-5.255582	down
MPF_LOC101476292.1.1	XM_004567039.1 PREDICTED: Maylandia zebra transgelin-like (LOC101476292), transcript variant X2, mRNA	0.035200294	-6.7138233	down
MPF_LOC100708025.2.2	XM_003456564.1 PREDICTED: Oreochromis niloticus cytohesin-4-like (LOC100708025), mRNA	0.017880041	-3.7307868	down
MPF_AHNK.20.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.033158198	-1.6717155	down
MPF_LOC100702843.2.2	XP_003455945.1 PREDICTED: protein-tyrosine kinase 2-beta-like [Oreochromis niloticus]	0.037894323	-2.7515202	down
MPF_LOC101474461.1.1	XM_004546190.1 PREDICTED: Maylandia zebra ataxin-1-like (LOC101474461), transcript variant X2, mRNA	0.006872254	-3.394105	down

MPF_CD276.6.9	CD276_XENLA (sp|Q68EV1) CD276 antigen homolog OS=Xenopus laevis GN=cd276 PE=2 SV=1	0.029333163	-3.2451096	down
MPF_LOC100697337.2.4	XP_003446015.1 PREDICTED: hypothetical protein LOC100697337 [Oreochromis niloticus]	0.037894323	-1.9846942	down
MPF_CD4.1.1	NP_001072091.1 T-cell surface glycoprotein CD4 [Takifugu rubripes]	0.03887031	0.86714846	up
MPF_contig_006498		0.025294997	-3.363094	down
MPF_contig_031891		0.0223594	-4.066507	down
MPF_LOC101487485.1.1	XM_004560899.1 PREDICTED: Maylandia zebra fibroleukin-like (LOC101487485), mRNA	0.022055771	-2.9019809	down
MPF_CD48.2.4	CD48_MOUSE (sp|P18181) CD48 antigen OS=Mus musculus GN=Cd48 PE=1 SV=1	0.019606845	-4.025452	down
MPF_contig_042687		0.031468377	-2.8822846	down
MPF_LOC100697522.1.1	XM_003447958.1 PREDICTED: Oreochromis niloticus N-acetylmuramoyl-L-alanine amidaselike (LOC100697522), mRNA	0.04634622	-2.5973258	down
MPF_contig_035115		0.049604226	-3.3895125	down
MPF_contig_023056		0.031770308	-3.1487613	down
MPF_LOC101168710.1.1	XP_004070984.1 PREDICTED: CD27 antigen-like [Oryzias latipes]	0.047965955	-3.8291776	down

MPF_LOC101473901.1.2	XM_004572233.1 PREDICTED: Maylandia zebra CDC42 small effector protein 1-like (LOC101473901), transcript variant X2, mRNA	0.01658866	-4.8563266	down
MPF_LOC101478250.3.3	XM_004538353.1 PREDICTED: Maylandia zebra flocculation protein FLO11-like (LOC101478250), transcript variant X3, mRNA	0.048438825	-5.1557446	down
MPF_LOC100696796.2.2	XM_003445884.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100696796 (LOC100696796), mRNA	0.035465773	-2.6305492	down
MPF_LOC100698701.1.2	XM_003455230.1 PREDICTED: Oreochromis niloticus protein S100-A13-like (LOC100698701), mRNA	0.015604368	-4.2309084	down
MPF_LOC101467030.1.1	XM_004563996.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 31-like (LOC101467030), mRNA	0.035200294	-2.4485562	down
MPF_LOC445921.1.1	XP_003979513.1 PREDICTED: Ig mu chain C region membrane-bound form [Takifugu rubripes]	0.033274923	-3.889231	down
MPF_LOC101477280.1.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.01718951	-3.8191347	down
MPF_LOC101160373.1.1	XP_004083232.1 PREDICTED: DNA damage-regulated autophagy modulator protein 1-like [Oryzias latipes]	0.031770308	-2.4222522	down
MPF_LOC101474504.4.5	XM_004557613.1 PREDICTED: Maylandia zebra anthrax toxin receptor 1-like (LOC101474504), mRNA	0.03701327	-3.9441426	down
MPF_contig_026208		0.040134653	-2.527882	down
MPF_contig_009643		0.040219318	-1.3434558	down
MPF_contig_044114		0.045032855	0.8461506	up
MPF_LOC101475513.1.1	XM_004545621.1 PREDICTED: Maylandia zebra EGF-containing fibulin-like extracellular matrix protein 2-like (LOC101475513), mRNA	0.013206946	-4.2691317	down
MPF_contig_026183	XM_004548669.1 PREDICTED: Maylandia zebra uncharacterized LOC101485992 (LOC101485992), transcript variant X3, mRNA	0.04634622	1.0258847	up
MPF_contig_027568		0.01718951	-3.908968	down
MPF_LOC101064915.1.1	XM_003967542.1 PREDICTED: Takifugu rubripes thromboxane-A synthase-like (LOC101064915), mRNA	0.01658866	-3.6639075	down
MPF_LOC100691990.2.2	XM_003445526.1 PREDICTED: Oreochromis niloticus annexin A1-like (LOC100691990), mRNA	0.016541727	-2.2146616	down
MPF_LOC101464899.2.4	XM_004553991.1 PREDICTED: Maylandia zebra protein bassoon-like (LOC101464899), transcript variant X2, mRNA	0.010997458	-2.9830122	down

MPF_LOC101479507.2.2	XM_004568789.1 PREDICTED: Maylandia zebra T-complex protein 1 subunit alpha-like (LOC101479507), mRNA	0.022882693	0.38876635	up
MPF_LOC101065219.1.3	XM_003969289.1 PREDICTED: Takifugu rubripes protein S100-A1-like (LOC101065219), mRNA	0.010997458	-3.674676	down
MPF_LOC100711484.7.8	XM_003448843.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100711484), mRNA	0.03525393	0.545639	up
MPF_LOC101155558.1.1	XM_004082371.1 PREDICTED: Oryzias latipes interferon alpha-inducible protein 27-like protein 2-like (LOC101155558), mRNA	0.017283726	-4.0751133	down
MPF_LOC101157426.1.1	XM_004085697.1 PREDICTED: Oryzias latipes translation machinery-associated protei 7like, transcript variant 2 (LOC101157426), mRNA	0.02901613	0.5686083	up
MPF_LOC101476071.1.1	XM_004541164.1 PREDICTED: Maylandia zebra uncharacterized LOC101476071 (LOC101476071), mRNA	0.002189767	-3.819736	down
MPF_LOC101486169.4.4	XM_004566076.1 PREDICTED: Maylandia zebra cyclin-T2-like (LOC101486169), mRNA	0.016467266	-7.072751	down
MPF_contig_014120		0.029391069	-4.472113	down
MPF_contig_031514		0.021755263	1.0588942	up
MPF_LOC101469505.1.1	XM_004563094.1 PREDICTED: Maylandia zebra ephrin-B2a-like (LOC101469505), transcript variant X2, mRNA	0.013472267	-3.8505988	down
MPF_contig_043487		0.04951666	-1.8741908	down
MPF_contig_016882		0.016467266	-2.162847	down
MPF_LOC100710612.1.1	XM_003454616.1 PREDICTED: Oreochromis niloticus macrophage mannose receptor 1-like (LOC100710612), mRNA	0.041477904	-3.2701144	down
MPF_ACBD5.1.1	ACBD5_PONAB (sp|Q5R7V3) Acyl-CoA-binding domain-containing protein 5 OS=Pongo abelii GN=ACBD5 PE=2 SV=1	0.022055771	-2.5841773	down
MPF_contig_020194		0.006872254	-4.9962163	down
MPF_LOC101465099.1.1	XM_004557394.1 PREDICTED: Maylandia zebra moesin-like (LOC101465099), mRNA	0.043628942	-4.632845	down
MPF_LOC101487032.1.1	XM_004543159.1 PREDICTED: Maylandia zebra ADM-like (LOC101487032), transcript variant X1, mRNA	0.017283726	-4.5682974	down
MPF_LOC101476871.1.3	XM_004569314.1 PREDICTED: Maylandia zebra nuclear factor 1 C-type-like (LOC101476871), transcript variant X2, mRNA	0.017880041	-2.796393	down
MPF_AHNK.11.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.044109177	-4.8392076	down
MPF_contig_021336		0.01658866	-2.1453156	down
MPF_LOC101467829.1.2	XM_004565458.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase pim-1-like (LOC101467829), mRNA	0.044087984	-2.981595	down
MPF_LOC101481552.2.41	XM_004575656.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101481552), mRNA	0.041477904	0.6230984	up
MPF_LOC101487208.1.1	XM_004564346.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase ZFP91-like (LOC101487208), transcript variant X3, mRNA	0.010780305	-3.611361	down
MPF_LOC101475700.1.3	XM_004564763.1 PREDICTED: Maylandia zebra phosphate carrier protein, mitochondriallike (LOC101475700), transcript variant X2, mRNA	0.047965955	-2.7636485	down
MPF_LOC101065219.2.3	XM_003969289.1 PREDICTED: Takifugu rubripes protein S100-A1-like (LOC101065219), mRNA	0.003644191	-3.984394	down
MPF_LOC101479628.3.3	XM_004554593.1 PREDICTED: Maylandia zebra proto-oncogene c-Rel-like (LOC101479628), mRNA	0.035200294	-1.8009694	down
MPF_contig_011981		0.03864547	-4.681638	down
MPF_LOC101156484.2.2	XM_004067491.1 PREDICTED: Oryzias latipes CD81 antigen-like (LOC101156484), mRNA	0.027233807	-3.211	down
MPF_LOC101478816.1.1	XM_004541641.1 PREDICTED: Maylandia zebra ubiquitin carboxyl-terminal hydrolase 45-like (LOC101478816), transcript variant X1, mRNA	0.036863893	-2.7429338	down

MPF_CFAH.6.15	CFAH_HUMAN (sp|P08603) Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	0.019606845	-3.2214508	down
MPF_LOC101473855.2.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA	0.035200294	-2.5401993	down
MPF_LOC101469207.1.1	XM_004560645.1 PREDICTED: Maylandia zebra c-Jun-amino-terminal kinase-interacting protein 3-like (LOC101469207), transcript variant X10, mRNA	0.04634622	-2.568541	down
MPF_LOC101482347.1.1	XR_191458.1 PREDICTED: Maylandia zebra TBC1 domain family member 13-like (LOC101482347), transcript variant X2, misc_RNA	0.02544578	-2.3810208	down
MPF_LOC100712330.1.2	XM_003438072.1 PREDICTED: Oreochromis niloticus ATP synthase subunit g, mitochondrial-like (LOC100712330), mRNA	0.04305904	1.2014871	up
MPF_LOC101168049.1.1	XM_004072873.1 PREDICTED: Oryzias latipes sushi domain-containing protein 1-like (LOC101168049), mRNA	0.01658866	-2.69384	down
MPF_LOC101486284.3.3	XM_004546431.1 PREDICTED: Maylandia zebra transmembrane protein 189-like (LOC101486284), mRNA	0.01718951	0.5727554	up
MPF_LOC101159641.5.35	XM_004085298.1 PREDICTED: Oryzias latipes tenascin-like (LOC101159641), mRNA	0.01658866	-2.5029268	down
MPF_LOC101479481.1.1	XM_004563952.1 PREDICTED: Maylandia zebra latent-transforming growth factor betabinding protein 3-like (LOC101479481), transcript variant X2, mRNA	0.03465091	-2.7391267	down
MPF_LOC100707166.2.2	XM_003442172.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100707166 (LOC100707166), mRNA	0.02901613	-2.9961112	down
MPF_LOC101077496.1.1	XM_003968940.1 PREDICTED: Takifugu rubripes gamma-glutamylcyclotransferase-like (LOC101077496), mRNA	0.019181546	-3.4338012	down
MPF_LOC101063002.1.1	XP_003971894.1 PREDICTED: LOW QUALITY PROTEIN: T-cell activation Rho GTPaseactivating protein-like [Takifugu rubripes]	0.024553591	-2.8804612	down
MPF_LOC101474649.1.2	XM_004569663.1 PREDICTED: Maylandia zebra zinc finger protein 729-like (LOC101474649), mRNA	0.037730373	-2.0256357	down
MPF_LOC101469758.1.3	XM_004558073.1 PREDICTED: Maylandia zebra estradiol 17-beta-dehydrogenase 12-B-like (LOC101469758), mRNA	0.032686193	-0.63258356	down
MPF_contig_017190		0.02051149	-3.4494839	down
MPF_RS7.10.10	RS7_TAKRU (sp|P50894) 40S ribosomal protein S7 OS=Takifugu rubripes GN=rps7 PE=3 SV=1	0.012938407	-2.1997745	down
MPF_IKBKB.2.2	XM_003451030.1 PREDICTED: Oreochromis niloticus inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta (IKBKB), mRNA	0.025189415	-2.711544	down
MPF_LOC101161674.2.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA	0.031770308	-3.3750997	down
MPF_LOC101483532.1.2	XM_004543245.1 PREDICTED: Maylandia zebra transcription factor PU.1-like (LOC101483532), transcript variant X2, mRNA	0.031770308	-2.1617374	down
MPF_RS6.6.11	RS6_PROMA (sp|Q7V9F9) 30S ribosomal protein S6 OS=Prochlorococcus marinus (strain SARG / CCMP1375 / SS120) GN=rpsF PE=3 SV=1	0.033274923	-4.0922112	down
MPF_LOC101071928.1.1	XP_003978669.1 PREDICTED: uncharacterized protein LOC101071928 [Takifugu rubripes]	0.001188962	-4.166593	down
MPF_LOC101487772.1.2	XM_004559324.1 PREDICTED: Maylandia zebra alcohol dehydrogenase 1-like (LOC101487772), mRNA	0.036863893	0.89219093	up
SR48_70+ vs SR48_45-				
Phylofish Gene ID	Gene description	p (Corr FDR)	Log FC	Regulation
MPF_LOC101472355.1.1	XM_004556700.1 PREDICTED: Maylandia zebra peripheral myelin protein 22-like (LOC101472355), mRNA	6.24E-04	3.5051188	up
MPF_contig_015482		9.70E-04	-0.45319363	down
MPF_LOC101476572.2.2	XM_004541074.1 PREDICTED: Maylandia zebra tetraspanin-17-like (LOC101476572), mRNA	6.24E-04	2.825408	up
MPF_AHNAK.3.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]	6.24E-04	4.0749545	up
MPF_LOC101475665.1.3	XM_004554127.1 PREDICTED: Maylandia zebra mucin-2-like (LOC101475665), transcript variant X2, mRNA	8.67E-04	0.81580013	up
MPF_contig_020534		8.66E-04	2.415676	up
MPF_LOC100694500.1.1	XP_003444166.1 PREDICTED: cytoplasmic dynein 1 light intermediate chain 1-like [Oreochromis niloticus]	8.44E-04	-0.8144378	down

MPF_LOC101483521.1.1	XM_004540909.1 PREDICTED: Maylandia zebra early growth response protein 1-like (LOC101483521), mRNA	6.24E-04	3.3486705	up
MPF_LOC101476812.1.3	XM_004575484.1 PREDICTED: Maylandia zebra DNA-directed RNA polymerase III subunit RPC8-like (LOC101476812), mRNA	9.70E-04	-0.81263727	down
MPF_LOC100711025.1.1	XP_003444057.1 PREDICTED: putative helicase Mov10l1-like [Oreochromis niloticus]	9.45E-04	-0.5037498	down
MPF_LOC100702817.2.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	6.84E-04	4.1965423	up
MPF_LOC101156898.4.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	7.06E-04	3.5543485	up
MPF_ZN214.3.8	ZN214_HUMAN (sp|Q9UL59) Zinc finger protein 214 OS=Homo sapiens GN=ZNF214 PE=2 SV=2	9.37E-04	-0.42941186	down
MPF_LOC100690258.1.1	XP_003440479.1 PREDICTED: annexin A2-A-like [Oreochromis niloticus]	9.70E-04	3.331645	up
MPF_LOC101477280.2.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	9.45E-04	2.7907078	up
MPF_contig_024155		9.75E-04	-0.60469157	down
MPF_LOC101156898.1.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	6.84E-04	3.0306187	up
MPF_LOC101480875.1.1	XM_004574330.1 PREDICTED: Maylandia zebra proline-, glutamic acid- and leucine-rich protein 1-like (LOC101480875), transcript variant X2, mRNA	9.45E-04	-0.4583011	down
MPF_contig_044643		9.65E-04	-0.49297327	down
MPF_contig_013399		6.24E-04	-0.559927	down
MPF_contig_002534		8.67E-04	-1.7499447	down
MPF_LOC100703477.2.2	XM_003456383.1 PREDICTED: Oreochromis niloticus DCN1-like protein 5-like (LOC100703477), mRNA	9.65E-04	-0.7809991	down
MPF_LOC100933241.9.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	9.70E-04	2.7508416	up

MPF_SELMODRAFT_443953.1.1	XP_002978779.1 hypothetical protein SELMODRAFT_443953 [Selaginella moellendorffii]	7.88E-04	-0.95196223	down
MPF_LOC100698096.4.4	XM_003457021.1 PREDICTED: Oreochromis niloticus H/ACA ribonucleoprotein complex subunit 2like protein-like (LOC100698096), mRNA	6.92E-04	-0.97915936	down
MPF_ZGC_77149.2.2	NM_200959.2 Danio rerio zgc:77149 (zgc:77149), mRNA gb|BC065678.1| Danio rerio zgc:55886, mRNA (cDNA clone MGC:77149 IMAGE:6961245), complete cds	9.65E-04	-0.40807444	down
MPF_LOC101477280.5.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	6.24E-04	2.7085342	up
MPF_contig_032146		9.03E-04	2.447113	up
MPF_contig_020082		9.65E-04	3.4221072	up
MPF_LOC101466982.1.2	XM_004574455.1 PREDICTED: Maylandia zebra pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial-like (LOC101466982), mRNA	8.79E-04	-1.0784574	down
MPF_LOC101469173.1.1	XM_004548596.1 PREDICTED: Maylandia zebra uncharacterized LOC101469173 (LOC101469173), mRNA	8.79E-04	-0.7733393	down
MPF_LOC101480826.9.9	XM_004564784.1 PREDICTED: Maylandia zebra ubiquitin-60S ribosomal protein L40-like (LOC101480826), mRNA	8.79E-04	-0.5256958	down
MPF_LOC100933241.11.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	6.24E-04	-1.2428627	down
MPF_LOC101477280.4.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	6.24E-04	2.7693615	up
MPF_LOC764806.1.1	XP_003730203.1 PREDICTED: uncharacterized protein LOC764806 [Strongylocentrotus purpuratus]	9.45E-04	-0.28547052	down

MPF_HACE1.3.3	[BBH] HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2	6.24E-04	2.0656605	up
MPF_LOC101161674.1.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA	9.45E-04	2.2401323	up
MPF_contig_018948	WP_006047458.1 hypothetical protein [Burkholderia graminis]	8.67E-04	2.0558333	up
MPF_LOC101161574.14.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	9.63E-04	3.070199	up
MPF_LAMP2.1.1	NP_001133282.1 lysosomal membrane glycoprotein 2 precursor [Salmo salar]	8.67E-04	-1.819005	down
MPF_contig_048773		9.92E-04	-0.7706427	down
MPF_LOC101467885.1.2	XM_004574029.1 PREDICTED: Maylandia zebra calpain-1 catalytic subunit-like (LOC101467885), transcript variant X1, mRNA	9.45E-04	-0.43612197	down
MPF_LOC100702318.5.5	XP_003458375.1 PREDICTED: galectin-9-like [Oreochromis niloticus]	6.42E-04	2.549489	up
MPF_contig_008714		3.61E-04	2.6475496	up
MPF_contig_043137		9.65E-04	-1.0286634	down
MPF_CJ032.1.1	CJ032_DANRE (sp|Q4V8S9) UPF0693 protein C10orf32 homolog OS=Danio rerio GN=si:ch211-67n3.3 PE=3 SV=1	6.24E-04	-0.71631575	down
MPF_contig_038580		6.24E-04	-1.3982686	down
MPF_LOC101468983.2.2	XR_191999.1 PREDICTED: Maylandia zebra uncharacterized LOC101468983 (LOC101468983), misc_RNA	9.45E-04	1.4403348	up
MPF_AHNAK.4.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]	6.24E-04	4.1078434	up
MPF_contig_037980		6.84E-04	3.1817553	up
MPF_AHNK.16.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	6.24E-04	3.792429	up
MPF_LOC101467642.1.1	XM_004565102.1 PREDICTED: Maylandia zebra ubiquitin-like-conjugating enzyme ATG10-like (LOC101467642), transcript variant X3, mRNA	8.58E-04	-0.57292604	down
MPF_LOC101156898.3.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	6.24E-04	3.1026058	up
MPF_LOC100695691.2.2	XM_003455952.1 PREDICTED: Oreochromis niloticus actin-related protein 2/3 complex subunit 1Blike (LOC100695691), mRNA	8.67E-04	3.436186	up
MPF_contig_036627		8.67E-04	-0.8752179	down
MPF_LOC100699383.1.6	XM_003445310.1 PREDICTED: Oreochromis niloticus translationally-controlled tumor protein homolog (LOC100699383), mRNA	8.67E-04	-1.131875	down
MPF_LOC101486559.2.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA	7.68E-04	3.5304594	up
MPF_contig_020945	XM_004542601.1 PREDICTED: Maylandia zebra muscleblind-like protein 1-like (LOC101483053), transcript variant X16, mRNA	6.24E-04	3.2228398	up
MPF_contig_001265	XM_004544289.1 PREDICTED: Maylandia zebra rab11 family-interacting protein 1-like (LOC101463597), transcript variant X1, mRNA	6.24E-04	-0.7746916	down
MPF_MYO1B.1.2	XP_003443378.1 PREDICTED: myosin-Ib isoform 2 [Oreochromis niloticus]	6.24E-04	-0.5991754	down
MPF_contig_023403		8.44E-04	1.0066733	up
MPF_LOC100696784.1.1	XP_003441680.1 PREDICTED: HHIP-like protein 1-like [Oreochromis niloticus]	8.44E-04	2.4692407	up
MPF_LOC101170487.4.4	XM_004085086.1 PREDICTED: Oryzias latipes low-density lipoprotein receptor 2-like (LOC101170487), mRNA	9.26E-04	1.8254471	up
MPF_contig_017097		5.95E-04	2.8509126	up

MPF_LOC100690793.2.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]	9.45E-04	3.5592828	up
MPF_LOC101468488.3.7	XM_004552241.1 PREDICTED: Maylandia zebra 40S ribosomal protein S11-like (LOC101468488), mRNA	9.06E-04	-0.6105609	down
MPF_LOC101167402.1.2	XM_004080364.1 PREDICTED: Oryzias latipes uncharacterized LOC101167402 (LOC101167402), mRNA	6.24E-04	-0.9832983	down
MPF_contig_033424		3.61E-04	5.293371	up
MPF_LOC101477532.1.1	XM_004569581.1 PREDICTED: Maylandia zebra claudin-4-like (LOC101477532), mRNA	9.30E-04	-0.8764033	down
MPF_LOC100685053.1.1	XP_003434657.1 PREDICTED: polyubiquitin-like [Canis lupus familiaris]	9.75E-04	-0.4011717	down
MPF_LOC100769042.1.1	XP_003512927.1 PREDICTED: hypothetical protein LOC100769042 [Cricetulus griseus]	8.67E-04	-0.7657208	down

MPF_LOC100697017.2.2	XM_003455478.1 PREDICTED: Oreochromis niloticus ubiquitin-40S ribosomal protein S27a-like (LOC100697017), mRNA	6.24E-04	-0.37040326	down
MPF_LOC101481611.1.2	XM_004544911.1 PREDICTED: Maylandia zebra elongation factor Ts, mitochondrial-like (LOC101481611), mRNA	6.24E-04	-0.4832001	down
MPF_contig_020192		9.45E-04	-0.46445462	down
MPF_LOC101480093.7.8	XM_004574589.1 PREDICTED: Maylandia zebra tripartite motif-containing protein 16-like (LOC101480093), mRNA	6.84E-04	-0.894649	down
MPF_ENPP1.1.2	XM_003446358.1 PREDICTED: Oreochromis niloticus ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA	6.24E-04	2.8688421	up
MPF_LOC101468606.1.3	XM_004561834.1 PREDICTED: Maylandia zebra protein PBDC1-like (LOC101468606), transcript variant X2, mRNA	8.67E-04	-0.44503593	down
MPF_contig_030749		9.26E-04	2.4091377	up
MPF_UBC.1.5	UBC_RAT (sp|Q63429) Polyubiquitin-C OS=Rattus norvegicus GN=Ubc PE=1 SV=1	9.37E-04	-0.36294174	down
MPF_LOC101465148.1.1	XM_004569455.1 PREDICTED: Maylandia zebra brain acid soluble protein 1-like (LOC101465148), transcript variant X1, mRNA	9.75E-04	3.291632	up
MPF_LOC100698764.2.2	XM_003449126.1 PREDICTED: Oreochromis niloticus probable cation-transporting ATPase 13A2-like (LOC100698764), mRNA	9.75E-04	-0.4149217	down
MPF_LOC101465079.2.2	XM_004551108.1 PREDICTED: Maylandia zebra basal cell adhesion molecule-like (LOC101465079), mRNA	6.24E-04	2.5876179	up
MPF_LOC100695799.6.7	XM_003460096.1 PREDICTED: Oreochromis niloticus leukocyte elastase inhibitor-like (LOC100695799), mRNA	3.61E-04	-1.176157	down
MPF_LOC100697750.1.3	XM_003459604.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 14-like (LOC100697750), mRNA	6.84E-04	2.8654587	up
MPF_contig_037474		7.54E-04	0.8591571	up
MPF_contig_024281		8.67E-04	-0.6671085	down
MPF_MXAN_5876.1.1	YP_634013.1 hypothetical protein MXAN_5876 [Myxococcus xanthus DK 1622]	6.84E-04	1.6162633	up
MPF_contig_011640		6.24E-04	3.4892435	up
MPF_LOC101062526.1.1	XP_003962815.1 PREDICTED: d-2-hydroxyglutarate dehydrogenase, mitochondrial-like [Takifugu rubripes]	3.61E-04	-0.78702354	down
MPF_LOC101476475.1.1	XM_004562669.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 3-like (LOC101476475), mRNA	8.67E-04	4.247687	up
MPF_contig_002650	XM_004079020.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 1 (LOC101161674), mRNA	8.79E-04	2.3218417	up
MPF_LOC101485532.1.1	XM_004573748.1 PREDICTED: Maylandia zebra nuclear receptor-interacting protein 2-like	6.84E-04	-1.090391	down

	(LOC101485532), mRNA			
MPF_contig_032831		6.24E-04	2.514372	up
MPF_LOC100702817.1.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	6.24E-04	3.594905	up
MPF_LOC101486209.1.4	XM_004551098.1 PREDICTED: Maylandia zebra uncharacterized LOC101486209 (LOC101486209), mRNA	9.65E-04	3.1252005	up
MPF_LOC100698399.1.1	XM_003444297.1 PREDICTED: Oreochromis niloticus non-specific lipid-transfer protein-like (LOC100698399), mRNA	8.67E-04	-0.68436533	down
MPF_LOC101078462.1.1	XP_003965271.1 PREDICTED: lysosome membrane protein 2-like [Takifugu rubripes]	8.58E-04	3.4092422	up
MPF_LOC100711510.1.8	XM_003455849.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100711510), mRNA	6.24E-04	2.6063309	up
MPF_contig_023699		9.45E-04	3.1259406	up
MPF_contig_011009		8.67E-04	-0.69504046	down
MPF_LOC100712435.2.2	XP_003459327.1 PREDICTED: major histocompatibility complex class I-related gene protein-like [Oreochromis niloticus]	9.65E-04	-1.8616748	down
MPF_LOC101477091.1.3	XM_004574318.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101477091), transcript variant X5, mRNA	9.42E-04	1.2305627	up
MPF_LOC100690401.1.3	XP_003454006.1 PREDICTED: hypothetical protein LOC100690401 [Oreochromis niloticus]	6.24E-04	3.5442069	up
MPF_LOC100703589.1.1	XM_003460117.1 PREDICTED: Oreochromis niloticus plasminogen activator inhibitor 1-like (LOC100703589), mRNA	7.88E-04	4.0867443	up
MPF_contig_032132		6.24E-04	-0.8449049	down
MPF_AHNK.21.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	6.24E-04	3.5961099	up
MPF_contig_024444		6.24E-04	-1.1961498	down
MPF_LOC101075004.1.1	XM_003964966.1 PREDICTED: Takifugu rubripes uncharacterized LOC101075004 (LOC101075004), mRNA	6.24E-04	3.717568	up
MPF_LOC100696821.2.2	XM_003452445.1 PREDICTED: Oreochromis niloticus ictacalcin-like (LOC100696821), mRNA	9.65E-04	3.3833156	up
MPF_LOC101172863.1.1	XP_004082959.1 PREDICTED: splicing factor 45-like [Oryzias latipes]	8.67E-04	-0.5717406	down
MPF_LOC100693306.9.13	XP_003458501.1 PREDICTED: protein NLRC3-like [Oreochromis niloticus]	8.67E-04	2.3602946	up
MPF_contig_028541		7.60E-04	3.1797981	up
MPF_contig_014987		9.75E-04	-0.6804562	down
MPF_LOC101464487.2.5	XM_004571832.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase BRSK2-like (LOC101464487), transcript variant X8, mRNA	3.61E-04	-0.8501808	down
MPF_B3AT.2.2	B3AT_ONCMY (sp|P32847) Band 3 anion exchange protein OS=Oncorhynchus mykiss GN=slc4a1 PE=2 SV=2	8.67E-04	2.5152674	up
MPF_LOC101465872.1.1	XM_004558783.1 PREDICTED: Maylandia zebra extended synaptotagmin-1-like (LOC101465872), mRNA	6.24E-04	4.0485525	up
MPF_LOC100700533.4.5	XM_003459971.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100700533), partial mRNA	9.45E-04	-0.47105932	down
MPF_LOC100708802.1.1	XM_003447173.1 PREDICTED: Oreochromis niloticus prolyl endopeptidase-like (LOC100708802), mRNA	6.24E-04	-0.49328426	down
MPF_LOC101467113.4.4	XM_004559889.1 PREDICTED: Maylandia zebra nuclear ubiquitous casein and cyclin-dependent kinase substrate 1-like (LOC101467113), mRNA	6.24E-04	-0.48424345	down

MPF_contig_049002		9.45E-04	-0.5309681	down

MPF_LOC100690793.1.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]	6.24E-04	3.949597	up
MPF_contig_034810		9.45E-04	-0.67648226	down
MPF_contig_040346		6.84E-04	-0.6683101	down
MPF_LOC101473612.4.5	XM_004550873.1 PREDICTED: Maylandia zebra sodium/potassium-transporting ATPase subunit alpha-3-like (LOC101473612), transcript variant X2, mRNA	6.24E-04	2.847055	up
MPF_contig_048017		6.24E-04	-0.9067097	down
MPF_contig_005684		9.61E-04	-0.53424364	down
MPF_LOC100697415.3.3	XP_003444759.1 PREDICTED: neuroblast differentiation-associated protein AHNAK-like [Oreochromis niloticus]	6.24E-04	3.9313726	up
MPF_LOC101068359.1.1	XP_003962600.1 PREDICTED: gap junction beta-4 protein-like [Takifugu rubripes]	7.06E-04	-0.8237357	down
MPF_K1C18.1.2	K1C18_DANRE (sp|Q7ZTS4) Keratin, type I cytoskeletal 18 OS=Danio rerio GN=krt18 PE=1 SV=2	6.24E-04	3.7538111	up
MPF_contig_021996		9.06E-04	-0.43759245	down
MPF_LOC101472401.1.1	XM_004544882.1 PREDICTED: Maylandia zebra coiled-coil domain-containing protein 174-like (LOC101472401), transcript variant X2, mRNA	9.65E-04	-0.5085897	down
MPF_LOC100692032.2.6	XP_003458104.1 PREDICTED: E3 ubiquitin/ISG15 ligase TRIM25-like [Oreochromis niloticus]	9.53E-04	-0.60870457	down
MPF_MYH11.1.2	MYH11_MOUSE (sp|O08638) Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1	6.24E-04	1.6554677	up
MPF_contig_036789		9.04E-04	2.1751413	up
MPF_LOC101482854.4.4	XM_004540267.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(q) subunit alpha-like (LOC101482854), transcript variant X3, mRNA	8.79E-04	-0.59591204	down
MPF_contig_017017		7.54E-04	-0.57417816	down
MPF_LOC101481869.4.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA	6.89E-04	1.2682614	up
MPF_LOC101159408.1.1	XP_004084885.1 PREDICTED: putative nuclease HARBI1-like [Oryzias latipes]	8.67E-04	-0.7754073	down
MPF_RBBP5.1.1	XP_003447710.1 PREDICTED: retinoblastoma-binding protein 5 [Oreochromis niloticus]	9.65E-04	-1.1332698	down
MPF_TNF6B.1.1	TNF6B_HUMAN (sp|O95407) Tumor necrosis factor receptor superfamily member 6B OS=Homo sapiens GN=TNFRSF6B PE=1 SV=1	8.67E-04	4.0148683	up
MPF_LOC100705618.1.1	XP_003453815.1 PREDICTED: protogenin-like [Oreochromis niloticus]	6.24E-04	2.5146198	up
MPF_LOC100702817.3.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	6.24E-04	4.2587743	up
MPF_LOC100692493.1.1	XP_003457870.1 PREDICTED: autophagy-related protein 16-1-like [Oreochromis niloticus]	8.79E-04	-0.5424442	down
MPF_LOC100712517.2.2	XM_003459650.1 PREDICTED: Oreochromis niloticus RNA (guanine-9-)-methyltransferase domaincontaining protein 2-like (LOC100712517), mRNA	6.24E-04	1.6498246	up
MPF_LOC101480609.1.2	XM_004539422.1 PREDICTED: Maylandia zebra homeodomain-interacting protein kinase 3-like (LOC101480609), transcript variant X2, mRNA	6.24E-04	3.097261	up
MPF_LOC101465129.6.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA	9.45E-04	1.5067023	up
MPF_LOC100710921.1.1	XM_003442353.1 PREDICTED: Oreochromis niloticus protein FAM63B-like (LOC100710921), mRNA	6.24E-04	-1.2020749	down
MPF_LOC101475183.1.1	XM_004539771.1 PREDICTED: Maylandia zebra tyrosyl-DNA phosphodiesterase 1-like (LOC101475183), mRNA	9.45E-04	-0.618043	down

MPF_contig_026589		6.69E-04	-1.3070453	down
MPF_LOC101483933.1.1	XM_004547257.1 PREDICTED: Maylandia zebra coiled-coil domain-containing protein 112-like (LOC101483933), transcript variant X2, mRNA	9.45E-04	-0.6256819	down
MPF_LOC100707046.4.12	XM_003454686.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100707046), mRNA	9.45E-04	1.8931532	up
MPF_contig_046542	XP_003443377.1 PREDICTED: myosin-Ib isoform 1 [Oreochromis niloticus]	6.24E-04	-0.6297569	down
MPF_HACE1.1.3	HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2	6.24E-04	4.919301	up
MPF_LOC100696180.1.1	XR_134816.1 PREDICTED: Oreochromis niloticus fibronectin-like (LOC100696180), miscRNA	8.67E-04	4.274227	up
MPF_LOC100700407.1.1	XM_003454414.1 PREDICTED: Oreochromis niloticus IGF-like family receptor 1-like (LOC100700407), mRNA	6.24E-04	3.105501	up
MPF_PSV.1.1	PSV_DICDI (sp|P08798) Prespore vesicle protein OS=Dictyostelium discoideum GN=psvA PE=2 SV=3	9.45E-04	1.7956417	up
MPF_LOC101161574.4.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	6.24E-04	2.5310562	up
MPF_LOC101487484.1.1	XM_004560337.1 PREDICTED: Maylandia zebra pleckstrin homology domain-containing family G member 5-like (LOC101487484), transcript variant X1, mRNA	6.24E-04	-0.7259841	down
MPF_contig_003837		9.45E-04	3.1450782	up
MPF_LOC101161574.3.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	8.67E-04	1.2808323	up
MPF_LOC100690809.1.1	XM_003441690.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100690809 (LOC100690809), mRNA	6.89E-04	-0.62096167	down
MPF_contig_015500		6.86E-04	2.7865279	up
MPF_LOC101477280.6.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	9.65E-04	2.5988617	up
MPF_contig_032919		9.32E-04	-0.73196095	down
MPF_LOC100695799.7.7	XP_003460144.1 PREDICTED: leukocyte elastase inhibitor-like [Oreochromis niloticus]	8.23E-04	-1.0026789	down
MPF_contig_022962		7.56E-04	2.4242296	up
MPF_contig_027052		6.24E-04	2.0921338	up
MPF_contig_019111		6.24E-04	-1.1021113	down
MPF_contig_032148		6.24E-04	-0.62106085	down
MPF_LOC101482854.3.4	XM_004540267.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(q) subunit alpha-like (LOC101482854), transcript variant X3, mRNA	9.65E-04	-0.58405495	down
MPF_LOC101473056.1.1	XM_004560837.1 PREDICTED: Maylandia zebra interferon-related developmental regulator 1-like (LOC101473056), mRNA	9.45E-04	-0.79186964	down
MPF_contig_026907		9.65E-04	3.0954356	up
MPF_LOC101469089.4.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA	5.95E-04	1.5033767	up
MPF_contig_032259		8.99E-04	2.6173453	up
MPF_LOC100694383.1.2	XP_003458505.1 PREDICTED: protein artemis-like [Oreochromis niloticus]	6.24E-04	-0.56521505	down
MPF_contig_021708		6.24E-04	1.6471925	up

MPF_LOC101465192.1.6	XM_004554818.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2Blike (LOC101465192), mRNA	9.75E-04	2.0831175	up
MPF_LOC101476137.1.1	XM_004574406.1 PREDICTED: Maylandia zebra baculoviral IAP repeat-containing protein 6-like (LOC101476137), transcript variant X5, mRNA	4.56E-04	-0.41531703	down
MPF_LOC101486605.3.3	XM_004551948.1 PREDICTED: Maylandia zebra protein CDV3 homolog (LOC101486605), transcript variant X2, mRNA	9.45E-04	-0.5266233	down
MPF_contig_026973	XM_004553863.1 PREDICTED: Maylandia zebra poly [ADP-ribose] polymerase 12-like (LOC101480887), transcript variant X1, mRNA	6.24E-04	2.3735785	up
MPF_LOC101166773.1.1	XP_004085184.1 PREDICTED: uncharacterized protein LOC101166773, partial [Oryzias latipes]	6.69E-04	1.2007871	up
MPF_LOC101468908.1.1	XM_004539040.1 PREDICTED: Maylandia zebra tuberin-like (LOC101468908), transcript variant X5, mRNA	9.53E-04	-0.6478333	down
MPF_CD4.1.1	NP_001072091.1 T-cell surface glycoprotein CD4 [Takifugu rubripes]	8.58E-04	-0.6067982	down
MPF_contig_031891		8.67E-04	3.105239	up
MPF_LOC101473901.1.2	XM_004572233.1 PREDICTED: Maylandia zebra CDC42 small effector protein 1-like (LOC101473901), transcript variant X2, mRNA	8.67E-04	3.0652912	up
MPF_LOC101471998.1.1	XM_004540134.1 PREDICTED: Maylandia zebra MFS-type transporter SLC18B1-like (LOC101471998), mRNA	6.24E-04	-1.6795368	down
MPF_LOC101471898.1.1	XM_004561201.1 PREDICTED: Maylandia zebra short/branched chain specific acyl-CoA dehydrogenase, mitochondrial-like (LOC101471898), mRNA	8.79E-04	-0.7201429	down
MPF_LOC101067922.3.6	XM_003966993.1 PREDICTED: Takifugu rubripes metallothionein A-like (LOC101067922), mRNA	8.67E-04	-0.3202352	down
MPF_LOC100692406.1.1	XP_003439388.1 PREDICTED: nucleolar MIF4G domain-containing protein 1-like [Oreochromis niloticus]	9.45E-04	-0.8811007	down
MPF_LOC101477280.1.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	7.88E-04	2.5314064	up
MPF_LOC100699053.1.1	XM_003453494.1 PREDICTED: Oreochromis niloticus trophoblast glycoprotein-like (LOC100699053), mRNA	9.06E-04	-0.80437326	down
MPF_LOC101475513.1.1	XM_004545621.1 PREDICTED: Maylandia zebra EGF-containing fibulin-like extracellular matrix protein 2-like (LOC101475513), mRNA	6.24E-04	3.264319	up
MPF_LOC101073669.1.1	XM_003964261.1 PREDICTED: Takifugu rubripes coatomer subunit zeta-2-like (LOC101073669), mRNA	6.24E-04	-1.2159114	down
MPF_LOC100691896.1.1	XM_003445111.1 PREDICTED: Oreochromis niloticus tetratricopeptide repeat protein 4-like (LOC100691896), mRNA	6.76E-04	-0.67800903	down
MPF_LOC101486169.4.4	XM_004566076.1 PREDICTED: Maylandia zebra cyclin-T2-like (LOC101486169), mRNA	8.67E-04	4.6730275	up
MPF_contig_031422		9.30E-04	-0.4295015	down
MPF_contig_016882		6.24E-04	1.6413908	up
MPF_contig_020194		6.24E-04	3.1553206	up
MPF_LOC101475468.3.3	XM_004560663.1 PREDICTED: Maylandia zebra Na(+)/H(+) exchange regulatory cofactor NHE-RF1like (LOC101475468), mRNA	6.24E-04	-0.5896334	down
MPF_AHNK.11.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	9.45E-04	3.5885096	up
MPF_LOC100691661.1.1	XM_003451671.1 PREDICTED: Oreochromis niloticus THO complex subunit 5 homolog (LOC100691661), mRNA	9.45E-04	-0.28898996	down
MPF_LOC101165175.3.3	XM_004078345.1 PREDICTED: Oryzias latipes cathepsin S-like (LOC101165175), mRNA	9.45E-04	2.4482179	up
MPF_LOC101156484.2.2	XM_004067491.1 PREDICTED: Oryzias latipes CD81 antigen-like (LOC101156484), mRNA	9.47E-04	2.134348	up
MPF_LOC101482619.1.3	XM_004556458.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase TAO2-like (LOC101482619), transcript variant X2, mRNA	9.47E-04	-0.9538708	down

MPF_LOC100701266.1.1	XM_003442151.1 PREDICTED: Oreochromis niloticus peptidyl-prolyl cis-trans isomerase FKBP10-like (LOC100701266), mRNA	8.67E-04	-0.92839617	down
MPF_contig_000382	XM_004569524.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 29-like (LOC101484386), transcript variant X1, mRNA	9.37E-04	-0.7513342	down
MPF_LOC101466776.2.2	XM_004567004.1 PREDICTED: Maylandia zebra sodium-dependent serotonin transporter-like (LOC101466776), transcript variant X3, mRNA	9.30E-04	-0.65571785	down
MPF_LOC101484929.2.3	XM_004542976.1 PREDICTED: Maylandia zebra CMP-N-acetylneuraminate-beta-1,4-galactoside alpha-2,3-sialyltransferase-like (LOC101484929), mRNA	8.93E-04	2.4420035	up
MPF_LOC101487772.1.2	XM_004559324.1 PREDICTED: Maylandia zebra alcohol dehydrogenase 1-like (LOC101487772), mRNA	6.84E-04	-0.6448822	down
MPF_contig_022673		8.67E-04	-0.86894363	down
MPF_LOC101482854.1.4	XM_004540267.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(q) subunit alpha-like (LOC101482854), transcript variant X3, mRNA	6.41E-04	-0.56171364	down

SR48_80+ vs SR48_45-

Phylofish Gene ID	Gene description	p (Corr FDR)	Log FC	Regulation
MPF_CD99.1.1	CD99_HUMAN (sp|P14209) CD99 antigen OS=Homo sapiens GN=CD99 PE=1 SV=1	0.033979006	-1.8039584	down
MPF_LOC100698998.2.7	XM_003439446.1 PREDICTED: Oreochromis niloticus myosin heavy chain, fast skeletal muscle-like (LOC100698998), mRNA	0.031504437	-2.33992	down
MPF_LOC101472355.1.1	XM_004556700.1 PREDICTED: Maylandia zebra peripheral myelin protein 22-like (LOC101472355), mRNA	0.024688901	-3.4958048	down
MPF_LOC101472505.3.3	XM_004567307.1 PREDICTED: Maylandia zebra sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1-like (LOC101472505), transcript variant X4, mRNA	0.04894557	1.1553993	up
MPF_contig_013127	XM_004539189.1 PREDICTED: Maylandia zebra ATP-binding cassette sub-family A member 1-like (LOC101484083), transcript variant X1, mRNA	0.043771714	-1.4095926	down
MPF_contig_042359		0.041183017	-1.7516935	down
MPF_LOC100702435.1.1	XM_003442073.1 PREDICTED: Oreochromis niloticus hemoglobin subunit alpha-1-like (LOC100702435), mRNA	0.033915687	-2.02146	down
MPF_LOC101476572.2.2	XM_004541074.1 PREDICTED: Maylandia zebra tetraspanin-17-like (LOC101476572), mRNA	0.024688901	-3.1541338	down
MPF_AHNAK.3.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]	0.024688901	-4.113111	down
MPF_contig_020534		0.032478802	-2.3529625	down
MPF_contig_005089		0.043236237	1.3731189	up
MPF_LOC101483521.1.1	XM_004540909.1 PREDICTED: Maylandia zebra early growth response protein 1-like (LOC101483521), mRNA	0.024688901	-3.319308	down
MPF_LOC100690512.1.1	XP_003438469.1 PREDICTED: hypothetical protein LOC100690512 [Oreochromis niloticus]	0.03115698	-2.4780061	down
MPF_LOC100693359.2.6	XM_003449442.1 PREDICTED: Oreochromis niloticus microfibril-associated glycoprotein 4-like (LOC100693359), mRNA	0.047354784	1.0657802	up
MPF_contig_016274		0.043771714	-1.2331853	down
MPF_contig_015023		0.04957513	-1.0413246	down
MPF_LOC101464589.2.3	XM_004548947.1 PREDICTED: Maylandia zebra exostosin-1b-like (LOC101464589), mRNA	0.039815266	1.0400944	up
MPF_LOC100701693.2.4	XM_003459252.1 PREDICTED: Oreochromis niloticus mamu class II histocompatibility antigen, DR alpha chain-like (LOC100701693), mRNA	0.04068399	-1.7950892	down

MPF_LOC100693335.1.4	XM_003443944.1 PREDICTED: Oreochromis niloticus gliomedin-like (LOC100693335), mRNA	0.03115698	1.2407374	up
MPF_LOC100174873.3.10	NM_001267638.1 Gasterosteus aculeatus beta globin (LOC100174873), mRNA gb|AY184355.1| Gasterosteus aculeatus beta globin mRNA, complete cds	0.041156992	-1.5348117	down
MPF_contig_022617		0.024688901	-3.5232246	down
MPF_RL17.5.5	RL17_RAT (sp|P24049) 60S ribosomal protein L17 OS=Rattus norvegicus GN=Rpl17 PE=2 SV=3	0.041156992	-1.5225286	down
MPF_LOC100702817.2.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.024688901	-4.458973	down
MPF_LECG.4.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.048683308	-3.8633642	down
MPF_LOC101156898.4.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	0.032626204	-3.2050607	down
MPF_LOC100690258.1.1	XP_003440479.1 PREDICTED: annexin A2-A-like [Oreochromis niloticus]	0.030160543	-3.6751878	down
MPF_LOC101075367.4.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]	0.041156992	-1.5677385	down
MPF_LOC101477280.2.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.032478802	-2.8302884	down
MPF_LOC101156898.1.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	0.032626204	-2.7036748	down
MPF_contig_035424		0.02948326	-1.184248	down
MPF_LOC100710548.2.4	XP_003459320.1 PREDICTED: major histocompatibility complex class I-related gene protein-like [Oreochromis niloticus]	0.047354784	-1.8140421	down
MPF_LOC101463600.1.1	XM_004544939.1 PREDICTED: Maylandia zebra class E basic helix-loop-helix protein 40-like (LOC101463600), mRNA	0.047354784	-1.1820817	down
MPF_contig_002534		0.033979006	1.5713253	up
MPF_LOC101474121.17.17	XM_004575391.1 PREDICTED: Maylandia zebra stonustoxin subunit beta-like (LOC101474121), mRNA	0.047976535	-2.4621167	down
MPF_LOC100933241.9.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.024688901	-3.0646846	down
MPF_LOC101162897.1.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]	0.034762036	-2.9712648	down
MPF_LOC100706224.1.1	XM_003450725.1 PREDICTED: Oreochromis niloticus transmembrane protein 168-A-like (LOC100706224), mRNA	0.024688901	1.0472946	up
MPF_contig_033674		0.042485975	-1.80056	down
MPF_LOC101482220.3.3	XM_004571715.1 PREDICTED: Maylandia zebra h-2 class II histocompatibility antigen gamma chainlike (LOC101482220), mRNA	0.043236237	-2.784182	down
MPF_LOC100698173.2.3	XP_003456090.1 PREDICTED: hypothetical protein LOC100698173 [Oreochromis niloticus]	0.041156992	1.1314921	up
MPF_LOC100698096.4.4	XM_003457021.1 PREDICTED: Oreochromis niloticus H/ACA ribonucleoprotein complex subunit 2like protein-like (LOC100698096), mRNA	0.01925946	1.1830797	up
MPF_RL37P.1.1	RL37P_RAT (sp|P61515) Putative 60S ribosomal protein L37a OS=Rattus norvegicus GN=Rpl37a-ps1 PE=5 SV=2	0.032880154	-2.3522925	down
MPF_BRAFLDRAFT_92923.4.11	XP_002605501.1 hypothetical protein BRAFLDRAFT_92923 [Branchiostoma floridae]	0.03836361	1.2250032	up
MPF_MIR142A.1.1	NR_030090.1 Danio rerio microRNA 142a (mir142a), microRNA	0.0393948	-2.6007173	down
MPF_SGS4.2.10	SGS4_DROME (sp|Q00725) Salivary glue protein Sgs-4 OS=Drosophila melanogaster GN=Sgs4 PE=2 SV=1	0.03451082	-1.014946	down
MPF_LOC101477280.5.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.024688901	-2.8472934	down
MPF_LOC101479225.2.2	XM_004571532.1 PREDICTED: Maylandia zebra glucose-6-phosphate isomerase-like (LOC101479225), mRNA	0.032880154	1.041143	up

MPF_contig_041411		0.032880154	1.0639949	up
MPF_LOC100711796.2.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA	0.041950908	-1.8414593	down
MPF_contig_032146		0.032626204	-2.4429407	down
MPF_contig_020082		0.031431407	-3.4211159	down

MPF_LOC101167377.1.1	XP_004073716.1 PREDICTED: snRNA-activating protein complex subunit 1-like [Oryzias latipes]	0.030369533	1.2305183	up
MPF_contig_024224		0.026987117	-3.859468	down
MPF_LOC100933241.11.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.01925946	1.4217939	up
MPF_contig_032481		0.041406687	-1.5706005	down
MPF_LOC101477280.4.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.024688901	-2.8699994	down
MPF_contig_027060		0.045526285	-1.4809246	down
MPF_HACE1.3.3	[BBH] HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2	0.024688901	-1.9798722	down
MPF_LOC101161674.1.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA	0.030160543	-2.3934135	down
MPF_contig_018948	WP_006047458.1 hypothetical protein [Burkholderia graminis]	0.032626204	-2.020534	down
MPF_LECG.21.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.043771714	-3.3182898	down
MPF_LOC101161574.14.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.030160543	-3.349689	down
MPF_LAMP2.1.1	NP_001133282.1 lysosomal membrane glycoprotein 2 precursor [Salmo salar]	0.033915687	1.6008554	up
MPF_LOC100701823.1.2	XM_003446064.1 PREDICTED: Oreochromis niloticus protamine-like protein-like (LOC100701823), mRNA	0.047354784	-1.8819895	down
MPF_HBA.6.8	HBA_ARTOR (sp|P0C237) Hemoglobin subunit alpha OS=Artedidraco orianae GN=hba PE=1 SV=2	0.039267194	-1.5135356	down
MPF_LOC100702318.5.5	XP_003458375.1 PREDICTED: galectin-9-like [Oreochromis niloticus]	0.03115698	-2.250668	down
MPF_LOC101485836.2.2	XM_004559956.1 PREDICTED: Maylandia zebra muscle M-line assembly protein unc-89-like (LOC101485836), transcript variant X1, mRNA	0.036592614	2.1728005	up
MPF_LOC101075367.1.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]	0.038560603	-1.7010746	down
MPF_contig_008714		0.01925946	-2.9679985	down
MPF_LOC101475324.3.5	XM_004570832.1 PREDICTED: Maylandia zebra MOB kinase activator 2-like (LOC101475324), transcript variant X4, mRNA	0.046404414	-1.144021	down
MPF_LOC101075590.1.1	XP_003966053.1 PREDICTED: uncharacterized protein LOC101075590 [Takifugu rubripes]	0.037768055	1.1336284	up
MPF_POPTRDRAFT_794775.3.5	XP_002338344.1 predicted protein [Populus trichocarpa]	0.042485975	-1.0261029	down
MPF_contig_035342		0.042485975	-1.1948116	down
MPF_contig_043137		0.030687563	1.101102	up
MPF_LOC101155699.2.2	XM_004073699.1 PREDICTED: Oryzias latipes protein S100-A10-like (LOC101155699), mRNA	0.030160543	-3.8910525	down
MPF_LOC101474419.1.1	XM_004554493.1 PREDICTED: Maylandia zebra sperm-associated antigen 17-like (LOC101474419), mRNA	0.047354784	1.3013914	up
MPF_LOC100699721.2.2	XP_003460016.1 PREDICTED: bifunctional protein NCOAT-like, partial [Oreochromis niloticus]	0.032880154	-2.0012288	down

MPF_contig_038580		0.01925946	1.4857029	up
MPF_LOC101061679.1.1	XM_003975895.1 PREDICTED: Takifugu rubripes cAMP-responsive element modulator-like (LOC101061679), mRNA	0.043771714	-1.2620554	down
MPF_LOC101468983.2.2	XR_191999.1 PREDICTED: Maylandia zebra uncharacterized LOC101468983 (LOC101468983), misc_RNA	0.031431407	-1.5097914	down
MPF_AHNAK.4.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]	0.024688901	-4.2022033	down
MPF_LOC100707140.3.4	XP_003458392.1 PREDICTED: hypothetical protein LOC100707140 [Oreochromis niloticus]	0.04079872	-1.4531894	down
MPF_contig_037980		0.03233395	-2.989553	down
MPF_AHNK.16.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.027709274	-3.7773104	down
MPF_RSSA.9.9	RSSA_SPAAU (sp|Q4QY71) 40S ribosomal protein SA OS=Sparus aurata GN=rpsa PE=2 SV=2	0.04157155	-1.296341	down
MPF_LY9.3.3	LY9_HUMAN (sp|Q9HBG7) T-lymphocyte surface antigen Ly-9 OS=Homo sapiens GN=LY9 PE=1 SV=3	0.024688901	-2.7365234	down
MPF_LOC100710050.5.6	XM_003446256.1 PREDICTED: Oreochromis niloticus 6.8 kDa mitochondrial proteolipid-like (LOC100710050), mRNA	0.041156992	1.3091834	up
MPF_LOC101156898.3.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	0.03135899	-2.8181329	down
MPF_LOC100707640.1.2	XP_003451524.1 PREDICTED: hypothetical protein LOC100707640 [Oreochromis niloticus]	0.035701096	-1.0252099	down
MPF_LOC100695691.2.2	XM_003455952.1 PREDICTED: Oreochromis niloticus actin-related protein 2/3 complex subunit 1Blike (LOC100695691), mRNA	0.027373271	-3.580705	down
MPF_LOC101475950.3.3	XM_004553845.1 PREDICTED: Maylandia zebra cAMP-specific 3',5'-cyclic phosphodiesterase 4B-like (LOC101475950), transcript variant X3, mRNA	0.030160543	-3.0580988	down
MPF_C1QA.2.2	[BBH] C1QA_PIG (sp|Q69DL0) Complement C1q subcomponent subunit A OS=Sus scrofa GN=C1QA PE=2 SV=1	0.043321703	-2.818112	down
MPF_contig_014059		0.041156992	-1.2429074	down
MPF_contig_032442		0.032880154	-2.4109073	down
MPF_RL37A.1.1	RL37A_XENLA (sp|Q7SZB4) 60S ribosomal protein L37a OS=Xenopus laevis GN=rpl37a PE=3 SV=3	0.035223186	-2.2811093	down
MPF_LOC100933241.12.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.024688901	1.0339613	up
MPF_LOC100699383.1.6	XM_003445310.1 PREDICTED: Oreochromis niloticus translationally-controlled tumor protein homolog (LOC100699383), mRNA	0.033915687	1.0645695	up
MPF_contig_026335		0.03115698	-2.9948354	down
MPF_FBXW5.1.1	XP_003445226.1 PREDICTED: F-box/WD repeat-containing protein 5 [Oreochromis niloticus]	0.03949431	1.6999495	up
MPF_contig_034209	XM_003198881.1 PREDICTED: Danio rerio retrotransposable element Tf2 155 kDa protein type 1-like (LOC100535308), mRNA	0.029057328	-1.9413002	down
MPF_contig_006465		0.045952104	-1.082622	down
MPF_LOC101486559.2.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA	0.030111242	-3.5655718	down
MPF_LOC100703996.2.2	XM_003450220.1 PREDICTED: Oreochromis niloticus armadillo repeat-containing protein 4-like (LOC100703996), mRNA	0.033979006	1.0124278	up
MPF_LOC101486920.1.1	XM_004539290.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12like (LOC101486920), mRNA	0.043321703	2.1765082	up

MPF_LOC101487453.1.2	XM_004548571.1 PREDICTED: Maylandia zebra aflatoxin B1 aldehyde reductase member 2-like (LOC101487453), mRNA	0.02598959	1.3973098	up
MPF_contig_020945	XM_004542601.1 PREDICTED: Maylandia zebra muscleblind-like protein 1-like (LOC101483053), transcript variant X16, mRNA	0.024688901	-3.269763	down
MPF_LOC101486124.4.4	XM_004575749.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12like (LOC101486124), mRNA	0.043321703	-2.3694315	down
MPF_contig_023403		0.024688901	-1.1046804	down
MPF_LOC101482220.2.3	XM_004571715.1 PREDICTED: Maylandia zebra h-2 class II histocompatibility antigen gamma chainlike (LOC101482220), mRNA	0.041156992	-2.8753114	down
MPF_LOC101475790.3.3	XM_004565656.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101475790), mRNA	0.024688901	1.0403771	up
MPF_LOC100696784.1.1	XP_003441680.1 PREDICTED: HHIP-like protein 1-like [Oreochromis niloticus]	0.01925946	-3.1757147	down
MPF_LOC101170487.4.4	XM_004085086.1 PREDICTED: Oryzias latipes low-density lipoprotein receptor 2-like (LOC101170487), mRNA	0.03451082	-1.746056	down
MPF_contig_017097		0.024688901	-2.807589	down
MPF_LOC100690793.2.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]	0.027373271	-3.802396	down
MPF_LOC100707240.2.2	XP_003459468.1 PREDICTED: ATPase family AAA domain-containing protein 2-like [Oreochromis niloticus]	0.03521828	1.6878386	up
MPF_contig_033424		0.01925946	-5.3322434	down
MPF_contig_037687		0.045952104	1.8031929	up
MPF_contig_029284		0.024688901	1.5889122	up
MPF_LOC101466239.3.3	XM_004550939.1 PREDICTED: Maylandia zebra apolipoprotein Eb-like (LOC101466239), mRNA	0.042485975	-2.856666	down
MPF_LOC100711789.5.22	XP_003457783.1 PREDICTED: neural cell adhesion molecule 2-like [Oreochromis niloticus]	0.047354784	-2.2433248	down
MPF_LOC101069588.3.3	XM_003963279.1 PREDICTED: Takifugu rubripes transketolase-like protein 2-like, transcript variant 1 (LOC101069588), mRNA	0.038344156	1.022697	up
MPF_LOC100691160.2.2	XP_003459991.1 PREDICTED: 5-hydroxytryptamine receptor 3A-like [Oreochromis niloticus]	0.032880154	-1.3871772	down
MPF_ANXA1.1.2	NP_001098295.1 annexin max3 [Oryzias latipes]	0.041950908	-1.3816938	down
MPF_LOC101484400.1.5	XM_004572910.1 PREDICTED: Maylandia zebra 60S ribosomal protein L22-like 1-like (LOC101484400), mRNA	0.04229652	-1.763629	down
MPF_LOC101477695.1.9	XM_004564867.1 PREDICTED: Maylandia zebra 60S ribosomal protein L18a-like (LOC101477695), transcript variant X2, mRNA	0.031431407	-1.2683074	down
MPF_LOC101169293.6.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.03395561	-1.1377358	down
MPF_ENPP1.1.2	XM_003446358.1 PREDICTED: Oreochromis niloticus ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA	0.024688901	-2.9961026	down
MPF_contig_030749		0.032993812	-2.3795571	down
MPF_LOC101465148.1.1	XM_004569455.1 PREDICTED: Maylandia zebra brain acid soluble protein 1-like (LOC101465148), transcript variant X1, mRNA	0.032880154	-3.3095505	down
MPF_LOC101483461.5.5	XM_004548470.1 PREDICTED: Maylandia zebra histone-lysine N-methyltransferase MLL5-like (LOC101483461), mRNA	0.04157155	1.1773987	up
MPF_LOC101465079.2.2	XM_004551108.1 PREDICTED: Maylandia zebra basal cell adhesion molecule-like (LOC101465079), mRNA	0.024688901	-2.7179325	down
MPF_LOC100695799.6.7	XM_003460096.1 PREDICTED: Oreochromis niloticus leukocyte elastase inhibitor-like (LOC100695799), mRNA	0.01925946	1.0511694	up

MPF_LOC100697750.1.3	XM_003459604.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 14-like (LOC100697750), mRNA	0.029980915	-2.7022126	down
MPF_LOC101471553.1.1	XM_004572678.1 PREDICTED: Maylandia zebra protein capicua homolog (LOC101471553), transcript variant X4, mRNA	0.043236237	-1.1123786	down
MPF_LOC100691105.1.2	XP_003449231.1 PREDICTED: cytochrome c oxidase subunit 8B, mitochondrial-like [Oreochromis niloticus]	0.047354784	-2.350727	down
MPF_LOC101480392.1.1	XM_004552287.1 PREDICTED: Maylandia zebra polymerase I and transcript release factor-like (LOC101480392), mRNA	0.043321703	2.076322	up
MPF_CFAH.8.15	CFAH_BOVIN (sp|Q28085) Complement factor H OS=Bos taurus GN=CFH PE=1 SV=3	0.043771714	-2.728477	down
MPF_MXAN_5876.1.1	YP_634013.1 hypothetical protein MXAN_5876 [Myxococcus xanthus DK 1622]	0.032626204	-1.4814458	down
MPF_contig_011640		0.024688901	-3.5154548	down
MPF_LOC101480355.1.1	XM_004569508.1 PREDICTED: Maylandia zebra crystallin J1C-like (LOC101480355), mRNA	0.031431407	-2.4289107	down
MPF_LOC101476997.1.2	XM_004552000.1 PREDICTED: Maylandia zebra microtubule-associated protein futsch-like (LOC101476997), mRNA	0.046055723	1.1200953	up
MPF_LOC101476475.1.1	XM_004562669.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 3-like (LOC101476475), mRNA	0.024688901	-4.600471	down
MPF_contig_028987		0.033979006	1.1091741	up
MPF_LOC101472370.1.1	XM_004538428.1 PREDICTED: Maylandia zebra gelsolin-like (LOC101472370), transcript variant X2, mRNA	0.041156992	-2.6688375	down
MPF_contig_047566		0.039009362	-1.3261628	down
MPF_LOC101487706.1.1	XM_004565535.1 PREDICTED: Maylandia zebra cAMP-responsive element modulator-like (LOC101487706), transcript variant X2, mRNA	0.045629505	-1.2269095	down
MPF_contig_002650	XM_004079020.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 1 (LOC101161674), mRNA	0.030111242	-2.4370394	down
MPF_LOC101467393.5.6	XM_004557584.1 PREDICTED: Maylandia zebra zinc finger CCCH domain-containing protein 7B-like (LOC101467393), mRNA	0.03207571	2.017076	up
MPF_LOC100696287.1.2	XP_003450735.1 PREDICTED: C-type lectin domain family 9 member A-like isoform 1 [Oreochromis niloticus]	0.032478802	-3.136027	down
MPF_LOC101169293.1.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.041156992	-1.5654278	down
MPF_LOC101485532.1.1	XM_004573748.1 PREDICTED: Maylandia zebra nuclear receptor-interacting protein 2-like (LOC101485532), mRNA	0.027373271	1.1303754	up
MPF_contig_032831		0.024688901	-2.5736687	down
MPF_contig_034792		0.03115698	-1.489891	down
MPF_LOC100702519.1.1	XM_003441393.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702519), mRNA	0.04546606	-2.5273888	down
MPF_LOC101485221.2.2	XM_004541104.1 PREDICTED: Maylandia zebra disintegrin and metalloproteinase domain-containing protein 19-like (LOC101485221), mRNA	0.031431407	-2.4748144	down
MPF_LOC100702817.1.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.024688901	-3.7960353	down
MPF_LOC100698726.1.1	XP_003460290.1 PREDICTED: hypothetical protein LOC100698726 [Oreochromis niloticus]	0.034953546	-3.606165	down
MPF_LOC101486209.1.4	XM_004551098.1 PREDICTED: Maylandia zebra uncharacterized LOC101486209 (LOC101486209), mRNA	0.037650954	-2.9522488	down

MPF_LOC101476584.9.11	XM_004568601.1 PREDICTED: Maylandia zebra 60S ribosomal protein L23-like (LOC101476584), transcript variant X2, mRNA	0.030398598	-1.3009806	down
MPF_LOC101487243.1.3	XM_004570967.1 PREDICTED: Maylandia zebra pleckstrin homology domain-containing family M member 2-like (LOC101487243), transcript variant X2, mRNA	0.04546606	-1.0398493	down
MPF_LECE.1.1	LECE_HELCR (sp|P06027) Echinoidin OS=Heliocidaris crassispina PE=1 SV=1	0.043960717	-3.483595	down
MPF_LOC101470535.2.3	XM_004560271.1 PREDICTED: Maylandia zebra cyclin-T1-like (LOC101470535), transcript variant X2, mRNA	0.045952104	1.0530119	up
MPF_LOC101156352.1.1	XP_004077953.1 PREDICTED: ictacalcin-like [Oryzias latipes]	0.037768055	-2.7776248	down
MPF_LOC101480831.3.3	XM_004565417.1 PREDICTED: Maylandia zebra putative 60S ribosomal protein L37a-like (LOC101480831), mRNA	0.033915687	-2.323359	down
MPF_LOC101078462.1.1	XP_003965271.1 PREDICTED: lysosome membrane protein 2-like [Takifugu rubripes]	0.024688901	-3.6827137	down
MPF_contig_027617		0.033979006	-1.1964536	down
MPF_contig_014802		0.03836361	-1.3666289	down
MPF_LOC101484400.2.5	XM_004572910.1 PREDICTED: Maylandia zebra 60S ribosomal protein L22-like 1-like (LOC101484400), mRNA	0.043236237	-1.6142516	down
MPF_LOC100711510.1.8	XM_003455849.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100711510), mRNA	0.024688901	-2.6660266	down
MPF_LOC100711484.2.8	XM_003448843.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100711484), mRNA	0.042485975	1.3095791	up
MPF_contig_023699		0.041156992	-2.683433	down
MPF_LOC101485244.1.1	XM_004568719.1 PREDICTED: Maylandia zebra zinc transporter 1-like (LOC101485244), mRNA	0.034953546	-1.7403393	down
MPF_LOC100712435.2.2	XP_003459327.1 PREDICTED: major histocompatibility complex class I-related gene protein-like [Oreochromis niloticus]	0.047354784	1.5361419	up
MPF_LOC101476648.1.1	XM_004538345.1 PREDICTED: Maylandia zebra chondroitin sulfate proteoglycan 4-like (LOC101476648), transcript variant X1, mRNA	0.032880154	2.5474324	up
MPF_LOC100712218.1.1	XM_003452499.1 PREDICTED: Oreochromis niloticus potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4-like (LOC100712218), mRNA	0.039267194	1.1473742	up
MPF_LOC101477091.1.3	XM_004574318.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101477091), transcript variant X5, mRNA	0.033979006	-1.1743917	down
MPF_LOC100690401.1.3	XP_003454006.1 PREDICTED: hypothetical protein LOC100690401 [Oreochromis niloticus]	0.024688901	-3.367925	down
MPF_LOC100703589.1.1	XM_003460117.1 PREDICTED: Oreochromis niloticus plasminogen activator inhibitor 1-like (LOC100703589), mRNA	0.024688901	-4.723201	down
MPF_AHNK.21.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.029597793	-3.475265	down
MPF_contig_024444		0.01925946	1.2493519	up
MPF_LOC101475556.1.1	XM_004575798.1 PREDICTED: Maylandia zebra junction plakoglobin-like (LOC101475556), transcript variant X2, mRNA	0.033915687	1.4802375	up
MPF_LOC101075004.1.1	XM_003964966.1 PREDICTED: Takifugu rubripes uncharacterized LOC101075004 (LOC101075004), mRNA	0.024688901	-3.864941	down
MPF_LOC100696821.2.2	XM_003452445.1 PREDICTED: Oreochromis niloticus ictacalcin-like (LOC100696821), mRNA	0.032880154	-3.2334173	down
MPF_LOC100693306.9.13	XP_003458501.1 PREDICTED: protein NLRC3-like [Oreochromis niloticus]	0.033979006	-2.2164085	down
MPF_contig_028541		0.024688901	-3.307468	down
MPF_LOC101164210.1.1	XM_004065888.1 PREDICTED: Oryzias latipes spermine oxidase-like (LOC101164210), mRNA	0.044679508	-1.7752393	down

MPF_HEPHL1.1.1	XM_003446729.1 PREDICTED: Oreochromis niloticus hephaestin-like 1 (HEPHL1), mRNA	0.047976535	-2.1388047	down
MPF_LOC100698649.6.10	XP_003460222.1 PREDICTED: complement C1q tumor necrosis factor-related protein 3-like [Oreochromis niloticus]	0.047354784	-3.1948647	down
MPF_LOC100689711.4.6	XP_003459483.1 PREDICTED: h-2 class I histocompatibility antigen, L-D alpha chain-like [Oreochromis niloticus]	0.031431407	-1.8276367	down
MPF_ATAD2.2.2	ATAD2_PONAB (sp|Q5RDX4) ATPase family AAA domain-containing protein 2 OS=Pongo abelii GN=ATAD2 PE=2 SV=1	0.03115698	1.2801588	up
MPF_LOC100174873.6.10	NM_001267638.1 Gasterosteus aculeatus beta globin (LOC100174873), mRNA gb|AY184355.1| Gasterosteus aculeatus beta globin mRNA, complete cds	0.032880154	-2.4676456	down
MPF_B3AT.2.2	B3AT_ONCMY (sp|P32847) Band 3 anion exchange protein OS=Oncorhynchus mykiss GN=slc4a1 PE=2 SV=2	0.024688901	-2.7211473	down
MPF_LOC101465872.1.1	XM_004558783.1 PREDICTED: Maylandia zebra extended synaptotagmin-1-like (LOC101465872), mRNA	0.024688901	-3.8944328	down
MPF_LOC100690727.1.1	XM_003443255.1 PREDICTED: Oreochromis niloticus ribosomal RNA processing protein 1 homolog Blike (LOC100690727), mRNA	0.041156992	-1.0812707	down

MPF_LOC101471935.1.1	XM_004545975.1 PREDICTED: Maylandia zebra transcription factor MafB-like (LOC101471935), mRNA	0.030160543	-2.518478	down
MPF_RL18A.5.14	RL18A_DANRE (sp|Q7ZWJ4) 60S ribosomal protein L18a OS=Danio rerio GN=rpl18a PE=2 SV=1	0.032880154	-1.0345562	down
MPF_ZG17.2.2	ZG17_XENLA (sp|P18713) Gastrula zinc finger protein XlCGF17.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.033979006	1.5453789	up
MPF_LOC100702234.6.6	XM_003459254.1 PREDICTED: Oreochromis niloticus mamu class II histocompatibility antigen, DR alpha chain-like (LOC100702234), mRNA	0.046404414	-1.4798436	down
MPF_LOC100690793.1.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]	0.024688901	-3.8568568	down
MPF_LOC101485836.1.2	XM_004559956.1 PREDICTED: Maylandia zebra muscle M-line assembly protein unc-89-like (LOC101485836), transcript variant X1, mRNA	0.033915687	2.283061	up
MPF_LOC100712420.1.5	XP_003456711.1 PREDICTED: adenine phosphoribosyltransferase-like [Oreochromis niloticus]	0.03395561	-1.1716766	down
MPF_LOC101473612.4.5	XM_004550873.1 PREDICTED: Maylandia zebra sodium/potassium-transporting ATPase subunit alpha-3-like (LOC101473612), transcript variant X2, mRNA	0.024688901	-3.0798852	down
MPF_LOC101464956.1.1	XM_004545486.1 PREDICTED: Maylandia zebra large neutral amino acids transporter small subunit 3like (LOC101464956), mRNA	0.043960717	-2.3104231	down
MPF_contig_047601		0.02814418	-2.1446846	down
MPF_LOC100693091.2.2	XM_003450261.1 PREDICTED: Oreochromis niloticus fucolectin-7-like (LOC100693091), mRNA	0.049220506	-2.6072502	down
MPF_LOC101472577.1.1	XM_004538960.1 PREDICTED: Maylandia zebra metal transporter CNNM2-like (LOC101472577), transcript variant X2, mRNA	0.046404414	-1.5584037	down
MPF_LOC100697415.3.3	XP_003444759.1 PREDICTED: neuroblast differentiation-associated protein AHNAK-like [Oreochromis niloticus]	0.024688901	-3.970909	down
MPF_K1C18.1.2	K1C18_DANRE (sp|Q7ZTS4) Keratin, type I cytoskeletal 18 OS=Danio rerio GN=krt18 PE=1 SV=2	0.024688901	-4.0734835	down
MPF_contig_018142		0.047354784	-1.430768	down
MPF_contig_037954		0.047976535	-1.0600753	down
MPF_MYH11.1.2	MYH11_MOUSE (sp|O08638) Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1	0.024688901	-1.6793444	down
MPF_LOC100693203.3.4	XM_003457748.1 PREDICTED: Oreochromis niloticus tetraspanin-5-like (LOC100693203), mRNA	0.033979006	-1.0704306	down
MPF_LOC101465015.1.1	XM_004562273.1 PREDICTED: Maylandia zebra MKL/myocardin-like protein 2-like (LOC101465015), transcript variant X4, mRNA	0.024688901	-1.3180543	down
MPF_contig_036789		0.024688901	-2.2140188	down

MPF_LOC100710548.3.4	XP_003459320.1 PREDICTED: major histocompatibility complex class I-related gene protein-like [Oreochromis niloticus]	0.043321703	-2.638665	down
MPF_contig_017105		0.03527128	1.3650597	up
MPF_LOC101481869.4.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA	0.024688901	-1.4318441	down
MPF_LOC100711796.1.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA	0.046404414	-1.7028723	down
MPF_LOC100701392.1.1	XM_003452212.1 PREDICTED: Oreochromis niloticus protein phosphatase 1K, mitochondrial-like (LOC100701392), mRNA	0.03451082	-1.5841196	down
MPF_RBBP5.1.1	XP_003447710.1 PREDICTED: retinoblastoma-binding protein 5 [Oreochromis niloticus]	0.02948326	1.1791353	up
MPF_contig_023721		0.04177806	-1.2506858	down
MPF_TNF6B.1.1	TNF6B_HUMAN (sp|O95407) Tumor necrosis factor receptor superfamily member 6B OS=Homo sapiens GN=TNFRSF6B PE=1 SV=1	0.024688901	-4.738618	down
MPF_LOC100705618.1.1	XP_003453815.1 PREDICTED: protogenin-like [Oreochromis niloticus]	0.024688901	-2.701024	down
MPF_LOC100711239.3.16	XM_003455848.1 PREDICTED: Oreochromis niloticus ribonuclease inhibitor-like (LOC100711239), mRNA	0.047976535	-1.7195752	down
MPF_LOC101487137.1.1	XM_004545126.1 PREDICTED: Maylandia zebra calcium/calmodulin-dependent protein kinase II inhibitor 2-like (LOC101487137), mRNA	0.043960717	-1.0342574	down
MPF_RS17.23.23	RS17_ICTPU (sp|Q90YQ6) 40S ribosomal protein S17 OS=Ictalurus punctatus GN=rps17 PE=2 SV=3	0.047354784	-1.4909742	down
MPF_LOC101486434.1.2	XM_004560149.1 PREDICTED: Maylandia zebra cathepsin K-like (LOC101486434), mRNA	0.039815266	-3.191424	down
MPF_LOC100702817.3.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.024688901	-4.6740623	down
MPF_LOC100488485.5.10	XP_002941723.1 PREDICTED: hypothetical protein LOC100488485 [Xenopus (Silurana) tropicalis]	0.033591364	-2.9010024	down
MPF_LOC101472640.3.4	XM_004574391.1 PREDICTED: Maylandia zebra microtubule-associated serine/threonine-protein kinase 3-like (LOC101472640), transcript variant X2, mRNA	0.04751419	-1.2063723	down
MPF_LOC101482128.1.2	XM_004574739.1 PREDICTED: Maylandia zebra MARCKS-related protein-like (LOC101482128), mRNA	0.01925946	2.8420649	up
MPF_LOC100712517.2.2	XM_003459650.1 PREDICTED: Oreochromis niloticus RNA (guanine-9-)-methyltransferase domaincontaining protein 2-like (LOC100712517), mRNA	0.024688901	-1.5494502	down
MPF_LOC101480609.1.2	XM_004539422.1 PREDICTED: Maylandia zebra homeodomain-interacting protein kinase 3-like (LOC101480609), transcript variant X2, mRNA	0.01925946	-3.5590432	down
MPF_LOC101465129.6.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA	0.031504437	-1.5873618	down
MPF_LOC100709671.1.2	XM_003460204.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100709671 (LOC100709671), mRNA	0.041950908	-1.4877119	down
MPF_contig_043890		0.041156992	-1.3188491	down
MPF_contig_037677		0.043236237	1.8711576	up
MPF_contig_030109		0.046404414	-1.8046865	down
MPF_LOC100705343.3.3	XM_003450141.1 PREDICTED: Oreochromis niloticus claudin-8-like (LOC100705343), mRNA	0.032626204	-3.143126	down
MPF_LOC100701823.2.2	XM_003446064.1 PREDICTED: Oreochromis niloticus protamine-like protein-like (LOC100701823), mRNA	0.042297408	-1.5753536	down
MPF_contig_009977		0.046404414	-1.1697617	down

MPF_LOC101487936.1.3	XM_004552317.1 PREDICTED: Maylandia zebra F-box/LRR-repeat protein 20-like (LOC101487936), transcript variant X2, mRNA	0.027373271	1.0602622	up
MPF_LOC101484083.3.3	XM_004539190.1 PREDICTED: Maylandia zebra ATP-binding cassette sub-family A member 1-like (LOC101484083), transcript variant X2, mRNA	0.041220345	-1.3363733	down
MPF_contig_026589		0.024688901	1.4386144	up
MPF_contig_004003		0.041156992	-1.9576013	down
MPF_LOC100692490.2.4	XM_003457423.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L37a-like (LOC100692490), mRNA	0.032478802	-2.3682723	down
MPF_LOC100706186.1.2	XM_003460059.1 PREDICTED: Oreochromis niloticus calpain-2 catalytic subunit-like (LOC100706186), mRNA	0.03836361	-1.9066935	down
MPF_LOC100707046.4.12	XM_003454686.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100707046), mRNA	0.04177806	-1.6145034	down
MPF_HACE1.1.3	HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2	0.024688901	-4.775292	down
MPF_LOC101482220.1.3	XM_004571715.1 PREDICTED: Maylandia zebra h-2 class II histocompatibility antigen gamma chainlike (LOC101482220), mRNA	0.04259444	-2.7752671	down
MPF_LOC100696180.1.1	XR_134816.1 PREDICTED: Oreochromis niloticus fibronectin-like (LOC100696180), miscRNA	0.027697286	-4.545038	down
MPF_LOC101477376.3.3	XM_004553320.1 PREDICTED: Maylandia zebra ADP-ribosylation factor 5-like (LOC101477376), mRNA	0.024688901	1.1106267	up
MPF_LOC101162897.2.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]	0.041950908	-2.5928166	down
MPF_LOC100700407.1.1	XM_003454414.1 PREDICTED: Oreochromis niloticus IGF-like family receptor 1-like (LOC100700407), mRNA	0.03115698	-2.8799477	down
MPF_LOC101466143.1.18	XM_004574840.1 PREDICTED: Maylandia zebra 40S ribosomal protein S18-like (LOC101466143), mRNA	0.041220345	-1.5659657	down
MPF_LOC101473055.1.4	XM_004560375.1 PREDICTED: Maylandia zebra basement membrane-specific heparan sulfate proteoglycan core protein-like (LOC101473055), transcript variant X2, mRNA	0.03451082	-1.6583351	down
MPF_PSV.1.1	PSV_DICDI (sp|P08798) Prespore vesicle protein OS=Dictyostelium discoideum GN=psvA PE=2 SV=3	0.032993812	-1.8257377	down
MPF_LOC101161574.4.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.024688901	-2.4638107	down
MPF_LOC101467796.9.9	XM_004554825.1 PREDICTED: Maylandia zebra nesprin-2-like (LOC101467796), mRNA	0.04177806	-1.312479	down
MPF_LOC101488070.1.1	XM_004543546.1 PREDICTED: Maylandia zebra neprilysin-like (LOC101488070), transcript variant X1, mRNA	0.024688901	-4.9685006	down
MPF_contig_036850		0.027373271	-1.7104049	down
MPF_contig_003837		0.03395561	-3.001116	down
MPF_LOC101161574.3.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.024688901	-1.1379261	down
MPF_contig_015500		0.024688901	-2.95176	down
MPF_LOC101477280.6.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.032478802	-2.6694264	down
MPF_LOC100703120.2.3	XP_003458215.1 PREDICTED: hypothetical protein LOC100703120 [Oreochromis niloticus]	0.048683308	-1.3880771	down
MPF_PCGF1.2.2	PCGF1_DANRE (sp|Q7ZYZ7) Polycomb group RING finger protein 1 OS=Danio rerio GN=pcgf1 PE=3 SV=1	0.032626204	-2.2261598	down
MPF_LOC101464712.2.5	XM_004554817.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2Blike (LOC101464712), transcript variant X2, mRNA	0.041156992	-1.2253509	down
MPF_LOC100703239.1.1	XP_003440200.1 PREDICTED: hypothetical protein LOC100703239 [Oreochromis niloticus]	0.045873713	-2.3328488	down
MPF_LOC101486623.1.3	XM_004556475.1 PREDICTED: Maylandia zebra nuclear protein 1-like (LOC101486623), transcript variant X2, mRNA	0.047354784	-2.4323907	down

MPF_contig_022962		0.033979006	-2.1228285	down
MPF_LOC101488089.1.1	XM_004570084.1 PREDICTED: Maylandia zebra uncharacterized LOC101488089 (LOC101488089), transcript variant X3, mRNA	0.046055723	-2.3542953	down
MPF_contig_027052		0.024688901	-1.9684451	down
MPF_LOC101464848.5.5	XM_004545232.1 PREDICTED: Maylandia zebra bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]like (LOC101464848), transcript variant X2, mRNA	0.032478802	-1.3870525	down
MPF_LOC101468563.1.2	XM_004572588.1 PREDICTED: Maylandia zebra alkaline nuclease-like (LOC101468563), transcript variant X6, mRNA	0.047354784	-1.406703	down
MPF_LOC101068301.2.3	XM_003966217.1 PREDICTED: Takifugu rubripes protein S100-A11-like (LOC101068301), mRNA	0.04268631	-2.7717853	down
MPF_contig_019111		0.024688901	1.1144675	up
MPF_LOC101470306.1.1	XM_004574119.1 PREDICTED: Maylandia zebra uncharacterized LOC101470306 (LOC101470306), mRNA	0.036816116	-2.2788498	down
MPF_LOC101473855.10.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA	0.041156992	-1.5574255	down
MPF_LOC101481486.1.2	XM_004563678.1 PREDICTED: Maylandia zebra MARCKS-related protein-like (LOC101481486), mRNA	0.024688901	2.582404	up
MPF_LOC100696821.1.2	XP_003452493.1 PREDICTED: ictacalcin-like [Oreochromis niloticus]	0.032478802	-3.6229868	down
MPF_LOC100699007.2.2	XM_003442225.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100699007, transcript variant 2 (LOC100699007), mRNA	0.048554115	-3.1424496	down
MPF_contig_026907		0.032993812	-3.116148	down
MPF_LOC101475128.1.1	XM_004547410.1 PREDICTED: Maylandia zebra RNA-binding protein 12-like (LOC101475128), transcript variant X4, mRNA	0.039267194	1.0962877	up
MPF_LOC101469089.4.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA	0.01925946	-1.5926731	down
MPF_contig_032259		0.02848602	-2.8030698	down
MPF_contig_031639		0.04913515	-2.344394	down
MPF_contig_012573		0.031431407	-3.0338974	down
MPF_LOC100696805.1.1	XM_003448039.1 PREDICTED: Oreochromis niloticus putative G-protein coupled receptor 44-like (LOC100696805), mRNA	0.033979006	-1.1555449	down
MPF_LOC100709087.2.2	XP_003451700.1 PREDICTED: polyubiquitin-C-like [Oreochromis niloticus]	0.04023118	-1.1107984	down
MPF_contig_021708		0.029980915	-1.6097369	down
MPF_LOC101465192.1.6	XM_004554818.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2Blike (LOC101465192), mRNA	0.034953546	-1.6424483	down
MPF_C1QT3.4.4	C1QT3_MOUSE (sp|Q9ES30) Complement C1q tumor necrosis factor-related protein 3 OS=Mus musculus GN=C1qtnf3 PE=2 SV=1	0.03949431	-2.9352326	down
MPF_LOC100698649.3.10	XP_003460222.1 PREDICTED: complement C1q tumor necrosis factor-related protein 3-like [Oreochromis niloticus]	0.043771714	-3.0941136	down
MPF_LOC100695137.3.3	XP_003447509.1 PREDICTED: high affinity immunoglobulin epsilon receptor subunit gamma-like [Oreochromis niloticus]	0.033979006	-3.555051	down
MPF_LOC101476292.1.1	XM_004567039.1 PREDICTED: Maylandia zebra transgelin-like (LOC101476292), transcript variant X2, mRNA	0.032880154	-4.6097455	down
MPF_contig_026973	XM_004553863.1 PREDICTED: Maylandia zebra poly [ADP-ribose] polymerase 12-like (LOC101480887), transcript variant X1, mRNA	0.03115698	-2.1420631	down

MPF_IGSF3.1.1	IGSF3_HUMAN (sp|O75054) Immunoglobulin superfamily member 3 OS=Homo sapiens GN=IGSF3 PE=2 SV=3	0.033591364	1.1039071	up
MPF_LOC101166773.1.1	XP_004085184.1 PREDICTED: uncharacterized protein LOC101166773, partial [Oryzias latipes]	0.024688901	-1.2888381	down
MPF_LOC100697337.2.4	XP_003446015.1 PREDICTED: hypothetical protein LOC100697337 [Oreochromis niloticus]	0.030369533	-1.3804333	down
MPF_LOC100698802.3.5	XM_003458154.1 PREDICTED: Oreochromis niloticus cytochrome c oxidase subunit 8A, mitochondrial-like (LOC100698802), mRNA	0.033979006	1.3092927	up
MPF_LOC101485004.5.8	XM_004560422.1 PREDICTED: Maylandia zebra serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C-like (LOC101485004), mRNA	0.031057589	1.591083	up
MPF_contig_031891		0.024688901	-3.3802004	down
MPF_CD48.2.4	CD48_MOUSE (sp|P18181) CD48 antigen OS=Mus musculus GN=Cd48 PE=1 SV=1	0.032626204	-2.7061439	down
MPF_NALP3.1.1	NALP3_BOVIN (sp|A6QLE5) NACHT, LRR and PYD domains-containing protein 3 OS=Bos taurus GN=NLRP3 PE=2 SV=1	0.02598959	-1.6579278	down
MPF_contig_043323		0.041156992	-1.0977736	down
MPF_LOC101468524.2.2	XM_004540307.1 PREDICTED: Maylandia zebra transcription factor Sp3-like (LOC101468524), transcript variant X2, mRNA	0.046055723	1.6975856	up
MPF_LOC101168710.1.1	XP_004070984.1 PREDICTED: CD27 antigen-like [Oryzias latipes]	0.033979006	-2.6992204	down
MPF_LOC101473901.1.2	XM_004572233.1 PREDICTED: Maylandia zebra CDC42 small effector protein 1-like (LOC101473901), transcript variant X2, mRNA	0.027908875	-3.310245	down
MPF_LOC101471998.1.1	XM_004540134.1 PREDICTED: Maylandia zebra MFS-type transporter SLC18B1-like (LOC101471998), mRNA	0.032880154	1.2948031	up
MPF_LOC101478250.3.3	XM_004538353.1 PREDICTED: Maylandia zebra flocculation protein FLO11-like (LOC101478250), transcript variant X3, mRNA	0.032626204	-3.5944993	down
MPF_LECG.42.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.047354784	-3.402804	down
MPF_LOC101476819.6.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0.047976535	-1.6785684	down
MPF_contig_048305		0.033979006	1.3836191	up
MPF_LOC100698701.1.2	XM_003455230.1 PREDICTED: Oreochromis niloticus protein S100-A13-like (LOC100698701), mRNA	0.033979006	-2.6580007	down
MPF_RL23.2.9	RL23_RAT (sp|P62832) 60S ribosomal protein L23 OS=Rattus norvegicus GN=Rpl23 PE=2 SV=1	0.047354784	-1.5304556	down
MPF_LOC101477280.1.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.027373271	-2.6524477	down
MPF_LOC101160373.1.1	XP_004083232.1 PREDICTED: DNA damage-regulated autophagy modulator protein 1-like [Oryzias latipes]	0.041156992	-1.7003902	down
MPF_LOC101475513.1.1	XM_004545621.1 PREDICTED: Maylandia zebra EGF-containing fibulin-like extracellular matrix protein 2-like (LOC101475513), mRNA	0.024688901	-3.2010589	down
MPF_RS7.7.10	RS7_TAKRU (sp|P50894) 40S ribosomal protein S7 OS=Takifugu rubripes GN=rps7 PE=3 SV=1	0.03233395	-1.7807193	down
MPF_LOC101464981.1.1	XM_004574536.1 PREDICTED: Maylandia zebra cyclic AMP-dependent transcription factor ATF-4-like (LOC101464981), mRNA	0.041156992	-2.040608	down
MPF_LOC100691990.2.2	XM_003445526.1 PREDICTED: Oreochromis niloticus annexin A1-like (LOC100691990), mRNA	0.042491622	-1.3795681	down
MPF_contig_032267		0.032478802	-3.1115725	down
MPF_LOC101073669.1.1	XM_003964261.1 PREDICTED: Takifugu rubripes coatomer subunit zeta-2-like (LOC101073669), mRNA	0.030160543	1.0211161	up
MPF_LOC101473819.2.3	XM_004552168.1 PREDICTED: Maylandia zebra hemoglobin embryonic subunit alpha-like (LOC101473819), transcript variant X2, mRNA	0.024688901	-3.3847356	down
MPF_LOC101486169.4.4	XM_004566076.1 PREDICTED: Maylandia zebra cyclin-T2-like (LOC101486169), mRNA	0.024688901	-5.1608295	down

MPF_contig_014120		0.03233395	-3.5124593	down
MPF_contig_043487		0.04957513	-1.129855	down
MPF_contig_016882		0.030160543	-1.5090685	down
MPF_ACBD5.1.1	ACBD5_PONAB (sp|Q5R7V3) Acyl-CoA-binding domain-containing protein 5 OS=Pongo abelii GN=ACBD5 PE=2 SV=1	0.047354784	-1.5679953	down
MPF_contig_020194		0.024688901	-3.4252381	down
MPF_LOC101465099.1.1	XM_004557394.1 PREDICTED: Maylandia zebra moesin-like (LOC101465099), mRNA	0.042485975	-3.0297184	down
MPF_AHNK.11.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.037175376	-3.352121	down
MPF_LOC101467829.1.2	XM_004565458.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase pim-1-like (LOC101467829), mRNA	0.037650954	-1.9425054	down
MPF_contig_038232		0.03115698	1.0327073	up
MPF_LOC101165175.3.3	XM_004078345.1 PREDICTED: Oryzias latipes cathepsin S-like (LOC101165175), mRNA	0.041156992	-2.1087332	down

MPF_LOC101478710.1.1	XM_004562050.1 PREDICTED: Maylandia zebra DEP domain-containing protein 1A-like (LOC101478710), transcript variant X2, mRNA	0.032665133	1.1548411	up
MPF_LOC100699721.1.2	XP_003460016.1 PREDICTED: bifunctional protein NCOAT-like, partial [Oreochromis niloticus]	0.04079872	-2.62965	down
MPF_LOC101480653.1.5	XM_004571444.1 PREDICTED: Maylandia zebra neurofascin-like (LOC101480653), mRNA	0.048683308	1.853548	up
MPF_contig_011981		0.033979006	-3.2700648	down
MPF_LOC101156484.2.2	XM_004067491.1 PREDICTED: Oryzias latipes CD81 antigen-like (LOC101156484), mRNA	0.033821132	-2.1375604	down
MPF_LOC101482619.1.3	XM_004556458.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase TAO2-like (LOC101482619), transcript variant X2, mRNA	0.024688901	1.0629468	up
MPF_LOC101473855.2.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA	0.03949431	-1.7079868	down
MPF_contig_030523		0.049220506	-2.3679085	down
MPF_MOG.5.5	NP_001158619.1 Myelin-oligodendrocyte glycoprotein precursor [Oncorhynchus mykiss]	0.04546606	-1.5772972	down
MPF_LOC101159641.5.35	XM_004085298.1 PREDICTED: Oryzias latipes tenascin-like (LOC101159641), mRNA	0.03836361	-1.6160531	down
MPF_LOC100701242.3.9	XM_003459250.1 PREDICTED: Oreochromis niloticus h-2 class II histocompatibility antigen, I-A beta chain-like, transcript variant 1 (LOC100701242), mRNA	0.047354784	-2.6431131	down
MPF_contig_028990		0.03115698	-2.0092273	down
MPF_HBB2.3.3	[BBH] HBB2_PSEUR (sp|P83625) Hemoglobin subunit beta-2 OS=Pseudaphritis urvillii GN=hbb2 PE=1 SV=1	0.043236237	-1.896483	down
MPF_LOC101161674.2.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA	0.032626204	-2.3657365	down
MPF_LOC101484929.2.3	XM_004542976.1 PREDICTED: Maylandia zebra CMP-N-acetylneuraminate-beta-1,4-galactoside alpha-2,3-sialyltransferase-like (LOC101484929), mRNA	0.03823759	-2.0960271	down

SR48_70+ vs SR48_30-

Phylofish Gene ID	Gene description	p (Corr FDR)	Log FC	Regulation

MPF_LOC101475165.1.1	XM_004557989.1 PREDICTED: Maylandia zebra secretory carrier-associated membrane protein 2-like (LOC101475165), transcript variant X1, mRNA	0.048044402	-0.6831598	down
MPF_contig_034181		8.62E-04	2.2343736	up
MPF_CD99.1.1	CD99_HUMAN (sp|P14209) CD99 antigen OS=Homo sapiens GN=CD99 PE=1 SV=1	0.013970896	2.51117	up
MPF_LOC101070622.1.2	XP_003976498.1 PREDICTED: glucose-6-phosphate isomerase-like isoform 1 [Takifugu rubripes]	0.038931586	-1.0670872	down
MPF_CD68.2.2	NP_001158857.1 Macrosialin precursor [Salmo salar]	3.86E-04	3.5787916	up
MPF_contig_030395		0.028497541	-0.8443699	down
MPF_LOC100696676.4.4	XP_003459127.1 PREDICTED: zinc finger protein 235-like [Oreochromis niloticus]	0.005661226	-0.4589615	down
MPF_LOC100698998.2.7	XM_003439446.1 PREDICTED: Oreochromis niloticus myosin heavy chain, fast skeletal muscle-like (LOC100698998), mRNA	0.001790945	3.174652	up
MPF_LOC100698790.1.2	XP_003455363.1 PREDICTED: mitotic spindle assembly checkpoint protein MAD2B-like [Oreochromis niloticus]	0.047509596	-0.79230595	down
MPF_LOC101157470.1.1	XM_004074516.1 PREDICTED: Oryzias latipes transportin-1-like (LOC101157470), mRNA	0.03135769	1.8795953	up
MPF_LOC100706528.4.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0.002055359	-1.0054412	down
MPF_TNR5.4.4	TNR5_HUMAN (sp|P25942) Tumor necrosis factor receptor superfamily member 5 OS=Homo sapiens GN=CD40 PE=1 SV=1	0.009727723	-0.808311	down
MPF_LOC101157594.1.1	XP_004065840.1 PREDICTED: uncharacterized protein LOC101157594 [Oryzias latipes]	8.62E-04	2.7195983	up
MPF_LOC101472355.1.1	XM_004556700.1 PREDICTED: Maylandia zebra peripheral myelin protein 22-like (LOC101472355), mRNA	2.92E-04	4.802478	up
MPF_GSK3AB.1.2	NM_131390.2 Danio rerio glycogen synthase kinase 3 alpha b (gsk3ab), mRNA gb|BC065952.1| Danio rerio glycogen synthase kinase 3 alpha, mRNA (cDNA clone MGC:76825 IMAGE:6964853), complete cds	0.03168701	-0.6196914	down
MPF_LOC100705746.1.3	XP_003443116.1 PREDICTED: trafficking protein particle complex subunit 5-like [Oreochromis niloticus]	0.03230088	-0.6968851	down
MPF_contig_045041		0.014163161	-0.7906684	down
MPF_RL36A.2.2	RL36A_TAKRU (sp|P61486) 60S ribosomal protein L36a OS=Takifugu rubripes GN=rpl36a PE=3 SV=2	0.018205103	-0.7097149	down
MPF_LOC100135188.1.5	NP_001107363.1 uncharacterized protein LOC100135188 [Xenopus (Silurana) tropicalis]	0.005308218	2.9527056	up
MPF_LOC100696526.1.1	XM_003444290.1 PREDICTED: Oreochromis niloticus probable phospholipid-transporting ATPase VAlike (LOC100696526), mRNA	0.036345366	-0.6039726	down
MPF_LOC100702375.2.2	XM_003450215.1 PREDICTED: Oreochromis niloticus 6-phosphofructokinase type C-like (LOC100702375), mRNA	0.001715593	2.2843442	up
MPF_LOC100708533.1.1	XM_003447172.1 PREDICTED: Oreochromis niloticus annexin A2-like (LOC100708533), mRNA	0.044269416	2.4765506	up
MPF_contig_003522	XM_004551014.1 PREDICTED: Maylandia zebra akirin-1-like (LOC101486208), transcript variant X1, mRNA	1.57E-04	3.3484383	up
MPF_LOC752725.1.2	XP_001179979.2 PREDICTED: uncharacterized protein LOC752725 isoform 1 [Strongylocentrotus purpuratus]	0.018603342	-1.3082721	down
MPF_LOC100711945.9.12	XP_003451200.1 PREDICTED: interferon-induced protein 44-like [Oreochromis niloticus]	0.039148536	-0.60232925	down
MPF_LOC101473402.1.1	XM_004548338.1 PREDICTED: Maylandia zebra protein kinase C and casein kinase substrate in neurons protein 2-like (LOC101473402), transcript variant X3, mRNA	0.004220047	1.4480165	up
MPF_contig_045446		7.16E-04	-0.5674915	down
MPF_LOC101472043.4.14	XM_004573789.1 PREDICTED: Maylandia zebra tight junction-associated protein 1-like (LOC101472043), transcript variant X4, mRNA	8.47E-04	2.1058066	up
MPF_contig_044869	XM_004575909.1 PREDICTED: Maylandia zebra neurabin-2-like (LOC101486611), transcript variant	0.006548257	2.5918832	up

	X1, mRNA			

MPF_contig_044599		0.034990955	-0.86396956	down
MPF_LOC101475041.3.3	XM_004549542.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 7-like (LOC101475041), transcript variant X2, mRNA	0.002760018	3.9838867	up
MPF_LOC101484531.1.1	XM_004559127.1 PREDICTED: Maylandia zebra ubiquitin carboxyl-terminal hydrolase 37-like (LOC101484531), transcript variant X2, mRNA	0.005032116	-0.74821997	down
MPF_MMP9.2.5	XM_003448139.1 PREDICTED: Oreochromis niloticus matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA	0.04716473	2.6351495	up
MPF_LOC100696802.1.1	XP_003447430.1 PREDICTED: Golgi reassembly-stacking protein 2-like [Oreochromis niloticus]	0.01113301	1.8562245	up
MPF_contig_023930		5.30E-04	3.931744	up
MPF_LOC101471392.1.2	XM_004556871.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase Siah2-like (LOC101471392), mRNA	0.047293946	-0.7394948	down
MPF_contig_023861		0.006498309	2.1009586	up
MPF_LOC101485376.1.3	XM_004557844.1 PREDICTED: Maylandia zebra thymosin beta-12-like (LOC101485376), mRNA	0.013726315	-0.6749773	down
MPF_LOC101065174.1.1	XM_003977503.1 PREDICTED: Takifugu rubripes RNA 3'-terminal phosphate cyclase-like (LOC101065174), mRNA	0.003720693	-0.7938533	down
MPF_LOC101468488.5.7	XM_004552241.1 PREDICTED: Maylandia zebra 40S ribosomal protein S11-like (LOC101468488), mRNA	0.0437016	-0.6257939	down
MPF_SRAP.2.3	SRAP_STAAN (sp|Q7A362) Serine-rich adhesin for platelets OS=Staphylococcus aureus (strain N315) GN=sraP PE=1 SV=1	0.03063811	2.7042677	up
MPF_LOC101160212.3.4	XP_004084697.1 PREDICTED: h-2 class II histocompatibility antigen, I-A beta chain-like [Oryzias latipes]	0.030548751	3.0175095	up
MPF_contig_040368		5.73E-04	3.1688268	up
MPF_LOC101156534.2.3	XR_177556.1 PREDICTED: Oryzias latipes synaptotagmin-1-like (LOC101156534), misc_RNA	0.020762017	-0.7934327	down
MPF_contig_038379		0.001791252	3.122687	up
MPF_LOC101168682.3.3	XM_004066371.1 PREDICTED: Oryzias latipes protein S100-B-like, transcript variant 2 (LOC101168682), mRNA	0.003943931	3.4771376	up
MPF_SSL-2.1.2	NP_001117194.1 serum lectin 2 precursor [Salmo salar]	1.40E-04	3.9467907	up
MPF_contig_013127	XM_004539189.1 PREDICTED: Maylandia zebra ATP-binding cassette sub-family A member 1-like (LOC101484083), transcript variant X1, mRNA	0.007902411	2.0382748	up
MPF_LOC101470583.3.3	XM_004571226.1 PREDICTED: Maylandia zebra TSC22 domain family protein 1-like (LOC101470583), mRNA	0.04093185	-1.0865691	down
MPF_LOC101466485.1.2	XM_004540856.1 PREDICTED: Maylandia zebra immunoglobulin lambda-like polypeptide 5-like (LOC101466485), mRNA	0.009207967	3.403067	up
MPF_LOC101062260.2.2	XP_003970925.1 PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit alpha-like [Takifugu rubripes]	0.030638218	1.9205372	up
MPF_TTC9B.1.1	NM_001078791.2 Xenopus (Silurana) tropicalis tetratricopeptide repeat domain 9B (ttc9b), mRNA	0.004268618	2.7366567	up
MPF_LOC101465862.1.1	XM_004555006.1 PREDICTED: Maylandia zebra C3 and PZP-like alpha-2-macroglobulin domaincontaining protein 8-like (LOC101465862), transcript variant X2, mRNA	0.04242951	-0.60454506	down
MPF_LOC100693642.1.1	XM_003454966.1 PREDICTED: Oreochromis niloticus adenylate kinase isoenzyme 1-like, transcript variant 1 (LOC100693642), mRNA	0.008621556	2.9964743	up
MPF_LOC101479293.1.1	XM_004543228.1 PREDICTED: Maylandia zebra protein FAM189A1-like (LOC101479293), transcript variant X2, mRNA	0.035689894	-1.3251184	down

MPF_POMT2.1.1	XP_003447845.1 PREDICTED: protein O-mannosyl-transferase 2 [Oreochromis niloticus]	0.025273811	-0.46102998	down
MPF_LOC101172154.1.1	XP_004068682.1 PREDICTED: epithelial membrane protein 3-like [Oryzias latipes]	2.59E-04	3.9270318	up
MPF_LOC100700496.3.3	XM_003453022.1 PREDICTED: Oreochromis niloticus probable ribonuclease ZC3H12D-like (LOC100700496), mRNA	1.81E-04	3.3547232	up
MPF_LOC101476572.2.2	XM_004541074.1 PREDICTED: Maylandia zebra tetraspanin-17-like (LOC101476572), mRNA	1.65E-04	4.200174	up
MPF_LOC101155471.2.2	XM_004080809.1 PREDICTED: Oryzias latipes cullin-1-like (LOC101155471), mRNA	0.008750069	-0.9331608	down
MPF_LOC100702147.4.11	XP_003459074.1 PREDICTED: hypothetical protein LOC100702147 [Oreochromis niloticus]	0.025398446	2.419604	up
MPF_LOC100699424.5.7	XM_003455807.1 PREDICTED: Oreochromis niloticus deleted in malignant brain tumors 1 protein-like (LOC100699424), mRNA	0.004862377	-1.232038	down
MPF_LOC100699557.1.1	XM_003443457.1 PREDICTED: Oreochromis niloticus extracellular sulfatase Sulf-1-like (LOC100699557), mRNA	0.032727864	-1.0114994	down
MPF_contig_045323		3.59E-04	4.191399	up
MPF_LOC101487704.1.1	XM_004564995.1 PREDICTED: Maylandia zebra transcription elongation factor SPT5-like (LOC101487704), mRNA	0.030225178	-1.5404644	down
MPF_contig_042533		0.03322063	2.1065695	up
MPF_LOC101474911.1.1	XM_004566844.1 PREDICTED: Maylandia zebra B-cell receptor CD22-like (LOC101474911), transcript variant X3, mRNA	0.003151855	3.7114043	up
MPF_LOC101471502.1.1	XM_004539386.1 PREDICTED: Maylandia zebra AFG3-like protein 1-like (LOC101471502), transcript variant X2, mRNA	0.015684035	-0.45000738	down
MPF_AHNAK.3.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]	6.00E-04	5.4723725	up
MPF_contig_009706		0.029445808	2.5684218	up
MPF_LOC101466716.1.1	XM_004550747.1 PREDICTED: Maylandia zebra C-type lectin domain family 9 member A-like (LOC101466716), transcript variant X2, mRNA	0.003676144	3.317322	up
MPF_LOC101475665.1.3	XM_004554127.1 PREDICTED: Maylandia zebra mucin-2-like (LOC101475665), transcript variant X2, mRNA	0.009384455	0.96852773	up
MPF_G6PCA.2.1.1	NP_001157278.1 im:6895556 [Danio rerio]	0.035858028	-1.153964	down
MPF_LOC101472002.1.2	XM_004541243.1 PREDICTED: Maylandia zebra histone-lysine N-methyltransferase ASH1L-like (LOC101472002), transcript variant X1, mRNA	4.17E-04	2.7772958	up
MPF_contig_020534		0.003787725	3.4784756	up
MPF_THAP9.1.1	[BBH] THAP9_HUMAN (sp|Q9H5L6) DNA transposase THAP9 OS=Homo sapiens GN=THAP9 PE=1 SV=2	1.57E-04	3.4232554	up
MPF_contig_044800		0.02861339	-0.87824535	down
MPF_LOC100704351.1.1	XM_003448735.1 PREDICTED: Oreochromis niloticus pleckstrin homology domain-containing family M member 1-like (LOC100704351), mRNA	0.019154161	-0.43653873	down
MPF_LOC101470829.1.1	XM_004557598.1 PREDICTED: Maylandia zebra desumoylating isopeptidase 1-like (LOC101470829), mRNA	5.19E-05	3.7115662	up
MPF_LOC101474125.1.1	XM_004553209.1 PREDICTED: Maylandia zebra membrane protein FAM174B-like (LOC101474125), transcript variant X2, mRNA	0.012382003	-0.7336951	down
MPF_LOC101485376.3.3	XM_004557844.1 PREDICTED: Maylandia zebra thymosin beta-12-like (LOC101485376), mRNA	0.02442365	-0.66625303	down
MPF_LOC101469812.1.2	XM_004571140.1 PREDICTED: Maylandia zebra polycomb group RING finger protein 3-like (LOC101469812), mRNA	0.014495558	-0.44628003	down

MPF_contig_026757		0.001881666	2.5960357	up
MPF_LOC101482364.1.4	XM_004541093.1 PREDICTED: Maylandia zebra cytoplasmic polyadenylation element-binding protein 4-like (LOC101482364), mRNA	0.035858028	-0.6225048	down
MPF_contig_026572		0.025726486	-0.9692588	down
MPF_LOC101483521.1.1	XM_004540909.1 PREDICTED: Maylandia zebra early growth response protein 1-like (LOC101483521), mRNA	1.57E-04	4.8337517	up
MPF_LOC101466706.1.1	XM_004548787.1 PREDICTED: Maylandia zebra coiled-coil domain-containing protein 66-like (LOC101466706), transcript variant X4, mRNA	0.04231967	-0.9022875	down
MPF_LOC100690512.1.1	XP_003438469.1 PREDICTED: hypothetical protein LOC100690512 [Oreochromis niloticus]	0.003471285	3.3703363	up
MPF_FGL1.1.1	FGL1_BOVIN (sp|Q3SZZ7) Fibrinogen-like protein 1 OS=Bos taurus GN=FGL1 PE=2 SV=1	0.035858028	2.9554758	up
MPF_contig_006224		0.031663816	1.6508346	up
MPF_LOC101170712.1.1	XM_004080140.1 PREDICTED: Oryzias latipes hemoglobin subunit beta-1-like (LOC101170712), mRNA	0.002546	2.4253085	up
MPF_LOC101169532.18.45	XP_004070110.1 PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Oryzias latipes]	0.049991075	1.8341756	up
MPF_LOC101476812.1.3	XM_004575484.1 PREDICTED: Maylandia zebra DNA-directed RNA polymerase III subunit RPC8-like (LOC101476812), mRNA	0.00977722	-1.1440401	down
MPF_LOC101476936.1.1	XM_004565493.1 PREDICTED: Maylandia zebra peptidyl-prolyl cis-trans isomerase FKBP1A-like (LOC101476936), mRNA	7.08E-04	2.7210138	up
MPF_LOC101464855.1.1	XM_004546244.1 PREDICTED: Maylandia zebra signal peptide, CUB and EGF-like domain-containing protein 3-like (LOC101464855), transcript variant X1, mRNA	0.018118626	3.6888604	up
MPF_HBA1.2.5	HBA1_ANAMI (sp|P83270) Hemoglobin subunit alpha-1 OS=Anarhichas minor GN=hba1 PE=1 SV=2	0.032921147	2.1612496	up
MPF_contig_016274		0.012136511	1.9700112	up
MPF_LOC100711025.1.1	XP_003444057.1 PREDICTED: putative helicase Mov10l1-like [Oreochromis niloticus]	0.003504425	-0.7093525	down
MPF_LOC101486124.3.4	XM_004575749.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12like (LOC101486124), mRNA	0.005696483	2.5511613	up
MPF_LOC100711070.2.2	XM_003455767.1 PREDICTED: Oreochromis niloticus prefoldin subunit 6-like (LOC100711070), mRNA	0.048314296	-0.9720926	down
MPF_LOC101155669.1.1	XP_004067287.1 PREDICTED: globoside alpha-1,3-N-acetylgalactosaminyltransferase 1-like [Oryzias latipes]	0.014686909	1.4525199	up
MPF_contig_015023		0.028385947	1.4848795	up
MPF_LOC100693993.1.1	XM_003453809.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693993 (LOC100693993), mRNA	0.003151855	2.7282796	up
MPF_LOC101479407.1.1	XM_004547238.1 PREDICTED: Maylandia zebra macrophage-expressed gene 1 protein-like (LOC101479407), mRNA	3.59E-04	2.882822	up
MPF_LOC100712028.1.5	XM_003450493.1 PREDICTED: Oreochromis niloticus apolipoprotein C-I-like (LOC100712028), mRNA	0.008428021	3.8216743	up
MPF_LOC101473623.3.9	XM_004576627.1 PREDICTED: Maylandia zebra ferritin, middle subunit-like (LOC101473623), mRNA	0.03619735	-0.49326128	down
MPF_LOC101487734.2.2	XM_004571292.1 PREDICTED: Maylandia zebra cytohesin-4-like (LOC101487734), mRNA	0.001464735	3.068108	up
MPF_LOC101481567.1.1	XM_004560226.1 PREDICTED: Maylandia zebra uncharacterized LOC101481567 (LOC101481567), mRNA	0.035858028	2.1430914	up
MPF_LOC101484489.10.10	XM_004548851.1 PREDICTED: Maylandia zebra 14-3-3 protein beta/alpha-A-like (LOC101484489), mRNA	0.047293946	-0.45960996	down

MPF_contig_015898	XM_004556609.1 PREDICTED: Maylandia zebra calcium/calmodulin-dependent protein kinase type II subunit gamma-like (LOC101474026), transcript variant X6, mRNA	0.015642129	-0.6286955	down
MPF_contig_038012		8.62E-04	2.8940485	up
MPF_LOC101471089.1.1	XM_004552818.1 PREDICTED: Maylandia zebra transmembrane protein 131-like (LOC101471089), mRNA	0.03942728	-2.0323896	down
MPF_LOC101464455.7.13	XM_004542249.1 PREDICTED: Maylandia zebra calmodulin-like (LOC101464455), mRNA	0.026520038	1.1084404	up
MPF_LOC100708275.1.1	XM_003449495.1 PREDICTED: Oreochromis niloticus alpha-aspartyl dipeptidase-like (LOC100708275), mRNA	0.001031627	2.8476782	up
MPF_LOC100701693.2.4	XM_003459252.1 PREDICTED: Oreochromis niloticus mamu class II histocompatibility antigen, DR alpha chain-like (LOC100701693), mRNA	0.01605041	2.3591661	up
MPF_YTHDF1.1.1	XP_003439071.1 PREDICTED: YTH domain family protein 1 [Oreochromis niloticus]	0.028843079	-0.90522766	down
MPF_LOC101472907.1.4	XM_004570821.1 PREDICTED: Maylandia zebra oxysterol-binding protein-related protein 5-like (LOC101472907), transcript variant X4, mRNA	0.037678413	-0.72862816	down
MPF_LOC101464789.7.10	XM_004574915.1 PREDICTED: Maylandia zebra heat shock cognate 71 kDa protein-like (LOC101464789), mRNA	0.03249635	-0.47857955	down
MPF_LOC100694958.1.2	XM_003449949.1 PREDICTED: Oreochromis niloticus clathrin light chain A-like, transcript variant 3 (LOC100694958), mRNA	0.01979235	-0.57812214	down
MPF_contig_002218		0.034726255	-0.48893833	down
MPF_LOC101478889.3.3	XM_004561424.1 PREDICTED: Maylandia zebra protein yippee-like 2-like (LOC101478889), transcript variant X2, mRNA	0.04557982	2.6200554	up
MPF_LOC101476889.1.1	XM_004550785.1 PREDICTED: Maylandia zebra 39S ribosomal protein L51, mitochondrial-like (LOC101476889), mRNA	0.025258163	-0.6723308	down

MPF_LOC101486244.2.2	XM_004539011.1 PREDICTED: Maylandia zebra transcription factor MafG-like (LOC101486244), transcript variant X3, mRNA	1.57E-04	2.7429407	up
MPF_LOC101079843.1.1	XM_003972061.1 PREDICTED: Takifugu rubripes coiled-coil and C2 domain-containing protein 1A-like (LOC101079843), mRNA	0.024698121	-0.9213896	down
MPF_LOC100706528.6.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0.008659684	-1.0862107	down
MPF_LOC101172990.11.36	XM_004073898.1 PREDICTED: Oryzias latipes uncharacterized LOC101172990 (LOC101172990), mRNA	0.031094607	2.8457348	up
MPF_contig_022617		0.01577848	3.626842	up
MPF_LOC101483928.1.2	XM_004570429.1 PREDICTED: Maylandia zebra sodium-driven chloride bicarbonate exchanger-like (LOC101483928), transcript variant X2, mRNA	0.039148536	1.1863574	up
MPF_LOC101470866.3.3	XM_004566111.1 PREDICTED: Maylandia zebra protein spire homolog 2-like (LOC101470866), mRNA	0.049876817	-0.8357949	down
MPF_LOC100692032.5.6	XM_003458056.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100692032), mRNA	0.016257549	-0.6258487	down
MPF_RL17.5.5	RL17_RAT (sp|P24049) 60S ribosomal protein L17 OS=Rattus norvegicus GN=Rpl17 PE=2 SV=3	0.006380456	2.1581526	up
MPF_LOC101477684.3.4	XM_004539594.1 PREDICTED: Maylandia zebra small EDRK-rich factor 2-like (LOC101477684), mRNA	0.035663363	-0.77311707	down
MPF_LOC100702817.2.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.001348924	5.9223247	up
MPF_LOC101486439.1.1	XM_004561632.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 21-like (LOC101486439), mRNA	7.19E-04	2.40851	up

MPF_LOC101487373.24.24	XM_004576282.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101487373), mRNA	0.019337732	2.791614	up
MPF_LOC101156898.4.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	0.002822743	4.846303	up
MPF_LOC101173244.5.8	XM_004076629.1 PREDICTED: Oryzias latipes ATP synthase subunit g, mitochondrial-like (LOC101173244), mRNA	0.006937477	-1.1294831	down
MPF_LOC101476286.1.1	XM_004541073.1 PREDICTED: Maylandia zebra synaptopodin 2-like protein-like (LOC101476286), mRNA	0.008195538	3.7189617	up
MPF_LOC100693692.3.3	XM_003444116.1 PREDICTED: Oreochromis niloticus protein asteroid homolog 1-like (LOC100693692), mRNA	0.020049248	-1.0303807	down
MPF_ZN214.3.8	ZN214_HUMAN (sp|Q9UL59) Zinc finger protein 214 OS=Homo sapiens GN=ZNF214 PE=2 SV=2	0.011377938	-0.5411343	down
MPF_LOC101156534.3.3	XR_177556.1 PREDICTED: Oryzias latipes synaptotagmin-1-like (LOC101156534), misc_RNA	0.021505397	1.8559871	up
MPF_contig_030947	XM_004572764.1 PREDICTED: Maylandia zebra agrin-like (LOC101470011), transcript variant X2, mRNA	0.012953717	2.6542559	up
MPF_contig_006781	XM_004572062.1 PREDICTED: Maylandia zebra polypyrimidine tract-binding protein 2-like (LOC101478106), transcript variant X2, mRNA	0.03571405	-0.698698	down
MPF_LOC100690258.1.1	XP_003440479.1 PREDICTED: annexin A2-A-like [Oreochromis niloticus]	0.003779727	4.7181945	up
MPF_LOC101075367.4.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]	0.006909485	2.2242785	up
MPF_ZG57.7.12	ZG57_XENLA (sp|P18729) Gastrula zinc finger protein XlCGF57.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.006389125	-1.0756254	down
MPF_PHUM_PHUM529360.1.2	XP_002431439.1 ngd5/osm-6/ift52, putative [Pediculus humanus corporis]	0.003673072	2.9606552	up
MPF_contig_044718		0.040316716	-0.41289812	down
MPF_LOC101477280.2.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.001715593	3.9215386	up
MPF_LOC100712254.1.1	XM_003439410.1 PREDICTED: Oreochromis niloticus anamorsin-like (LOC100712254), mRNA	0.015695732	-0.7204972	down
MPF_LOC100699178.1.1	XM_003438369.1 PREDICTED: Oreochromis niloticus inositol 1,4,5-triphosphate receptor-interacting protein-like (LOC100699178), mRNA	0.027092082	2.5038452	up
MPF_contig_044194		0.002189675	3.2587004	up
MPF_contig_046342		0.04220178	-0.52699274	down
MPF_MOR1A.1.1	[BBH] MOR1A_CHICK (sp|Q2YHT7) Cell surface glycoprotein CD200 receptor 1-A OS=Gallus gallus GN=CD200R1A PE=1 SV=1	2.92E-04	3.4145606	up
MPF_LOC100689854.15.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0.049854793	-0.8327861	down
MPF_LOC101166874.5.6	XP_004071207.1 PREDICTED: 60S ribosomal protein L3-like [Oryzias latipes]	0.019503621	-0.59341425	down
MPF_contig_014917		0.04488326	1.5635953	up
MPF_LOC101156898.1.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	0.00237142	4.1634417	up
MPF_LOC101073280.1.1	XM_003962805.1 PREDICTED: Takifugu rubripes striatin-3-like (LOC101073280), mRNA	0.018142981	-0.7525711	down
MPF_contig_036689		0.024343735	-0.8153062	down
MPF_LOC101480875.1.1	XM_004574330.1 PREDICTED: Maylandia zebra proline-, glutamic acid- and leucine-rich protein 1-like (LOC101480875), transcript variant X2, mRNA	0.030548751	-0.558002	down
MPF_contig_035424		0.008002973	1.5533767	up
MPF_LOC101480576.2.3	XM_004574067.1 PREDICTED: Maylandia zebra uncharacterized LOC101480576 (LOC101480576), mRNA	0.030765753	1.8719338	up
MPF_contig_044643		0.01852906	-0.61155987	down

MPF_LOC101482372.2.4	XM_004542967.1 PREDICTED: Maylandia zebra macrophage mannose receptor 1-like (LOC101482372), mRNA	0.012094057	3.995102	up
MPF_LOC101468108.1.2	XM_004559699.1 PREDICTED: Maylandia zebra protein FAM160B1-like (LOC101468108), mRNA	0.02104948	-0.75576776	down
MPF_contig_044390		0.046004083	-1.2094517	down
MPF_contig_013399		0.005249367	-0.70688295	down
MPF_LOC101474121.17.17	XM_004575391.1 PREDICTED: Maylandia zebra stonustoxin subunit beta-like (LOC101474121), mRNA	5.89E-04	4.0112934	up

MPF_contig_028214	XM_004556613.1 PREDICTED: Maylandia zebra calcium/calmodulin-dependent protein kinase type II subunit gamma-like (LOC101474026), transcript variant X10, mRNA	0.04246915	-0.86120844	down
MPF_LOC101477399.1.1	XM_004538348.1 PREDICTED: Maylandia zebra uncharacterized LOC101477399 (LOC101477399), mRNA	0.001031627	2.3188996	up
MPF_LOC100703477.2.2	XM_003456383.1 PREDICTED: Oreochromis niloticus DCN1-like protein 5-like (LOC100703477), mRNA	0.01613487	-0.9895644	down
MPF_LOC100705400.2.2	XP_003441709.1 PREDICTED: hypothetical protein LOC100705400 [Oreochromis niloticus]	0.03078744	1.0269275	up
MPF_LOC100933241.9.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.019318828	3.3618774	up
MPF_LOC101465578.1.2	XM_004538015.1 PREDICTED: Maylandia zebra far upstream element-binding protein 3-like (LOC101465578), mRNA	0.013049964	-0.8107867	down
MPF_LOC101474259.2.2	XM_004541897.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF19B-like (LOC101474259), transcript variant X2, mRNA	0.006673529	2.8181815	up
MPF_LOC101472694.2.4	XM_004542457.1 PREDICTED: Maylandia zebra ephrin type-A receptor 3-like (LOC101472694), transcript variant X2, mRNA	0.001464735	-0.55862236	down
MPF_contig_015342		9.13E-04	2.4605036	up
MPF_LOC100701273.27.44	XP_003444276.1 PREDICTED: NACHT, LRR and PYD domains-containing protein 12-like [Oreochromis niloticus]	0.008428021	2.7458448	up
MPF_LOC100695404.1.1	XM_003448451.1 PREDICTED: Oreochromis niloticus PDZ domain-containing protein GIPC1-like (LOC100695404), mRNA	0.016427044	-1.0032806	down
MPF_LOC101486883.2.2	XM_004552510.1 PREDICTED: Maylandia zebra granulins-like (LOC101486883), transcript variant X2, mRNA	0.00394884	2.2134929	up
MPF_LOC101162897.1.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]	0.00368609	4.23808	up
MPF_LOC101466775.1.1	XM_004543278.1 PREDICTED: Maylandia zebra sulfotransferase family cytosolic 2B member 1-like (LOC101466775), mRNA	0.041324485	-1.1037912	down
MPF_LOC101482220.3.3	XM_004571715.1 PREDICTED: Maylandia zebra h-2 class II histocompatibility antigen gamma chainlike (LOC101482220), mRNA	0.004681449	4.2362013	up
MPF_LOC101485932.1.1	XM_004538480.1 PREDICTED: Maylandia zebra phosphatidylinositol 4-phosphate 5-kinase type-1 beta-like (LOC101485932), transcript variant X2, mRNA	0.009140064	2.1812842	up
MPF_LOC100695994.23.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.03944329	-1.1594162	down
MPF_SELMODRAFT_443953.1.1	XP_002978779.1 hypothetical protein SELMODRAFT_443953 [Selaginella moellendorffii]	0.024193214	-1.1460123	down
MPF_contig_018234		0.044863876	-0.5213485	down
MPF_LOC101486061.1.1	XM_004563154.1 PREDICTED: Maylandia zebra protein FAM199X-like (LOC101486061), transcript variant X1, mRNA	0.027153343	-0.89196867	down
MPF_LOC101481939.1.1	XM_004553518.1 PREDICTED: Maylandia zebra zinc finger CCCH domain-containing protein 15-like (LOC101481939), mRNA	0.023313882	-1.1447916	down
MPF_LOC101486684.1.2	XM_004572189.1 PREDICTED: Maylandia zebra erythropoietin-like (LOC101486684), transcript variant X3, mRNA	0.047651947	-1.0984435	down

MPF_LOC100698096.4.4	XM_003457021.1 PREDICTED: Oreochromis niloticus H/ACA ribonucleoprotein complex subunit 2like protein-like (LOC100698096), mRNA	0.016665542	-1.063992	down
MPF_contig_016131		0.002951977	2.909297	up
MPF_LOC101469708.2.2	XM_004545599.1 PREDICTED: Maylandia zebra transmembrane protein 179-like (LOC101469708), mRNA	0.04242951	-1.0379901	down
MPF_RL37P.1.1	RL37P_RAT (sp|P61515) Putative 60S ribosomal protein L37a OS=Rattus norvegicus GN=Rpl37a-ps1 PE=5 SV=2	0.005802855	3.1592999	up
MPF_contig_003939		0.009991959	1.5477347	up
MPF_MIR142A.1.1	NR_030090.1 Danio rerio microRNA 142a (mir142a), microRNA	0.002183195	4.0363693	up
MPF_LOC100690793.3.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]	0.003551828	2.2757883	up
MPF_SGS4.2.10	SGS4_DROME (sp|Q00725) Salivary glue protein Sgs-4 OS=Drosophila melanogaster GN=Sgs4 PE=2 SV=1	0.020129085	1.4254117	up
MPF_LOC101477280.5.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	6.98E-04	3.839201	up
MPF_LOC101479551.1.1	XM_004555792.1 PREDICTED: Maylandia zebra SEC14-like protein 2-like (LOC101479551), mRNA	0.014269128	1.6865752	up
MPF_AHNK.17.22	[BBH] AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	4.83E-04	4.9614263	up
MPF_LOC101062855.1.1	XM_003970797.1 PREDICTED: Takifugu rubripes polyubiquitin-B-like, transcript variant 2 (LOC101062855), mRNA	0.011953841	-0.40426257	down
MPF_LOC101474370.1.1	XM_004568239.1 PREDICTED: Maylandia zebra mitochondrial glutamate carrier 1-like (LOC101474370), transcript variant X3, mRNA	0.004987546	2.3362894	up
MPF_LOC101479225.2.2	XM_004571532.1 PREDICTED: Maylandia zebra glucose-6-phosphate isomerase-like (LOC101479225), mRNA	0.049222965	-1.3085871	down
MPF_LOC100706657.3.3	XP_003447550.1 PREDICTED: CD48 antigen-like [Oreochromis niloticus]	0.001495702	3.51991	up
MPF_LOC101469586.1.1	XM_004560825.1 PREDICTED: Maylandia zebra striatin-interacting protein 1 homolog (LOC101469586), transcript variant X3, mRNA	0.009151258	-0.8611526	down
MPF_LOC101468502.1.1	XM_004555833.1 PREDICTED: Maylandia zebra copper homeostasis protein cutC homolog (LOC101468502), transcript variant X3, mRNA	0.037923776	-0.50196266	down
MPF_LOC101487738.1.1	XM_004571562.1 PREDICTED: Maylandia zebra aryl hydrocarbon receptor-like (LOC101487738), transcript variant X1, mRNA	0.021990225	-0.9250541	down
MPF_LOC100689746.1.1	XP_003445067.1 PREDICTED: proline-rich protein 5-like [Oreochromis niloticus]	0.047466762	-0.69914675	down
MPF_LOC100704894.10.13	XM_003450635.1 PREDICTED: Oreochromis niloticus glyceraldehyde-3-phosphate dehydrogenaselike (LOC100704894), mRNA	0.006384192	2.7946272	up
MPF_LOC100693135.1.1	XP_003439646.1 PREDICTED: exosome complex component MTR3-like [Oreochromis niloticus]	0.014143591	-0.53008264	down
MPF_LOC101078877.1.1	XP_003976004.1 PREDICTED: mitochondrial 2-oxoglutarate/malate carrier protein-like [Takifugu rubripes]	0.036034927	-0.763577	down
MPF_contig_029689		0.029477285	-0.9607243	down
MPF_LOC100711796.2.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA	0.00248689	2.7711182	up
MPF_contig_032146		0.001865535	3.4228344	up
MPF_LOC101473866.1.1	XM_004539673.1 PREDICTED: Maylandia zebra iroquois-class homeodomain protein IRX-5-like (LOC101473866), mRNA	0.028377142	-0.9599862	down
MPF_LOC101485578.1.1	XM_004539623.1 PREDICTED: Maylandia zebra CD276 antigen-like (LOC101485578), mRNA	0.00237142	2.4913077	up

MPF_LOC101484489.8.10	XM_004548851.1 PREDICTED: Maylandia zebra 14-3-3 protein beta/alpha-A-like (LOC101484489), mRNA	0.010483236	-0.6647124	down
MPF_contig_014852		0.044635	1.4418163	up
MPF_contig_020082		0.007460561	4.4267287	up
MPF_LOC101466982.1.2	XM_004574455.1 PREDICTED: Maylandia zebra pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial-like (LOC101466982), mRNA	0.04721877	-1.3259172	down
MPF_LOC100701946.1.1	XP_003453886.1 PREDICTED: uncharacterized protein KIAA1143 homolog [Oreochromis niloticus]	0.032921147	-0.75571275	down
MPF_LOC100692757.1.1	XM_003457189.1 PREDICTED: Oreochromis niloticus polypeptide N-acetylgalactosaminyltransferase 11-like (LOC100692757), mRNA	0.04372874	-2.0373988	down
MPF_LOC101464182.1.1	XM_004542248.1 PREDICTED: Maylandia zebra 26S protease regulatory subunit 4-like (LOC101464182), mRNA	0.013745132	0.63454056	up
MPF_LOC101466143.5.18	XM_004574840.1 PREDICTED: Maylandia zebra 40S ribosomal protein S18-like (LOC101466143), mRNA	0.03158049	1.8162508	up
MPF_contig_024224		0.003170146	4.853693	up
MPF_MYHM2126-2.1.3	XP_003975582.1 PREDICTED: myosin-7 [Takifugu rubripes]	1.57E-04	3.597402	up
MPF_contig_029610		0.027153343	1.227561	up
MPF_LOC101480826.9.9	XM_004564784.1 PREDICTED: Maylandia zebra ubiquitin-60S ribosomal protein L40-like (LOC101480826), mRNA	0.003333047	-0.7570371	down
MPF_contig_032441		0.01988097	1.978102	up
MPF_LOC101466151.1.1	XM_004575929.1 PREDICTED: Maylandia zebra transcription factor 20-like (LOC101466151), transcript variant X4, mRNA	0.049854334	-0.49611756	down
MPF_LOC100933241.11.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.007546911	-1.5423899	down
MPF_EIF3K.3.3	EIF3K_DANRE (sp|Q567V6) Eukaryotic translation initiation factor 3 subunit K OS=Danio rerio GN=eif3k PE=2 SV=1	0.024629418	2.079353	up
MPF_contig_028781		0.028843079	2.3921137	up
MPF_B2MG.3.10	B2MG_CYPCA (sp|Q03422) Beta-2-microglobulin OS=Cyprinus carpio GN=b2m PE=3 SV=1	6.65E-04	4.112689	up
MPF_LOC101069906.1.1	XP_003969359.1 PREDICTED: tissue factor pathway inhibitor-like [Takifugu rubripes]	0.001790945	2.68599	up
MPF_LOC100712143.1.1	XM_003454540.1 PREDICTED: Oreochromis niloticus metalloproteinase inhibitor 4-like (LOC100712143), mRNA	0.04709241	-0.8243584	down
MPF_LOC101477280.4.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.001206346	3.7916284	up
MPF_contig_040419	XM_004539772.1 PREDICTED: Maylandia zebra bifunctional glutamate/proline--tRNA ligase-like (LOC101475483), transcript variant X1, mRNA	0.039302945	-0.42145827	down
MPF_contig_012860		0.015260316	-1.3336394	down
MPF_contig_004922		0.003892398	2.976838	up
MPF_LOC100711864.1.1	XP_003452941.1 PREDICTED: abhydrolase domain-containing protein 13-like [Oreochromis niloticus]	0.044625193	-0.56877804	down
MPF_contig_028928	XM_004556251.1 PREDICTED: Maylandia zebra anoctamin-1-like (LOC101474501), transcript variant X1, mRNA	0.031621985	2.2673516	up
MPF_HACE1.3.3	[BBH] HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2	0.017651657	2.1440287	up

MPF_LOC101161674.1.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA	0.001464735	3.220993	up
MPF_LOC100693501.1.2	XP_003440491.1 PREDICTED: 3-hydroxyacyl-CoA dehydratase-like [Oreochromis niloticus]	0.046479017	-0.5822163	down
MPF_EIF4A2.1.1	NM_001102893.1 Xenopus (Silurana) tropicalis eukaryotic translation initiation factor 4A2 (eif4a2), mRNA gb|BC135871.1| Xenopus tropicalis hypothetical protein LOC100124955, mRNA (cDNA clone MGC:121826 IMAGE:7637784), complete cds	0.04495993	1.5962806	up
MPF_contig_035601		0.037279557	-1.6868583	down
MPF_contig_018948	WP_006047458.1 hypothetical protein [Burkholderia graminis]	0.001564096	2.9886103	up
MPF_contig_035116	XM_004567038.1 PREDICTED: Maylandia zebra transgelin-like (LOC101476292), transcript variant X1, mRNA	0.006510166	5.355307	up
MPF_LECG.21.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.026502624	4.1054606	up
MPF_HAGOROMO.1.1	XM_003456673.1 PREDICTED: Oreochromis niloticus F-box/WD repeat-containing protein 4-like (LOC100691948), mRNA	0.016250055	-0.9859161	down
MPF_LOC101161574.14.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.002593347	4.4699316	up
MPF_LOC101468278.2.3	XM_004545962.1 PREDICTED: Maylandia zebra tumor protein p53-inducible nuclear protein 2-like (LOC101468278), transcript variant X3, mRNA	0.026679114	3.1703823	up
MPF_contig_045428		0.04215111	-0.6928849	down
MPF_LOC101468208.2.2	XM_004554732.1 PREDICTED: Maylandia zebra eukaryotic translation initiation factor 5-like (LOC101468208), mRNA	0.047293946	0.8646299	up
MPF_LOC101481543.7.7	XM_004550249.1 PREDICTED: Maylandia zebra zinc finger BED domain-containing protein 1-like (LOC101481543), mRNA	1.57E-04	4.270958	up
MPF_LOC101474346.2.2	XM_004540807.1 PREDICTED: Maylandia zebra protein phosphatase 1 regulatory subunit 14B-like (LOC101474346), mRNA	0.041324485	-0.70789486	down
MPF_LOC101470279.4.4	XM_004544778.1 PREDICTED: Maylandia zebra mitochondrial inner membrane organizing system protein 1-like (LOC101470279), transcript variant X2, mRNA	0.016832741	-0.7570791	down
MPF_contig_021317		0.002943268	2.1387203	up
MPF_LOC101481234.4.12	XM_004569866.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2Blike (LOC101481234), mRNA	0.003420229	2.357244	up

MPF_HECTD1.2.4	XM_003451209.1 PREDICTED: Oreochromis niloticus HECT domain containing 1 (HECTD1), mRNA	0.016622968	-0.775794	down
MPF_LECG.27.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.022744646	3.8466096	up
MPF_LOC100700248.5.5	XP_003459295.1 PREDICTED: butyrophilin-like protein 2-like [Oreochromis niloticus]	0.0434344	1.6262441	up
MPF_LOC100703703.2.2	XM_003443559.1 PREDICTED: Oreochromis niloticus ribosome biogenesis regulatory protein homolog (LOC100703703), mRNA	0.02424857	-0.59104395	down
MPF_LOC101467885.1.2	XM_004574029.1 PREDICTED: Maylandia zebra calpain-1 catalytic subunit-like (LOC101467885), transcript variant X1, mRNA	0.005381975	-0.64635754	down
MPF_LOC100488485.6.10	XP_002941723.1 PREDICTED: hypothetical protein LOC100488485 [Xenopus (Silurana) tropicalis]	0.04495993	-0.54324865	down
MPF_contig_048496	XM_004571963.1 PREDICTED: Maylandia zebra neurofilament heavy polypeptide-like (LOC101475636), transcript variant X2, mRNA	0.022590887	-0.97028637	down
MPF_LOC101471756.4.4	XM_004573212.1 PREDICTED: Maylandia zebra trichohyalin-like (LOC101471756), mRNA	0.023023611	-0.5476794	down
MPF_contig_028822		0.035111103	-0.97229767	down
MPF_contig_029207		0.012076636	2.8875623	up

MPF_LOC100702318.5.5	XP_003458375.1 PREDICTED: galectin-9-like [Oreochromis niloticus]	0.002220721	3.5387306	up
MPF_CAL6303_1855.1.3	YP_007136861.1 hypothetical protein Cal6303_1855 [Calothrix sp. PCC 6303]	0.001778002	2.860886	up
MPF_LOC101065219.3.3	XM_003969289.1 PREDICTED: Takifugu rubripes protein S100-A1-like (LOC101065219), mRNA	0.001715593	2.8412173	up
MPF_LOC100704742.1.1	XP_003458221.1 PREDICTED: c-C motif chemokine 2-like [Oreochromis niloticus]	0.042345475	2.0712125	up
MPF_LOC101075367.1.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]	0.002856029	2.46949	up
MPF_CICA.1.1	XP_003200581.1 PREDICTED: hypothetical protein LOC560266 [Danio rerio]	0.00738922	1.1698823	up
MPF_LOC101159291.2.2	XM_004078003.1 PREDICTED: Oryzias latipes sodium/potassium-transporting ATPase subunit alpha-3like (LOC101159291), mRNA	3.60E-04	4.042153	up
MPF_contig_008714		0.003151855	2.8241475	up
MPF_LOC101173086.4.5	XP_004077318.1 PREDICTED: G-protein coupled receptor 4-like [Oryzias latipes]	0.029445808	0.93179935	up
MPF_contig_023224		1.65E-04	3.9644713	up
MPF_LOC101475324.3.5	XM_004570832.1 PREDICTED: Maylandia zebra MOB kinase activator 2-like (LOC101475324), transcript variant X4, mRNA	0.011033013	1.7548437	up
MPF_LOC100696002.1.1	XM_003445297.1 PREDICTED: Oreochromis niloticus carbamoyl-phosphate synthase [ammonia], mitochondrial-like (LOC100696002), mRNA	0.026158698	-0.5561442	down
MPF_contig_009283		0.03554348	2.3222506	up
MPF_LOC100694460.1.2	XM_003437761.1 PREDICTED: Oreochromis niloticus gamma-interferon-inducible lysosomal thiol reductase-like (LOC100694460), mRNA	0.049479105	-0.6891059	down
MPF_contig_045616		0.00170503	3.8673997	up
MPF_LOC100692360.1.1	XM_003449271.1 PREDICTED: Oreochromis niloticus seryl-tRNA synthetase, mitochondrial-like (LOC100692360), mRNA	0.041035186	-0.7287941	down
MPF_LOC100698256.2.2	XM_003454320.1 PREDICTED: Oreochromis niloticus tubulin beta-6 chain-like (LOC100698256), mRNA	0.020129085	1.8254261	up
MPF_LOC100695788.1.1	XP_003437652.1 PREDICTED: ribonuclease P protein subunit p29-like [Oreochromis niloticus]	0.046004508	-0.8758497	down
MPF_contig_028716		0.01829461	2.320643	up
MPF_contig_035342		0.033321362	1.6588507	up
MPF_contig_025434	XM_004558699.1 PREDICTED: Maylandia zebra disco-interacting protein 2 homolog B-A-like (LOC101469003), transcript variant X1, mRNA	0.036837943	-0.6119485	down
MPF_contig_043137		0.008587733	-1.0861783	down
MPF_ADH.1.1	ADH_SULAC (sp|Q4J781) NAD-dependent alcohol dehydrogenase OS=Sulfolobus acidocaldarius (strain ATCC 33909 / DSM 639 / JCM 8929 / NBRC 15157 / NCIMB 11770) GN=adh PE=3 SV=1	0.016034812	-0.7086744	down
MPF_LOC100698082.2.2	XR_134880.1 PREDICTED: Oreochromis niloticus keratin, type I cytoskeletal 13-like (LOC100698082), miscRNA	0.002926805	5.636846	up
MPF_LOC101174720.1.1	XP_004084001.1 PREDICTED: protein Z-dependent protease inhibitor-like [Oryzias latipes]	0.043794505	1.3962855	up
MPF_LOC101155699.2.2	XM_004073699.1 PREDICTED: Oryzias latipes protein S100-A10-like (LOC101155699), mRNA	0.002516571	5.2483907	up
MPF_LOC101077514.3.5	XP_003974477.1 PREDICTED: complement factor H-like [Takifugu rubripes]	0.002376923	4.2732105	up
MPF_LOC100693648.1.1	XM_003456513.1 PREDICTED: Oreochromis niloticus probable methyltransferase C20orf7 homolog, mitochondrial-like (LOC100693648), mRNA	0.002398221	-0.787385	down
MPF_CJ032.1.1	CJ032_DANRE (sp|Q4V8S9) UPF0693 protein C10orf32 homolog OS=Danio rerio GN=si:ch211-67n3.3 PE=3 SV=1	0.022966782	-0.75186056	down
MPF_LOC100705559.1.1	XM_003439386.1 PREDICTED: Oreochromis niloticus dihydrolipoyl dehydrogenase, mitochondriallike (LOC100705559), mRNA	0.035721064	-0.5026541	down

MPF_LOC100709346.1.1	XM_003448170.1 PREDICTED: Oreochromis niloticus baculoviral IAP repeat-containing protein 5.1-Alike (LOC100709346), mRNA	0.036034927	-1.1270522	down
MPF_LOC101474419.1.1	XM_004554493.1 PREDICTED: Maylandia zebra sperm-associated antigen 17-like (LOC101474419), mRNA	0.040316716	-1.7454786	down
MPF_LOC100699721.2.2	XP_003460016.1 PREDICTED: bifunctional protein NCOAT-like, partial [Oreochromis niloticus]	0.00832412	2.6734452	up
MPF_contig_038580		0.042317577	-1.412281	down
MPF_LOC101061679.1.1	XM_003975895.1 PREDICTED: Takifugu rubripes cAMP-responsive element modulator-like (LOC101061679), mRNA	0.015485545	1.960743	up
MPF_LOC101464318.1.2	XM_004575444.1 PREDICTED: Maylandia zebra HLA class II histocompatibility antigen, DR alpha chainlike (LOC101464318), mRNA	0.003943931	2.8671656	up
MPF_LOC100700605.10.27	XM_003458555.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100700605), mRNA	0.005523806	1.8562161	up
MPF_LOC100712299.1.1	XM_003451996.1 PREDICTED: Oreochromis niloticus myoferlin-like (LOC100712299), mRNA	7.93E-04	4.0090528	up
MPF_LOC100690401.2.3	XP_003454006.1 PREDICTED: hypothetical protein LOC100690401 [Oreochromis niloticus]	0.003800863	4.3792787	up
MPF_LOC101466558.2.2	XM_004561006.1 PREDICTED: Maylandia zebra 3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial-like (LOC101466558), transcript variant X2, mRNA	0.045100138	-1.005231	down
MPF_LOC100709891.1.1	XP_003449549.1 PREDICTED: succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial-like [Oreochromis niloticus]	0.03554348	-0.6496711	down
MPF_RL13.2.5	RL13_DANRE (sp|Q90Z10) 60S ribosomal protein L13 OS=Danio rerio GN=rpl13 PE=2 SV=3	0.044792734	1.6137781	up
MPF_contig_047103	XM_004572518.1 PREDICTED: Maylandia zebra collagen alpha-1(I) chain-like (LOC101476419), transcript variant X1, mRNA	0.046252906	-0.95166826	down
MPF_LOC101470279.1.4	XM_004544778.1 PREDICTED: Maylandia zebra mitochondrial inner membrane organizing system protein 1-like (LOC101470279), transcript variant X2, mRNA	0.018603342	-0.74577904	down
MPF_LOC101472257.1.1	XM_004556797.1 PREDICTED: Maylandia zebra pyruvate dehydrogenase [lipoamide] kinase isozyme 2-like (LOC101472257), mRNA	0.035626117	-0.87707806	down
MPF_LOC101478586.2.2	XM_004550792.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 6like (LOC101478586), transcript variant X2, mRNA	0.00237142	2.9760356	up
MPF_contig_027404	XM_004568351.1 PREDICTED: Maylandia zebra protein kinase C beta type-like (LOC101478005), transcript variant X1, mRNA	0.017876474	3.0479813	up
MPF_contig_019917		0.004918171	3.2648008	up
MPF_LOC101156017.1.1	XP_004072239.1 PREDICTED: prostate stem cell antigen-like [Oryzias latipes]	0.015160592	1.2624879	up
MPF_LOC101468983.2.2	XR_191999.1 PREDICTED: Maylandia zebra uncharacterized LOC101468983 (LOC101468983), misc_RNA	0.012856492	1.8094993	up
MPF_AHNAK.4.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]	4.83E-04	5.5112004	up
MPF_LOC101466194.6.9	XM_004565547.1 PREDICTED: Maylandia zebra integrin beta-1-like (LOC101466194), transcript variant X2, mRNA	0.03884524	-0.6263633	down
MPF_LOC101477842.2.4	XM_004575054.1 PREDICTED: Maylandia zebra protein SET-like (LOC101477842), mRNA	0.046272654	-0.5390434	down
MPF_LOC100707140.3.4	XP_003458392.1 PREDICTED: hypothetical protein LOC100707140 [Oreochromis niloticus]	0.002248571	2.158657	up
MPF_LOC101465129.15.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA	0.023434808	-0.51675934	down
MPF_contig_027340		0.003891571	1.9658297	up
MPF_LOC101480926.1.1	XM_004544359.1 PREDICTED: Maylandia zebra survival motor neuron protein 1-like (LOC101480926), mRNA	0.006389125	-0.60840416	down
MPF_contig_037907		0.040892802	1.8208776	up

MPF_contig_037980		0.011953841	3.8879163	up
MPF_LOC101487021.1.1	XM_004540761.1 PREDICTED: Maylandia zebra thrombospondin-1-like (LOC101487021), transcript variant X2, mRNA	0.003892398	4.7555556	up
MPF_AHNK.16.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	5.91E-04	5.244092	up
MPF_LOC101485716.5.12	XM_004572825.1 PREDICTED: Maylandia zebra multivesicular body subunit 12B-like (LOC101485716), mRNA	0.001733547	3.3693595	up
MPF_LOC101467642.1.1	XM_004565102.1 PREDICTED: Maylandia zebra ubiquitin-like-conjugating enzyme ATG10-like (LOC101467642), transcript variant X3, mRNA	0.018603342	-0.5935478	down
MPF_LOC100700648.1.1	XP_003447359.1 PREDICTED: pyruvate dehydrogenase [lipoamide] kinase isozyme 1-like [Oreochromis niloticus]	0.036862258	-0.790782	down
MPF_LOC100697044.1.1	XM_003460170.1 PREDICTED: Oreochromis niloticus myc-induced nuclear antigen-like (LOC100697044), mRNA	0.008636351	-0.6875052	down
MPF_RS13.9.9	RS13_GILMI (sp|Q9DFR6) 40S ribosomal protein S13 OS=Gillichthys mirabilis GN=rps13 PE=2 SV=3	0.011032867	1.425096	up
MPF_LOC101480425.2.3	XM_004539268.1 PREDICTED: Maylandia zebra uncharacterized LOC101480425 (LOC101480425), transcript variant X2, mRNA	0.004120294	2.9301078	up
MPF_LOC101466474.1.1	XM_004562278.1 PREDICTED: Maylandia zebra inactive rhomboid protein 1-like (LOC101466474), transcript variant X3, mRNA	0.044512663	-0.41446447	down
MPF_RSSA.9.9	RSSA_SPAAU (sp|Q4QY71) 40S ribosomal protein SA OS=Sparus aurata GN=rpsa PE=2 SV=2	0.014163161	1.7713059	up
MPF_LOC101477831.3.3	XM_004548827.1 PREDICTED: Maylandia zebra complement C1q subcomponent subunit B-like (LOC101477831), mRNA	0.003146028	4.095808	up
MPF_LOC101478257.1.2	XM_004562938.1 PREDICTED: Maylandia zebra thioredoxin, mitochondrial-like (LOC101478257), mRNA	0.032921147	-0.6317645	down
MPF_ZKSC3.1.1	ZKSC3_HUMAN (sp|Q9BRR0) Zinc finger protein with KRAB and SCAN domains 3 OS=Homo sapiens GN=ZKSCAN3 PE=1 SV=2	0.022970537	-0.53665644	down
MPF_LOC100699307.1.1	XM_003449296.1 PREDICTED: Oreochromis niloticus serine/threonine-protein kinase SIK3 homolog (LOC100699307), mRNA	0.045614492	-0.6656738	down
MPF_LY9.3.3	LY9_HUMAN (sp|Q9HBG7) T-lymphocyte surface antigen Ly-9 OS=Homo sapiens GN=LY9 PE=1 SV=3	0.004987546	3.4805589	up
MPF_LOC101481756.1.2	XM_004554602.1 PREDICTED: Maylandia zebra RING finger protein 122-like (LOC101481756), mRNA	0.030309485	-1.270863	down
MPF_contig_006740		0.030302616	-0.3460999	down
MPF_LOC100706139.1.1	XM_003450227.1 PREDICTED: Oreochromis niloticus kinesin-1 heavy chain-like (LOC100706139), mRNA	0.045928992	-0.72531986	down
MPF_SI_CH211-125E6.5.1.1	XP_001337601.1 PREDICTED: type-2 ice-structuring protein-like [Danio rerio]	0.002285471	2.8875408	up
MPF_LOC100707411.2.2	XM_003458503.1 PREDICTED: Oreochromis niloticus E3 ubiquitin-protein ligase ZNRF2-like (LOC100707411), mRNA	0.001778002	3.795538	up
MPF_LOC101478685.2.2	XM_004553130.1 PREDICTED: Maylandia zebra ras-related protein Rab-8B-like (LOC101478685), mRNA	0.0402451	-0.9711418	down
MPF_LOC100700602.2.2	XP_003457975.1 PREDICTED: hypothetical protein LOC100700602 [Oreochromis niloticus]	0.008381675	3.5175319	up
MPF_LOC101479097.3.3	XM_004541459.1 PREDICTED: Maylandia zebra kinesin-like protein KIF13A-like (LOC101479097), transcript variant X2, mRNA	0.045819294	-0.48528096	down
MPF_LOC101468662.1.1	XM_004548594.1 PREDICTED: Maylandia zebra tripartite motif-containing protein 62-like (LOC101468662), transcript variant X1, mRNA	0.028426884	-1.0163822	down
MPF_LOC101482211.2.2	XM_004547151.1 PREDICTED: Maylandia zebra intracellular hyaluronan-binding protein 4-like (LOC101482211), mRNA	0.023423532	-0.6724076	down
MPF_contig_008271		0.026912019	2.4252048	up

MPF_MMP9.5.5	XM_003448139.1 PREDICTED: Oreochromis niloticus matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA	0.008187216	1.3623886	up
MPF_LIG3.1.1	XP_003453487.1 PREDICTED: DNA ligase 3 [Oreochromis niloticus]	0.027696673	-0.85679716	down
MPF_LOC100705972.2.3	XM_003455172.1 PREDICTED: Oreochromis niloticus ATP synthase subunit O, mitochondrial-like (LOC100705972), mRNA	0.031186622	-1.175806	down
MPF_LOC101469126.1.1	XM_004562729.1 PREDICTED: Maylandia zebra monocarboxylate transporter 13-like (LOC101469126), transcript variant X5, mRNA	0.001055023	3.0851784	up
MPF_LOC100703143.1.2	XP_003441111.1 PREDICTED: PDZ and LIM domain protein 1-like [Oreochromis niloticus]	0.006511546	3.6845596	up
MPF_LOC101486252.1.1	XM_004563697.1 PREDICTED: Maylandia zebra PQ-loop repeat-containing protein 1-like (LOC101486252), transcript variant X2, mRNA	0.045210335	-0.61618847	down
MPF_LOC101163454.2.2	XM_004083663.1 PREDICTED: Oryzias latipes glutaredoxin-related protein 5, mitochondrial-like (LOC101163454), mRNA	0.036705527	-0.8215918	down
MPF_LOC100697494.1.1	XP_003441006.1 PREDICTED: protein CNPPD1-like [Oreochromis niloticus]	0.049991075	-0.7153702	down
MPF_contig_009677		0.004586066	2.6467712	up
MPF_LOC101159473.1.1	XP_004081096.1 PREDICTED: suppressor of tumorigenicity 14 protein-like isoform 1 [Oryzias latipes]	0.044269416	-1.5655646	down
MPF_LOC101484255.1.1	XM_004555723.1 PREDICTED: Maylandia zebra SH2 domain-containing protein 3C-like (LOC101484255), transcript variant X1, mRNA	0.007866101	2.7605717	up
MPF_LOC101484994.1.2	XM_004555447.1 PREDICTED: Maylandia zebra UPF0524 protein C3orf70 homolog A-like (LOC101484994), mRNA	0.001733547	2.8781235	up
MPF_LOC101156898.3.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]	0.002117743	4.2133083	up
MPF_LOC100702758.9.10	XM_003455412.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L27a-like (LOC100702758), mRNA	0.023844074	-0.5185509	down
MPF_contig_004038		0.037981328	1.6198772	up
MPF_LOC100695691.2.2	XM_003455952.1 PREDICTED: Oreochromis niloticus actin-related protein 2/3 complex subunit 1Blike (LOC100695691), mRNA	0.001464735	4.989525	up
MPF_contig_024249		0.013726315	-0.73845905	down
MPF_LOC101475950.3.3	XM_004553845.1 PREDICTED: Maylandia zebra cAMP-specific 3',5'-cyclic phosphodiesterase 4B-like (LOC101475950), transcript variant X3, mRNA	0.024590846	3.3243127	up
MPF_contig_024077		0.044269416	1.0776033	up
MPF_LOC100707655.8.19	XM_003454192.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S6-like (LOC100707655), mRNA	0.019318828	2.2009203	up
MPF_contig_007460		0.049222965	-0.736485	down
MPF_LOC101478322.2.4	XM_004556897.1 PREDICTED: Maylandia zebra capZ-interacting protein-like (LOC101478322), mRNA	0.048314296	-0.82399124	down
MPF_LOC101483451.1.1	XM_004547058.1 PREDICTED: Maylandia zebra fumarylacetoacetate hydrolase domain-containing protein 2-like (LOC101483451), transcript variant X2, mRNA	0.009199617	2.132185	up
MPF_C1QA.2.2	[BBH] C1QA_PIG (sp|Q69DL0) Complement C1q subcomponent subunit A OS=Sus scrofa GN=C1QA PE=2 SV=1	0.002593422	4.330143	up
MPF_contig_014059		0.007460561	1.7101164	up
MPF_contig_032442		0.026520215	2.952764	up
MPF_contig_037846		0.007873528	-0.7469327	down

MPF_LOC100691043.5.5	XM_003457742.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 12-like (LOC100691043), mRNA	8.79E-04	2.6809669	up
MPF_LOC100710259.1.2	XM_003450909.1 PREDICTED: Oreochromis niloticus NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3-like (LOC100710259), mRNA	0.012135304	-0.8619966	down
MPF_LOC100692382.1.1	XM_003455542.1 PREDICTED: Oreochromis niloticus lecithin retinol acyltransferase-like (LOC100692382), mRNA	0.043416996	-0.5701363	down
MPF_RL37A.1.1	RL37A_XENLA (sp|Q7SZB4) 60S ribosomal protein L37a OS=Xenopus laevis GN=rpl37a PE=3 SV=3	0.005387819	3.130146	up
MPF_LOC100708534.1.1	XM_003447507.1 PREDICTED: Oreochromis niloticus myeloid-associated differentiation marker homolog (LOC100708534), mRNA	0.002680828	4.94132	up
MPF_contig_015878		0.029185193	-0.7353172	down
MPF_MAG.1.4	MAG_RAT (sp|P07722) Myelin-associated glycoprotein OS=Rattus norvegicus GN=Mag PE=1 SV=1	1.69E-04	3.359998	up
MPF_LOC101073876.2.2	XM_003978783.1 PREDICTED: Takifugu rubripes uncharacterized LOC101073876 (LOC101073876), mRNA	0.019503621	-0.8783613	down
MPF_contig_036627		0.022762315	-0.99748135	down
MPF_contig_020726		0.012153483	-0.8906956	down
MPF_contig_002148	XM_004541441.1 PREDICTED: Maylandia zebra centrosomal protein of 72 kDa-like (LOC101474536), transcript variant X1, mRNA	0.028789232	-0.5471382	down
MPF_LOC100707046.10.12	XM_003454686.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100707046), mRNA	0.010453924	-0.86166674	down
MPF_LOC100933241.12.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.04136194	-1.0704699	down
MPF_LOC101174682.1.1	XP_004074864.1 PREDICTED: cytosolic purine 5'-nucleotidase-like [Oryzias latipes]	0.013548153	1.7107844	up
MPF_LOC100692664.1.1	XP_003458729.1 PREDICTED: neutrophil cytosol factor 1-like [Oreochromis niloticus]	0.005421654	3.249103	up
MPF_LOC100705244.1.1	XM_003450063.1 PREDICTED: Oreochromis niloticus heme oxygenase 2-like (LOC100705244), mRNA	0.01613487	2.393456	up
MPF_LOC100700248.2.5	XP_003459295.1 PREDICTED: butyrophilin-like protein 2-like [Oreochromis niloticus]	0.016444676	1.7998142	up
MPF_LOC100699383.1.6	XM_003445310.1 PREDICTED: Oreochromis niloticus translationally-controlled tumor protein homolog (LOC100699383), mRNA	0.015184979	-1.3207245	down
MPF_contig_026335		0.006115756	3.46693	up
MPF_contig_034209	XM_003198881.1 PREDICTED: Danio rerio retrotransposable element Tf2 155 kDa protein type 1-like (LOC100535308), mRNA	0.014991251	2.6166582	up
MPF_LOC101473555.2.3	XM_004560383.1 PREDICTED: Maylandia zebra CDP-diacylglycerol--serine O-phosphatidyltransferaselike (LOC101473555), transcript variant X8, mRNA	0.007771755	1.9992012	up
MPF_contig_006465		0.03174563	1.6858044	up
MPF_LOC100705495.2.2	XR_134825.1 PREDICTED: Oreochromis niloticus apoptosis-stimulating of p53 protein 1-like (LOC100705495), miscRNA	0.018216645	-1.4667157	down
MPF_LOC101470894.1.1	XM_004572943.1 PREDICTED: Maylandia zebra exocyst complex component 3-like (LOC101470894), mRNA	0.03322063	-0.40123656	down
MPF_LOC101486559.2.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA	0.001573924	4.9563613	up
MPF_LOC100703996.2.2	XM_003450220.1 PREDICTED: Oreochromis niloticus armadillo repeat-containing protein 4-like (LOC100703996), mRNA	0.011032867	-1.4603214	down
MPF_LOC101486920.1.1	XM_004539290.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12like (LOC101486920), mRNA	0.036345366	-3.0179656	down
MPF_LOC100696381.1.2	XP_003452968.1 PREDICTED: G-protein coupled receptor 161-like [Oreochromis niloticus]	0.026052147	-0.93190503	down

MPF_LOC100701172.1.1	XP_003442116.1 PREDICTED: U11/U12 small nuclear ribonucleoprotein 25 kDa protein-like [Oreochromis niloticus]	0.045422815	1.8067201	up
MPF_LOC101469336.3.3	XM_004566007.1 PREDICTED: Maylandia zebra ras-related protein M-Ras-like (LOC101469336), mRNA	0.003673072	1.6029687	up
MPF_LOC101475205.1.2	XM_004543789.1 PREDICTED: Maylandia zebra lissencephaly-1 homolog (LOC101475205), transcript variant X4, mRNA	0.004853593	-1.1670103	down
MPF_contig_028086		0.010982486	3.9775963	up
MPF_contig_020945	XM_004542601.1 PREDICTED: Maylandia zebra muscleblind-like protein 1-like (LOC101483053), transcript variant X16, mRNA	0.001621344	4.384346	up
MPF_LOC101069688.1.1	XM_003973598.1 PREDICTED: Takifugu rubripes uncharacterized LOC101069688 (LOC101069688), mRNA	0.036862258	-1.2988334	down
MPF_contig_001265	XM_004544289.1 PREDICTED: Maylandia zebra rab11 family-interacting protein 1-like (LOC101463597), transcript variant X1, mRNA	0.007191924	-1.0229282	down
MPF_LOC101486124.4.4	XM_004575749.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12like (LOC101486124), mRNA	0.007585418	3.8474874	up
MPF_contig_024030		0.044863876	1.265913	up
MPF_contig_038692		0.032099064	-1.0758038	down
MPF_MYO1B.1.2	XP_003443378.1 PREDICTED: myosin-Ib isoform 2 [Oreochromis niloticus]	0.021234617	-0.6747865	down
MPF_LOC100706378.1.2	XM_003444576.1 PREDICTED: Oreochromis niloticus thioredoxin-related transmembrane protein 2-Blike (LOC100706378), mRNA	0.04069054	-0.87171745	down
MPF_LOC101477243.1.1	XM_004544896.1 PREDICTED: Maylandia zebra rho guanine nucleotide exchange factor 25-like (LOC101477243), transcript variant X3, mRNA	0.002908227	2.649619	up
MPF_contig_023403		0.011177988	1.4126196	up
MPF_LOC101482220.2.3	XM_004571715.1 PREDICTED: Maylandia zebra h-2 class II histocompatibility antigen gamma chainlike (LOC101482220), mRNA	0.006095142	4.1823044	up
MPF_LOC100696784.1.1	XP_003441680.1 PREDICTED: HHIP-like protein 1-like [Oreochromis niloticus]	0.02171858	2.9656394	up
MPF_LOC101479225.1.2	XM_004571532.1 PREDICTED: Maylandia zebra glucose-6-phosphate isomerase-like (LOC101479225), mRNA	0.046004083	-1.0723876	down
MPF_contig_036894		0.047009382	-0.6402244	down
MPF_LOC101170487.4.4	XM_004085086.1 PREDICTED: Oryzias latipes low-density lipoprotein receptor 2-like (LOC101170487), mRNA	3.57E-04	2.8749757	up
MPF_contig_024095		0.012171867	1.2039422	up
MPF_contig_032239		4.83E-04	3.6869204	up
MPF_contig_017097		2.92E-04	4.011688	up
MPF_LOC101485593.1.1	XM_004543054.1 PREDICTED: Maylandia zebra protein FAM65A-like (LOC101485593), transcript variant X2, mRNA	0.017736377	-0.76550573	down
MPF_contig_025403		0.045422815	-0.64916843	down
MPF_LOC101479522.1.2	XM_004547622.1 PREDICTED: Maylandia zebra acid-sensing ion channel 1-like (LOC101479522), transcript variant X5, mRNA	0.004160123	3.4780383	up
MPF_LOC101064038.1.1	XP_003971568.1 PREDICTED: methylmalonyl-CoA mutase, mitochondrial-like [Takifugu rubripes]	0.045389522	-0.6295395	down
MPF_LOC100690793.2.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]	0.002230029	5.234599	up
MPF_LOC101480396.1.1	XM_004552665.1 PREDICTED: Maylandia zebra 5'-AMP-activated protein kinase subunit gamma-2like (LOC101480396), transcript variant X2, mRNA	0.002061126	2.4472153	up
MPF_LOC101468488.3.7	XM_004552241.1 PREDICTED: Maylandia zebra 40S ribosomal protein S11-like (LOC101468488), mRNA	0.008877138	-0.85719115	down

MPF_contig_006069		0.002546	2.6688447	up
MPF_LOC101167402.1.2	XM_004080364.1 PREDICTED: Oryzias latipes uncharacterized LOC101167402 (LOC101167402), mRNA	0.008823011	-1.0755253	down
MPF_contig_015875		0.00237142	3.6729116	up
MPF_LOC100695994.26.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.04246915	-0.9137411	down
MPF_contig_007959		0.015664274	2.2230444	up
MPF_contig_033424		2.92E-04	5.977249	up
MPF_contig_035511	XM_004558926.1 PREDICTED: Maylandia zebra ketohexokinase-like (LOC101480218), transcript variant X3, mRNA	0.00237142	3.2283397	up
MPF_LOC101486605.1.3	XM_004551948.1 PREDICTED: Maylandia zebra protein CDV3 homolog (LOC101486605), transcript variant X2, mRNA	0.011699507	-0.6848984	down
MPF_LOC100701712.1.1	XM_003441390.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100701712 (LOC100701712), mRNA	0.037279557	2.2479064	up
MPF_LOC100697541.1.1	XP_003452659.1 PREDICTED: ADP-ribosylation factor GTPase-activating protein 2-like [Oreochromis niloticus]	0.035139468	-0.4742975	down
MPF_LOC101477532.1.1	XM_004569581.1 PREDICTED: Maylandia zebra claudin-4-like (LOC101477532), mRNA	0.047441483	-1.0919728	down
MPF_LOC100702236.1.1	XP_003459601.1 PREDICTED: hypothetical protein LOC100702236 [Oreochromis niloticus]	0.049762387	-0.6421943	down
MPF_LOC101476232.1.1	XM_004574138.1 PREDICTED: Maylandia zebra bone morphogenetic protein 7-like (LOC101476232), mRNA	0.029695949	-1.0462871	down

MPF_contig_036677	XM_004573888.1 PREDICTED: Maylandia zebra c-Maf-inducing protein-like (LOC101478585), transcript variant X3, mRNA	0.02712629	-0.5631184	down
MPF_LOC101468583.4.7	XM_004576296.1 PREDICTED: Maylandia zebra uncharacterized LOC101468583 (LOC101468583), mRNA	0.02299974	1.9723921	up
MPF_LOC101066134.1.1	XP_003970138.1 PREDICTED: magnesium transporter protein 1-like [Takifugu rubripes]	0.007866101	1.7152531	up
MPF_CD63.1.2	NM_001124496.1 Oncorhynchus mykiss Cd63 antigen (cd63), mRNA gb|AY593998.1| Oncorhynchus mykiss CD63 (CD63) mRNA, complete cds	8.01E-04	3.3872905	up
MPF_LOC100119490.1.1	XP_001603259.2 PREDICTED: hypothetical protein LOC100119490 [Nasonia vitripennis]	0.031447295	2.5882547	up
MPF_LOC101471492.3.3	XM_004559612.1 PREDICTED: Maylandia zebra rab11 family-interacting protein 2-like (LOC101471492), mRNA	0.031050768	-0.660162	down
MPF_LOC100685053.1.1	XP_003434657.1 PREDICTED: polyubiquitin-like [Canis lupus familiaris]	0.041324485	-0.43234065	down
MPF_LOC101471101.1.1	XM_004557599.1 PREDICTED: Maylandia zebra X-ray repair cross-complementing protein 5-like (LOC101471101), mRNA	0.027563581	-0.68928385	down
MPF_contig_035918		0.001937971	2.720636	up
MPF_LOC100769042.1.1	XP_003512927.1 PREDICTED: hypothetical protein LOC100769042 [Cricetulus griseus]	0.024629418	-0.96110773	down
MPF_LOC101466239.3.3	XM_004550939.1 PREDICTED: Maylandia zebra apolipoprotein Eb-like (LOC101466239), mRNA	0.008623262	4.3095737	up
MPF_LOC101482968.2.4	XM_004567436.1 PREDICTED: Maylandia zebra junctional adhesion molecule C-like (LOC101482968), mRNA	0.04093185	-0.91310495	down
MPF_LOC100534470.1.1	XM_003441599.1 PREDICTED: Oreochromis niloticus friend leukemia integration 1, transcript variant 2 (LOC100534470), mRNA	0.049182035	1.4182882	up
MPF_LOC101484769.1.1	XM_004571907.1 PREDICTED: Maylandia zebra transcription factor MafB-like (LOC101484769), mRNA	0.015485545	3.7084644	up
MPF_LOC100696246.4.5	XM_003460438.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100696246 (LOC100696246), partial mRNA	0.033269685	2.334446	up

MPF_LOC101174297.1.1	XP_004078597.1 PREDICTED: zinc finger protein 850-like [Oryzias latipes]	0.018118626	-1.0765672	down
MPF_LOC100691286.1.1	XM_003452172.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100691286 (LOC100691286), mRNA	0.022749815	2.0211833	up
MPF_LOC100697017.2.2	XM_003455478.1 PREDICTED: Oreochromis niloticus ubiquitin-40S ribosomal protein S27a-like (LOC100697017), mRNA	0.02011402	-0.41168216	down
MPF_contig_015308		0.028966445	-0.5018	down
MPF_ZG57.6.12	ZG57_XENLA (sp|P18729) Gastrula zinc finger protein XlCGF57.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.03719966	-0.46087167	down
MPF_LOC100707820.1.1	XP_003448547.1 PREDICTED: E3 ubiquitin-protein ligase HECTD3-like [Oreochromis niloticus]	0.035858028	-0.7559948	down
MPF_LOC101479573.1.2	XM_004565228.1 PREDICTED: Maylandia zebra lysosomal acid lipase/cholesteryl ester hydrolase-like (LOC101479573), mRNA	0.034609396	1.7061248	up
MPF_LOC101481611.1.2	XM_004544911.1 PREDICTED: Maylandia zebra elongation factor Ts, mitochondrial-like (LOC101481611), mRNA	0.003227499	-0.6572094	down
MPF_LOC100691160.2.2	XP_003459991.1 PREDICTED: 5-hydroxytryptamine receptor 3A-like [Oreochromis niloticus]	0.00891462	1.8370266	up
MPF_contig_045057		0.047854975	-0.9707742	down
MPF_LOC100709074.1.1	XM_003448084.1 PREDICTED: Oreochromis niloticus T-complex protein 1 subunit beta-like (LOC100709074), mRNA	4.83E-04	3.482873	up
MPF_ANXA1.1.2	NP_001098295.1 annexin max3 [Oryzias latipes]	0.001206346	2.1733017	up
MPF_LOC100697025.1.1	XM_003457097.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100697025 (LOC100697025), mRNA	0.015705863	2.3300025	up
MPF_LOC101477695.1.9	XM_004564867.1 PREDICTED: Maylandia zebra 60S ribosomal protein L18a-like (LOC101477695), transcript variant X2, mRNA	0.007014755	1.5702882	up
MPF_LOC101466911.1.1	XM_004557020.1 PREDICTED: Maylandia zebra sodium/hydrogen exchanger 7-like (LOC101466911), transcript variant X1, mRNA	0.02477162	-0.58205074	down
MPF_contig_045551		0.049325388	1.4054813	up
MPF_LOC101169293.6.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.002909877	1.7671547	up
MPF_LOC569742.1.1	XP_698239.5 PREDICTED: hypothetical protein LOC569742 [Danio rerio]	0.044094026	1.573303	up
MPF_PHUM_PHUM529360.2.2	XP_002431439.1 ngd5/osm-6/ift52, putative [Pediculus humanus corporis]	0.010954781	2.8763788	up
MPF_LOC101486883.1.2	XM_004552510.1 PREDICTED: Maylandia zebra granulins-like (LOC101486883), transcript variant X2, mRNA	0.009509102	2.0415978	up
MPF_LOC101487672.1.1	XM_004557853.1 PREDICTED: Maylandia zebra Fanconi anemia group B protein-like (LOC101487672), mRNA	0.03720423	-0.62149143	down
MPF_contig_010065		0.006428036	3.264686	up
MPF_ENPP1.1.2	XM_003446358.1 PREDICTED: Oreochromis niloticus ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA	3.53E-04	4.1682243	up
MPF_LOC101468606.1.3	XM_004561834.1 PREDICTED: Maylandia zebra protein PBDC1-like (LOC101468606), transcript variant X2, mRNA	0.001348924	-0.56095594	down
MPF_LOC101464439.2.2	XM_004539111.1 PREDICTED: Maylandia zebra CD97 antigen-like (LOC101464439), transcript variant X2, mRNA	0.04848525	1.2809596	up
MPF_LOC101484456.9.9	XM_004541102.1 PREDICTED: Maylandia zebra 60S ribosomal protein L26-like (LOC101484456), transcript variant X2, mRNA	0.03554348	-0.764019	down
MPF_LOC101470279.3.4	XM_004544778.1 PREDICTED: Maylandia zebra mitochondrial inner membrane organizing system protein 1-like (LOC101470279), transcript variant X2, mRNA	0.025398446	-0.71505255	down

MPF_LOC101469688.2.4	XM_004540788.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 18.2like (LOC101469688), mRNA	0.008428021	2.3247528	up
MPF_LOC101163263.1.1	XP_004075057.1 PREDICTED: galactose-1-phosphate uridylyltransferase-like [Oryzias latipes]	0.032422595	-0.6419601	down
MPF_contig_030749		0.0015351	3.397633	up
MPF_UBC.1.5	UBC_RAT (sp|Q63429) Polyubiquitin-C OS=Rattus norvegicus GN=Ubc PE=1 SV=1	0.004337069	-0.43835926	down
MPF_LOC101465148.1.1	XM_004569455.1 PREDICTED: Maylandia zebra brain acid soluble protein 1-like (LOC101465148), transcript variant X1, mRNA	0.002677907	4.7146225	up

MPF_LOC100701544.8.20	XM_003444229.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 3-like (LOC100701544), mRNA	0.01105963	3.221633	up
MPF_LOC100692629.1.1	XM_003448362.1 PREDICTED: Oreochromis niloticus complement C1q subcomponent subunit C-like, transcript variant 2 (LOC100692629), mRNA	0.002908227	4.150023	up
MPF_UBR4.2.2	XM_003444861.1 PREDICTED: Oreochromis niloticus ubiquitin protein ligase E3 component nrecognin 4 (UBR4), mRNA	0.003891571	-0.67508125	down
MPF_contig_019847		0.02877205	1.2552676	up
MPF_LOC101476819.3.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0.035689894	1.6975412	up
MPF_LOC100696885.2.2	XM_003446045.1 PREDICTED: Oreochromis niloticus C-type lectin domain family 10 member A-like (LOC100696885), mRNA	0.004685761	3.9063716	up
MPF_LOC100698764.2.2	XM_003449126.1 PREDICTED: Oreochromis niloticus probable cation-transporting ATPase 13A2-like (LOC100698764), mRNA	0.041065946	-0.4891415	down
MPF_LOC100694528.1.1	XP_003452879.1 PREDICTED: probable alpha-ketoglutarate-dependent dioxygenase ABH7-like [Oreochromis niloticus]	0.02788023	-0.8421698	down
MPF_contig_020594		0.037868377	-0.49601552	down
MPF_LOC101469933.1.1	XM_004575028.1 PREDICTED: Maylandia zebra zinc finger protein 578-like (LOC101469933), transcript variant X2, mRNA	0.013305112	-0.58443075	down
MPF_LOC101465079.2.2	XM_004551108.1 PREDICTED: Maylandia zebra basal cell adhesion molecule-like (LOC101465079), mRNA	1.57E-04	3.981815	up
MPF_LOC101466869.1.3	XM_004570894.1 PREDICTED: Maylandia zebra KRR1 small subunit processome component homolog (LOC101466869), mRNA	0.030765753	-0.8105851	down
MPF_contig_015478		0.007771755	3.2214813	up
MPF_LOC101483789.1.1	XM_004555262.1 PREDICTED: Maylandia zebra protein SOGA2-like (LOC101483789), transcript variant X4, mRNA	0.035858028	-1.042934	down
MPF_LOC101463710.1.1	XM_004570537.1 PREDICTED: Maylandia zebra transcription initiation factor IIB-like (LOC101463710), mRNA	0.028034749	-0.6722612	down
MPF_LOC100695799.6.7	XM_003460096.1 PREDICTED: Oreochromis niloticus leukocyte elastase inhibitor-like (LOC100695799), mRNA	0.006238447	-1.3011484	down
MPF_LOC101477400.4.4	XM_004538536.1 PREDICTED: Maylandia zebra cyclin-G2-like (LOC101477400), mRNA	0.02496145	-0.96425146	down
MPF_LOC101465647.1.1	XM_004550937.1 PREDICTED: Maylandia zebra apolipoprotein A-I-like (LOC101465647), mRNA	0.003165984	3.3362777	up
MPF_CD276.3.9	CD276_XENLA (sp|Q68EV1) CD276 antigen homolog OS=Xenopus laevis GN=cd276 PE=2 SV=1	0.001555588	2.4782667	up
MPF_LOC100697750.1.3	XM_003459604.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 14-like (LOC100697750), mRNA	0.001674232	4.0741096	up
MPF_LOC101479127.1.1	XM_004548455.1 PREDICTED: Maylandia zebra integrin-alpha FG-GAP repeat-containing protein 2like (LOC101479127), mRNA	0.048455328	-0.4437637	down
MPF_LOC101466968.1.1	XM_004549139.1 PREDICTED: Maylandia zebra cleft lip and palate transmembrane protein 1-like protein-like (LOC101466968), transcript variant X1, mRNA	0.013707273	-0.8994832	down

MPF_LEG8.1.2	NP_001133778.1 Galectin-8 [Salmo salar]	0.026520215	-0.62551355	down
MPF_LOC101469240.1.1	XM_004544118.1 PREDICTED: Maylandia zebra charged multivesicular body protein 7-like (LOC101469240), mRNA	0.03230088	-0.46672148	down
MPF_LOC101471553.1.1	XM_004572678.1 PREDICTED: Maylandia zebra protein capicua homolog (LOC101471553), transcript variant X4, mRNA	0.001566779	1.9323053	up
MPF_LOC101482450.2.2	XM_004556283.1 PREDICTED: Maylandia zebra putative tRNA (cytidine(32)/guanosine(34)-2'-O)methyltransferase-like (LOC101482450), mRNA	0.047009382	-0.71355057	down
MPF_LOC100691105.1.2	XP_003449231.1 PREDICTED: cytochrome c oxidase subunit 8B, mitochondrial-like [Oreochromis niloticus]	0.002546	3.7023592	up
MPF_LOC100700881.1.1	XP_003439170.1 PREDICTED: polyglutamine-binding protein 1-like [Oreochromis niloticus]	0.03554348	-0.82929516	down
MPF_LOC101169532.9.45	XP_004070110.1 PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Oryzias latipes]	0.03554348	0.9280138	up
MPF_CFAH.8.15	CFAH_BOVIN (sp|Q28085) Complement factor H OS=Bos taurus GN=CFH PE=1 SV=3	0.004495184	4.1804576	up
MPF_LOC101484951.3.3	XM_004546887.1 PREDICTED: Maylandia zebra myosin regulatory light chain 2, smooth muscle minor isoform-like (LOC101484951), mRNA	0.018591234	1.7341512	up
MPF_LOC101475776.4.7	XM_004539154.1 PREDICTED: Maylandia zebra ATP synthase subunit d, mitochondrial-like (LOC101475776), transcript variant X2, mRNA	0.006673529	-0.7890701	down
MPF_contig_025452		0.001464735	2.3450875	up
MPF_LOC101472043.8.14	XM_004573789.1 PREDICTED: Maylandia zebra tight junction-associated protein 1-like (LOC101472043), transcript variant X4, mRNA	0.041065946	2.7496033	up
MPF_contig_037474		0.010403333	1.019381	up
MPF_LOC101475253.3.3	XM_004551716.1 PREDICTED: Maylandia zebra apoptosis-stimulating of p53 protein 2-like (LOC101475253), transcript variant X2, mRNA	0.022809107	-0.45598987	down
MPF_contig_024281		0.015695732	-0.8495569	down
MPF_MXAN_5876.1.1	YP_634013.1 hypothetical protein MXAN_5876 [Myxococcus xanthus DK 1622]	2.84E-04	2.2948556	up
MPF_contig_011640		0.001529747	4.7599726	up
MPF_LOC101473892.1.1	XM_004569569.1 PREDICTED: Maylandia zebra transforming growth factor beta-1-like (LOC101473892), transcript variant X2, mRNA	0.001529747	3.9677536	up
MPF_LOC101474901.3.6	XM_004565653.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101474901), mRNA	0.01036082	2.9697804	up
MPF_LOC101158032.2.2	XM_004073072.1 PREDICTED: Oryzias latipes ubiquitin-conjugating enzyme E2 A-like, transcript variant 1 (LOC101158032), mRNA	0.049222965	-0.8348803	down
MPF_LOC101466169.1.1	XM_004558785.1 PREDICTED: Maylandia zebra formin-like protein 3-like (LOC101466169), transcript variant X2, mRNA	0.035689894	2.195868	up
MPF_LOC101062526.1.1	XP_003962815.1 PREDICTED: d-2-hydroxyglutarate dehydrogenase, mitochondrial-like [Takifugu rubripes]	0.003140961	-0.8720111	down
MPF_LOC100706528.2.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0.007945137	-1.0227757	down
MPF_contig_018156		0.038214285	-0.38975054	down
MPF_LOC101068670.1.1	XM_003961269.1 PREDICTED: Takifugu rubripes transcription elongation factor B polypeptide 2-like (LOC101068670), mRNA	0.036862258	1.7631779	up
MPF_LOC100696360.1.3	XP_003446837.1 PREDICTED: signal-induced proliferation-associated 1-like protein 2-like [Oreochromis niloticus]	0.001464735	2.59338	up
MPF_contig_027915	XM_004568424.1 PREDICTED: Maylandia zebra cytochrome P450 2K3-like (LOC101476301), transcript variant X1, mRNA	0.001009901	2.3479009	up

MPF_contig_017451		0.035858028	-1.6508975	down
MPF_LOC101167345.32.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA	0.004400212	3.3417048	up
MPF_contig_019843		0.004094244	0.99464464	up
MPF_LOC101480355.1.1	XM_004569508.1 PREDICTED: Maylandia zebra crystallin J1C-like (LOC101480355), mRNA	0.04204296	2.7230344	up
MPF_LOC100692372.1.1	XM_003453719.1 PREDICTED: Oreochromis niloticus serine/threonine/tyrosine-interacting-like protein 1-like (LOC100692372), mRNA	0.036837943	1.055768	up
MPF_LOC101480702.3.4	XM_004557634.1 PREDICTED: Maylandia zebra mitogen-activated protein kinase 8B-like (LOC101480702), mRNA	0.003779727	2.41828	up
MPF_LOC101478535.2.2	XM_004540728.1 PREDICTED: Maylandia zebra latent-transforming growth factor beta-binding protein 2-like (LOC101478535), mRNA	0.001649342	3.2278662	up
MPF_LOC101464586.2.2	XM_004571741.1 PREDICTED: Maylandia zebra tensin-3-like (LOC101464586), transcript variant X3, mRNA	3.86E-04	1.7776022	up
MPF_LOC101487230.3.3	XM_004568550.1 PREDICTED: Maylandia zebra pre-B-cell leukemia transcription factor 2-like (LOC101487230), mRNA	0.005032116	2.7520518	up
MPF_LOC101476997.1.2	XM_004552000.1 PREDICTED: Maylandia zebra microtubule-associated protein futsch-like (LOC101476997), mRNA	0.006908079	-1.5804	down
MPF_contig_043149		0.03554348	-0.78722095	down
MPF_contig_003919		0.03616174	-0.6745243	down
MPF_LOC101476475.1.1	XM_004562669.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 3-like (LOC101476475), mRNA	0.00209402	6.0633364	up
MPF_LECG.5.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.002104431	2.8874512	up
MPF_LOC101480885.1.1	XM_004553596.1 PREDICTED: Maylandia zebra probable E3 SUMO-protein ligase RNF212-like (LOC101480885), transcript variant X2, mRNA	0.044863876	-0.65183073	down
MPF_LOC101487747.1.2	XM_004573537.1 PREDICTED: Maylandia zebra membrane-spanning 4-domains subfamily A member 15-like (LOC101487747), transcript variant X3, mRNA	0.007230636	3.3178666	up
MPF_LOC101472370.1.1	XM_004538428.1 PREDICTED: Maylandia zebra gelsolin-like (LOC101472370), transcript variant X2, mRNA	0.003146028	4.074353	up
MPF_contig_047566		0.040898368	1.7220868	up
MPF_LOC100698899.1.1	XM_003457691.1 PREDICTED: Oreochromis niloticus protein PAT1 homolog 1-like (LOC100698899), mRNA	0.045422815	-1.2663393	down
MPF_LOC101487706.1.1	XM_004565535.1 PREDICTED: Maylandia zebra cAMP-responsive element modulator-like (LOC101487706), transcript variant X2, mRNA	0.016444676	1.9416289	up
MPF_contig_024757		0.019377887	-0.97866917	down
MPF_contig_028429		0.001031627	3.4180324	up
MPF_LOC100711656.2.2	XP_003446481.1 PREDICTED: cytosolic endo-beta-N-acetylglucosaminidase-like [Oreochromis niloticus]	0.044635	1.1878762	up
MPF_LOC101079502.1.2	XM_003962427.1 PREDICTED: Takifugu rubripes kunitz-type protease inhibitor 1-like (LOC101079502), mRNA	0.049876817	-0.6234789	down
MPF_LOC101158287.1.1	XP_004073601.1 PREDICTED: iduronate 2-sulfatase-like [Oryzias latipes]	0.021990225	-0.67955357	down
MPF_PRG4.3.4	PRG4_MOUSE (sp|Q9JM99) Proteoglycan 4 OS=Mus musculus GN=Prg4 PE=1 SV=2	0.010552216	2.2917278	up
MPF_HSD17B8.1.1	XM_003457993.1 PREDICTED: Oreochromis niloticus 17-beta hydroxysteroid dehydrogenase type 8 (HSD17B8), mRNA	0.002179556	-0.63911146	down

MPF_contig_002650	XM_004079020.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 1 (LOC101161674), mRNA	0.001159374	3.3286457	up
MPF_LOC101466590.1.1	XM_004569012.1 PREDICTED: Maylandia zebra partner and localizer of BRCA2-like (LOC101466590), transcript variant X5, mRNA	0.01113301	1.3783514	up
MPF_contig_022248		0.007866101	-0.6667261	down
MPF_contig_043239		0.039148536	-0.75447327	down
MPF_LOC101163218.1.1	XP_004083710.1 PREDICTED: integrator complex subunit 9-like [Oryzias latipes]	0.046004083	2.2511659	up
MPF_contig_030303		0.02580533	1.1947813	up
MPF_contig_033809		0.02255319	-1.5842447	down
MPF_contig_000796	XM_004539264.1 PREDICTED: Maylandia zebra alpha-1,6-mannosylglycoprotein 6-beta-Nacetylglucosaminyltransferase B-like (LOC101479752), transcript variant X1, mRNA	0.015485545	-0.6198015	down
MPF_LOC101480291.1.2	XM_004550897.1 PREDICTED: Maylandia zebra platelet-activating factor acetylhydrolase IB subunit gamma-like (LOC101480291), mRNA	0.010982486	-0.58374685	down
MPF_LOC100696287.1.2	XP_003450735.1 PREDICTED: C-type lectin domain family 9 member A-like isoform 1 [Oreochromis niloticus]	0.004883999	4.370824	up
MPF_LOC101169293.1.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.001881666	2.4346745	up
MPF_contig_014694		0.039148536	0.671083	up
MPF_LOC101477400.1.4	XM_004538536.1 PREDICTED: Maylandia zebra cyclin-G2-like (LOC101477400), mRNA	0.009977766	-1.4508959	down
MPF_LOC101485532.1.1	XM_004573748.1 PREDICTED: Maylandia zebra nuclear receptor-interacting protein 2-like (LOC101485532), mRNA	0.021014832	-1.3947501	down
MPF_LOC100702771.1.1	XP_003459231.1 PREDICTED: WD repeat-containing protein 78-like [Oreochromis niloticus]	0.046608854	-1.3840613	down
MPF_LOC101469089.3.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA	0.024406986	1.3984479	up
MPF_contig_027163		0.004282251	2.8222635	up

MPF_FZD6.5.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440 IMAGE:6971142), complete cds	0.026934538	2.709488	up
MPF_LOC100711086.1.1	XP_003459625.1 PREDICTED: tripartite motif-containing protein 62-like [Oreochromis niloticus]	0.02861339	-1.0034733	down
MPF_LOC101075919.1.1	XP_003972255.1 PREDICTED: protein dpy-30 homolog [Takifugu rubripes]	0.023717664	-1.1748981	down
MPF_contig_032831		0.004160123	3.2350297	up
MPF_LOC101482059.1.3	XM_004563140.1 PREDICTED: Maylandia zebra mitogen-activated protein kinase kinase kinase kinase 4-like (LOC101482059), transcript variant X2, mRNA	0.00394884	2.6881347	up
MPF_LOC101474833.3.3	XM_004570025.1 PREDICTED: Maylandia zebra bcl-2-like protein 11-like (LOC101474833), mRNA	0.007369091	2.7896094	up
MPF_LOC100705069.1.1	XP_003447626.1 PREDICTED: shootin-1-like [Oreochromis niloticus]	9.52E-04	3.4394193	up
MPF_contig_034792		0.004356874	2.0856318	up
MPF_LOC101483357.1.1	XM_004573344.1 PREDICTED: Maylandia zebra transgelin-like (LOC101483357), mRNA	0.001417114	3.5613363	up
MPF_BRAFLDRAFT_96790.1.1	XP_002595816.1 hypothetical protein BRAFLDRAFT_96790 [Branchiostoma floridae]	0.046252906	-0.6474166	down
MPF_LOC101483666.3.3	XM_004550438.1 PREDICTED: Maylandia zebra TATA box-binding protein-associated factor RNA polymerase I subunit A-like (LOC101483666), transcript variant X3, mRNA	0.016034812	2.6213248	up

MPF_LOC100700712.2.3	XP_003440431.1 PREDICTED: hypothetical protein LOC100700712 [Oreochromis niloticus]	0.003378735	3.6054807	up
MPF_LOC101477458.1.1	XM_004549361.1 PREDICTED: Maylandia zebra probable E3 ubiquitin-protein ligase HERC3-like (LOC101477458), transcript variant X1, mRNA	0.012803177	1.6689639	up
MPF_LOC100706528.1.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0.003840653	-1.1121497	down
MPF_LOC100702519.1.1	XM_003441393.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702519), mRNA	0.005421654	4.4075646	up
MPF_contig_036796		0.012715197	-0.8966818	down
MPF_LOC100555635.1.1	XP_003229374.1 PREDICTED: uncharacterized protein C14orf93-like [Anolis carolinensis]	0.006498309	1.9238107	up
MPF_LOC101473755.3.3	XM_004564853.1 PREDICTED: Maylandia zebra CCR4-NOT transcription complex subunit 2-like (LOC101473755), transcript variant X2, mRNA	0.001865535	2.3675117	up
MPF_LOC100702817.1.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	3.97E-04	5.086316	up
MPF_LOC100691671.1.1	XM_003454380.1 PREDICTED: Oreochromis niloticus 3-hydroxyisobutyrate dehydrogenase, mitochondrial-like (LOC100691671), mRNA	0.044876385	-0.7164275	down
MPF_LOC100693237.1.1	XM_003442623.1 PREDICTED: Oreochromis niloticus catechol O-methyltransferase-like (LOC100693237), mRNA	6.83E-04	3.193484	up
MPF_LOC101473182.1.3	XM_004566836.1 PREDICTED: Maylandia zebra sialoadhesin-like (LOC101473182), transcript variant X2, mRNA	3.74E-04	3.9706326	up
MPF_LOC100701273.12.44	XM_003444228.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 12-like (LOC100701273), mRNA	0.014163161	2.6639004	up
MPF_LOC100706875.1.1	XP_003458154.1 PREDICTED: transmembrane protein 129-like [Oreochromis niloticus]	0.027563581	-0.7675881	down
MPF_LOC100698726.1.1	XP_003460290.1 PREDICTED: hypothetical protein LOC100698726 [Oreochromis niloticus]	0.032160897	4.8053684	up
MPF_LOC101479305.2.6	XM_004546110.1 PREDICTED: Maylandia zebra cytosolic sulfotransferase 3-like (LOC101479305), transcript variant X2, mRNA	0.004596975	1.3914256	up
MPF_LOC101467496.2.4	XM_004556127.1 PREDICTED: Maylandia zebra cytochrome c oxidase subunit 5B, mitochondrial-like (LOC101467496), mRNA	0.027713144	-0.9130888	down
MPF_contig_020368	XM_004550291.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101467183), transcript variant X2, mRNA	8.44E-04	3.1824827	up
MPF_LOC101486209.1.4	XM_004551098.1 PREDICTED: Maylandia zebra uncharacterized LOC101486209 (LOC101486209), mRNA	0.001721078	4.642376	up
MPF_LOC100699757.1.2	XP_003449595.1 PREDICTED: leucine-rich repeat and calponin homology domain-containing protein 1-like [Oreochromis niloticus]	0.020464122	-0.36026293	down
MPF_LOC100753274.1.1	XP_003496316.1 PREDICTED: hypothetical protein LOC100753274 [Cricetulus griseus]	0.047140256	-1.1386461	down
MPF_LOC101464936.1.1	XM_004541956.1 PREDICTED: Maylandia zebra sex comb on midleg-like protein 4-like (LOC101464936), transcript variant X3, mRNA	0.006389125	1.8882964	up
MPF_RNA45S5.4.4	NR_046235.1 Homo sapiens RNA, 45S pre-ribosomal 5 (RNA45S5), ribosomal RNA	0.046671156	-0.5576686	down
MPF_contig_044271		0.036862258	-0.76281834	down
MPF_LOC101468855.3.3	XM_004569017.1 PREDICTED: Maylandia zebra protein tweety homolog 3-like (LOC101468855), transcript variant X1, mRNA	0.002620848	2.8350728	up
MPF_LOC101080012.1.1	XM_003977798.1 PREDICTED: Takifugu rubripes CDP-diacylglycerol--serine Ophosphatidyltransferase-like (LOC101080012), mRNA	0.010532966	1.825674	up
MPF_contig_009983		0.011847384	1.2342501	up
MPF_TNR1B.1.1	[BBH] TNR1B_MOUSE (sp|P25119) Tumor necrosis factor receptor superfamily member 1B OS=Mus musculus GN=Tnfrsf1b PE=2 SV=1	0.001231902	4.5056176	up

MPF_LOC101487243.1.3	XM_004570967.1 PREDICTED: Maylandia zebra pleckstrin homology domain-containing family M member 2-like (LOC101487243), transcript variant X2, mRNA	0.012755489	1.5416244	up
MPF_LECE.1.1	LECE_HELCR (sp|P06027) Echinoidin OS=Heliocidaris crassispina PE=1 SV=1	0.047274325	4.0328894	up
MPF_LOC100691365.1.2	XM_003446687.1 PREDICTED: Oreochromis niloticus UPF0463 transmembrane protein C6orf35 homolog (LOC100691365), mRNA	0.02104269	-0.68713236	down
MPF_LOC101464596.2.2	XM_004551025.1 PREDICTED: Maylandia zebra sodium/hydrogen exchanger 1-like (LOC101464596), transcript variant X2, mRNA	0.020453071	2.6942923	up
MPF_LOC100701666.1.1	XP_003452593.1 PREDICTED: LOW QUALITY PROTEIN: pre-mRNA cleavage complex 2 protein Pcf11like [Oreochromis niloticus]	0.008877138	-0.8478093	down
MPF_contig_019979		0.020049248	2.3080332	up
MPF_contig_004494		0.015427726	2.520746	up
MPF_LOC101465329.3.4	XM_004566526.1 PREDICTED: Maylandia zebra glutaminyl-peptide cyclotransferase-like (LOC101465329), mRNA	0.0079584	2.1509278	up

MPF_contig_036091		0.001464735	2.3191915	up
MPF_LOC101470916.2.3	XM_004553002.1 PREDICTED: Maylandia zebra synaptotagmin-7-like (LOC101470916), transcript variant X5, mRNA	0.033672724	-0.6199656	down
MPF_LOC101070379.1.1	XP_003974368.1 PREDICTED: uncharacterized protein LOC101070379 [Takifugu rubripes]	0.03502468	2.4596357	up
MPF_LOC101076088.1.1	XP_003977514.1 PREDICTED: Krueppel-like factor 11-like [Takifugu rubripes]	0.005249367	-0.54947656	down
MPF_contig_045322		0.001083207	3.320211	up
MPF_LOC101469557.1.1	XM_004575292.1 PREDICTED: Maylandia zebra monoacylglycerol lipase ABHD12-like (LOC101469557), transcript variant X3, mRNA	0.041324485	-1.0935884	down
MPF_SI_DKEY-65L23.2.1.1	NP_001093522.1 uncharacterized protein LOC793688 [Danio rerio] ref|XP_001923659.2| PREDICTED: hypothetical protein LOC100150789 [Danio rerio] ref|XP_001922919.2| PREDICTED: hypothetical protein LOC100150626 [Danio rerio]	0.020851027	-1.0752516	down
MPF_LOC101484489.6.10	XM_004548851.1 PREDICTED: Maylandia zebra 14-3-3 protein beta/alpha-A-like (LOC101484489), mRNA	0.021473808	0.79379034	up
MPF_LOC101482296.2.3	XM_004546497.1 PREDICTED: Maylandia zebra transmembrane protein 56-B-like (LOC101482296), transcript variant X2, mRNA	0.04405943	0.8866872	up
MPF_LOC101482523.1.10	XM_004574334.1 PREDICTED: Maylandia zebra 60S ribosomal protein L14-like (LOC101482523), mRNA	0.016324326	1.4644914	up
MPF_LOC100698399.1.1	XM_003444297.1 PREDICTED: Oreochromis niloticus non-specific lipid-transfer protein-like (LOC100698399), mRNA	0.006335941	-0.9846372	down
MPF_LOC101474179.2.3	XM_004568681.1 PREDICTED: Maylandia zebra nucleolin 2-like (LOC101474179), mRNA	5.13E-05	4.4959893	up
MPF_LOC101156352.1.1	XP_004077953.1 PREDICTED: ictacalcin-like [Oryzias latipes]	0.002112055	3.8008165	up
MPF_FZD6.6.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440 IMAGE:6971142), complete cds	9.01E-04	3.5989876	up
MPF_LOC101480831.3.3	XM_004565417.1 PREDICTED: Maylandia zebra putative 60S ribosomal protein L37a-like (LOC101480831), mRNA	0.004591258	3.1372542	up
MPF_LOC101078462.1.1	XP_003965271.1 PREDICTED: lysosome membrane protein 2-like [Takifugu rubripes]	0.002667826	4.6177444	up
MPF_LOC101074275.1.1	XP_003968653.1 PREDICTED: transforming growth factor beta-1-like [Takifugu rubripes]	0.002154824	3.7269304	up
MPF_contig_027617		0.042700395	1.5630935	up
MPF_LOC101468354.1.1	XM_004544958.1 PREDICTED: Maylandia zebra retinoic acid receptor gamma-A-like (LOC101468354), transcript variant X4, mRNA	0.028377142	-0.80498886	down

MPF_contig_002367		0.043133523	-0.46304035	down
MPF_LOC101484400.2.5	XM_004572910.1 PREDICTED: Maylandia zebra 60S ribosomal protein L22-like 1-like (LOC101484400), mRNA	0.015781011	2.1720085	up
MPF_LOC100711510.1.8	XM_003455849.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100711510), mRNA	8.47E-04	3.7378929	up
MPF_LOC101486559.1.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA	8.81E-04	5.37502	up
MPF_LOC101464886.1.1	XM_004575104.1 PREDICTED: Maylandia zebra anoctamin-5-like (LOC101464886), transcript variant X2, mRNA	8.47E-04	3.1141682	up
MPF_LOC100689895.3.13	XP_003459184.1 PREDICTED: coxsackievirus and adenovirus receptor homolog [Oreochromis niloticus]	0.013801208	2.2321625	up
MPF_contig_013338		0.006576244	4.2453265	up
MPF_contig_004556	XM_004555151.1 PREDICTED: Maylandia zebra myelin protein P0-like (LOC101480114), transcript variant X2, mRNA	0.049876817	-0.57132953	down
MPF_XIAP.1.2	XIAP_XENTR (sp|Q5BKL8) E3 ubiquitin-protein ligase XIAP OS=Xenopus tropicalis GN=xiap PE=2 SV=1	0.023434808	-0.7439031	down
MPF_LOC101477465.2.3	XM_004574488.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 3like (LOC101477465), mRNA	0.03554348	-1.4595326	down
MPF_LOC101073877.1.1	XP_003979148.1 PREDICTED: plectin-like, partial [Takifugu rubripes]	0.008195538	3.693092	up
MPF_contig_018575		0.017222	2.650241	up
MPF_LOC100703911.1.1	XM_003452308.1 PREDICTED: Oreochromis niloticus proto-oncogene c-Rel-like (LOC100703911), mRNA	0.02496145	-0.54220766	down
MPF_ATD1B.1.1	[BBH] ATD1B_DANRE (sp|Q503W7) ATPase family AAA domain-containing protein 1-B OS=Danio rerio GN=atad1b PE=2 SV=2	0.049479105	-0.8994255	down
MPF_LOC100710050.2.6	XM_003446256.1 PREDICTED: Oreochromis niloticus 6.8 kDa mitochondrial proteolipid-like (LOC100710050), mRNA	0.015371226	-0.9524374	down
MPF_LOC101466654.1.2	XM_004538580.1 PREDICTED: Maylandia zebra sodium-dependent phosphate transporter 1-B-like (LOC101466654), partial mRNA	6.10E-04	3.0167909	up
MPF_contig_004789		0.02128095	0.9590707	up
MPF_LOC100706330.1.1	XP_003457684.1 PREDICTED: hypothetical protein LOC100706330 [Oreochromis niloticus]	1.57E-04	3.0385256	up
MPF_contig_023699		0.004223576	4.395859	up
MPF_LOC100691396.1.1	XM_003452902.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100691396 (LOC100691396), mRNA	0.017876474	2.5401978	up
MPF_LOC101473669.4.4	XM_004545518.1 PREDICTED: Maylandia zebra uncharacterized LOC101473669 (LOC101473669), mRNA	0.020762017	2.228028	up
MPF_LOC101464934.1.3	XM_004565357.1 PREDICTED: Maylandia zebra matrix metalloproteinase-14-like (LOC101464934), mRNA	0.007984483	4.0199065	up
MPF_LOC101466346.1.1	XM_004553806.1 PREDICTED: Maylandia zebra tyrosine-protein kinase ZAP-70-like (LOC101466346), transcript variant X4, mRNA	6.43E-04	2.893316	up
MPF_contig_021187		0.029846255	-0.4842592	down
MPF_LOC101485244.1.1	XM_004568719.1 PREDICTED: Maylandia zebra zinc transporter 1-like (LOC101485244), mRNA	0.005135804	2.5361161	up
MPF_LOC100692921.1.1	XM_003454794.1 PREDICTED: Oreochromis niloticus P2Y purinoceptor 12-like (LOC100692921), mRNA	6.10E-04	2.411768	up
MPF_LOC101174554.1.1	XP_004084158.1 PREDICTED: V-set domain-containing T-cell activation inhibitor 1-like [Oryzias latipes]	0.049531132	3.212985	up

MPF_contig_028808		7.19E-04	4.7057257	up
MPF_LOC101476835.3.4	XM_004560209.1 PREDICTED: Maylandia zebra septin-7-like (LOC101476835), transcript variant X2, mRNA	0.046517294	-0.71511126	down
MPF_LOC101485628.1.3	XM_004574692.1 PREDICTED: Maylandia zebra beta-1,4-mannosyl-glycoprotein 4-beta-Nacetylglucosaminyltransferase-like (LOC101485628), transcript variant X5, mRNA	0.01089882	3.0291486	up
MPF_contig_031758	XM_004550291.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101467183), transcript variant X2, mRNA	0.002292059	3.1099062	up
MPF_LOC100694329.2.3	XM_003445703.1 PREDICTED: Oreochromis niloticus proteolipid protein 2-like (LOC100694329), mRNA	0.022966782	2.5603573	up
MPF_LOC101469549.1.2	XM_004573028.1 PREDICTED: Maylandia zebra interleukin-1 receptor-like 1-like (LOC101469549), mRNA	0.001464735	2.9166384	up
MPF_contig_043597		0.01526677	-0.7579293	down
MPF_RH42.1.1	RH42_ARATH (sp|Q8H0U8) DEAD-box ATP-dependent RNA helicase 42 OS=Arabidopsis thaliana GN=RH42 PE=1 SV=2	0.027395483	1.3416958	up
MPF_contig_029262		0.003151855	1.0968841	up
MPF_LOC100695279.1.1	XP_003441081.1 PREDICTED: coiled-coil domain-containing protein 75-like [Oreochromis niloticus]	0.04405943	-0.96955293	down
MPF_contig_001885		0.0223205	-1.0287347	down
MPF_contig_008230		0.001733547	3.2994196	up
MPF_LOC100692739.1.1	XP_003452643.1 PREDICTED: gamma-crystallin N-like [Oreochromis niloticus]	0.035858028	-1.5539622	down
MPF_LOC101477091.1.3	XM_004574318.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101477091), transcript variant X5, mRNA	2.20E-04	2.0282817	up
MPF_LOC100690401.1.3	XP_003454006.1 PREDICTED: hypothetical protein LOC100690401 [Oreochromis niloticus]	4.17E-04	4.791892	up
MPF_LOC101172990.32.36	XP_004073946.1 PREDICTED: uncharacterized protein LOC101172990 [Oryzias latipes]	0.034256127	2.4191458	up
MPF_LOC101474833.1.3	XM_004570025.1 PREDICTED: Maylandia zebra bcl-2-like protein 11-like (LOC101474833), mRNA	0.002965618	3.3585489	up
MPF_LOC101475334.1.1	XM_004550229.1 PREDICTED: Maylandia zebra coiled-coil domain-containing protein 92-like (LOC101475334), mRNA	0.030795254	-0.84313965	down
MPF_contig_015549		0.016460415	1.7229664	up
MPF_LOC100703589.1.1	XM_003460117.1 PREDICTED: Oreochromis niloticus plasminogen activator inhibitor 1-like (LOC100703589), mRNA	0.002546	5.7357273	up
MPF_LOC101168933.2.2	XP_004086950.1 PREDICTED: macrophage receptor MARCO-like [Oryzias latipes]	0.006380456	2.1978636	up
MPF_PIGR.3.3	XP_004177171.1 PREDICTED: polymeric immunoglobulin receptor [Taeniopygia guttata]	0.0494809	-0.49960238	down
MPF_LOC100706916.1.1	XP_003444541.1 PREDICTED: hypothetical protein LOC100706916 [Oreochromis niloticus]	0.030154571	-0.86982244	down
MPF_AHNK.21.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	3.34E-04	5.0101147	up
MPF_contig_037191		0.041035186	-2.1211019	down
MPF_contig_024444		0.045091927	-1.2298012	down
MPF_contig_029035		0.012135304	3.049004	up
MPF_LOC101475556.1.1	XM_004575798.1 PREDICTED: Maylandia zebra junction plakoglobin-like (LOC101475556), transcript variant X2, mRNA	0.024251195	-2.0401459	down

MPF_LOC100694437.1.2	XM_003451931.1 PREDICTED: Oreochromis niloticus NFU1 iron-sulfur cluster scaffold homolog, mitochondrial-like (LOC100694437), mRNA	0.009382586	2.4398806	up
MPF_LOC101473574.7.7	XM_004564566.1 PREDICTED: Maylandia zebra 60S ribosomal protein L27a-like (LOC101473574), mRNA	0.0379215	1.7119923	up
MPF_contig_023757		0.001464735	3.3638508	up
MPF_LOC101475584.3.5	XM_004561039.1 PREDICTED: Maylandia zebra thrombospondin type-1 domain-containing protein 7A-like (LOC101475584), mRNA	0.001826411	4.2173505	up
MPF_LOC101075004.1.1	XM_003964966.1 PREDICTED: Takifugu rubripes uncharacterized LOC101075004 (LOC101075004), mRNA	8.47E-04	4.934902	up
MPF_contig_037558		0.008428021	3.1245277	up
MPF_GPX1.2.3	NM_001124525.1 Oncorhynchus mykiss glutathione peroxidase 1 (gpx1), mRNA gb|AY622862.1| Oncorhynchus mykiss glutathione peroxidase type 2 mRNA, complete cds	0.02043502	1.7969394	up
MPF_LOC101475224.2.2	XM_004569937.1 PREDICTED: Maylandia zebra gephyrin-like (LOC101475224), mRNA	0.027302237	-0.6209779	down
MPF_LOC100710693.1.3	XP_003453586.1 PREDICTED: complement factor H-like [Oreochromis niloticus]	5.71E-04	3.5350356	up
MPF_contig_048789		0.030697	-0.86657184	down
MPF_LOC101472438.1.4	XM_004575387.1 PREDICTED: Maylandia zebra collagen alpha-5(IV) chain-like (LOC101472438), mRNA	0.01852906	2.5940309	up
MPF_LOC100180429.3.7	XM_002120912.1 PREDICTED: Ciona intestinalis uncharacterized LOC100180429 (LOC100180429), mRNA	0.002766633	2.2825103	up
MPF_LOC101485262.1.1	XM_004572362.1 PREDICTED: Maylandia zebra membrane-spanning 4-domains subfamily A member 12-like (LOC101485262), mRNA	0.001335114	3.2758656	up
MPF_LOC101469036.1.1	XM_004542267.1 PREDICTED: Maylandia zebra platelet-activating factor acetylhydrolase-like (LOC101469036), transcript variant X1, mRNA	0.031663816	2.7139258	up
MPF_LOC100696821.2.2	XM_003452445.1 PREDICTED: Oreochromis niloticus ictacalcin-like (LOC100696821), mRNA	0.006740812	4.648323	up
MPF_contig_012069	XM_004552661.1 PREDICTED: Maylandia zebra neuropilin-2-like (LOC101479614), transcript variant X1, mRNA	0.010982486	0.9651999	up
MPF_LOC100710259.2.2	XM_003450909.1 PREDICTED: Oreochromis niloticus NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3-like (LOC100710259), mRNA	0.02468457	-0.62607	down
MPF_LOC100693569.1.1	XM_003457192.1 PREDICTED: Oreochromis niloticus 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase-like (LOC100693569), mRNA	0.036284976	1.8505689	up
MPF_LOC101481807.1.1	XR_191693.1 PREDICTED: Maylandia zebra plectin-like (LOC101481807), transcript variant X11, misc_RNA	0.003165984	3.139759	up
MPF_LOC100693952.2.2	XM_003442713.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693952 (LOC100693952), mRNA	0.04748985	-0.5893583	down
MPF_PABPC4.1.2	XM_003446180.1 PREDICTED: Oreochromis niloticus poly(A) binding protein, cytoplasmic 4 (inducible form) (PABPC4), mRNA	0.045249682	1.8697466	up
MPF_contig_029236		0.029445808	-0.43114227	down
MPF_contig_047891		3.41E-04	3.7367375	up
MPF_LOC100712302.1.1	XP_003452302.1 PREDICTED: aminoacyl tRNA synthase complex-interacting multifunctional protein 1like [Oreochromis niloticus]	0.001464735	3.3660479	up
MPF_LOC100709883.1.1	XP_003447642.1 PREDICTED: nitrilase homolog 1-like [Oreochromis niloticus]	0.03521311	-0.7039976	down
MPF_contig_010111		0.037083685	1.6830621	up
MPF_LOC101468994.1.1	XM_004555202.1 PREDICTED: Maylandia zebra poly [ADP-ribose] polymerase 2-like (LOC101468994), mRNA	0.037011933	-0.7318611	down

MPF_LOC101169190.1.1	XP_004068046.1 PREDICTED: Usher syndrome type-1C protein-binding protein 1-like [Oryzias latipes]	0.041324485	1.8648741	up
MPF_LOC100708796.1.1	XP_003446218.1 PREDICTED: adenylyltransferase and sulfurtransferase MOCS3-like [Oreochromis niloticus]	0.035934754	-0.8968518	down
MPF_MCM3AP.1.1	XM_003458357.1 PREDICTED: Oreochromis niloticus minichromosome maintenance complex component 3 associated protein (MCM3AP), mRNA	0.012941425	-0.69149774	down
MPF_LOC101172863.1.1	XP_004082959.1 PREDICTED: splicing factor 45-like [Oryzias latipes]	0.017736377	-0.76615095	down
MPF_contig_024382		0.044269416	-0.6355705	down
MPF_LOC101470525.1.1	XM_004556790.1 PREDICTED: Maylandia zebra vesicle-fusing ATPase-like (LOC101470525), mRNA	0.029695949	-0.5989246	down
MPF_contig_026897		0.026436092	1.1274894	up
MPF_LOC100706878.5.6	XP_003458391.1 PREDICTED: hypothetical protein LOC100706878 [Oreochromis niloticus]	1.57E-04	3.3009346	up
MPF_contig_029231		0.003678716	2.773309	up
MPF_contig_049090		0.044764053	-0.6804709	down
MPF_LOC101476391.1.1	XM_004544891.1 PREDICTED: Maylandia zebra GTP-binding protein Rheb-like (LOC101476391), mRNA	0.004110267	2.8528762	up
MPF_LOC101472409.2.3	XM_004570385.1 PREDICTED: Maylandia zebra formin-2-like (LOC101472409), mRNA	0.030638218	-2.8311515	down
MPF_contig_028541		0.00377114	3.9534621	up
MPF_LOC101470101.3.4	XM_004572496.1 PREDICTED: Maylandia zebra collagen alpha-1(XIII) chain-like (LOC101470101), mRNA	0.046662536	-0.6061454	down
MPF_LOC101075032.1.1	XM_003972203.1 PREDICTED: Takifugu rubripes mitochondrial import receptor subunit TOM20 homolog (LOC101075032), mRNA	0.011377938	-0.8905377	down
MPF_THAP8.1.1	THAP8_HUMAN (sp|Q8NA92) THAP domain-containing protein 8 OS=Homo sapiens GN=THAP8 PE=2 SV=1	0.024193214	-0.7792215	down
MPF_LOC101062276.1.1	XP_003976236.1 PREDICTED: nidogen-1-like [Takifugu rubripes]	0.015545127	2.9984255	up
MPF_LOC101469089.2.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA	0.04557982	1.7793063	up
MPF_LOC100692490.4.4	XM_003457423.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L37a-like (LOC100692490), mRNA	0.015861724	-2.8332896	down
MPF_HEPHL1.1.1	XM_003446729.1 PREDICTED: Oreochromis niloticus hephaestin-like 1 (HEPHL1), mRNA	8.81E-04	3.489735	up
MPF_LOC100698649.6.10	XP_003460222.1 PREDICTED: complement C1q tumor necrosis factor-related protein 3-like [Oreochromis niloticus]	0.028639114	4.53865	up
MPF_contig_014987		0.047293946	-0.65178156	down
MPF_LOC101464487.2.5	XM_004571832.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase BRSK2-like (LOC101464487), transcript variant X8, mRNA	0.014529526	-0.8511529	down
MPF_LOC101077970.2.2	XP_003974563.1 PREDICTED: tight junction protein ZO-2-like [Takifugu rubripes]	0.006389125	3.5214255	up
MPF_LOC100703454.2.2	XM_003450883.1 PREDICTED: Oreochromis niloticus protein S100-A1-like (LOC100703454), mRNA	0.049392886	1.7125487	up
MPF_contig_031644		0.03571405	-0.4011669	down
MPF_LOC100689711.4.6	XP_003459483.1 PREDICTED: h-2 class I histocompatibility antigen, L-D alpha chain-like [Oreochromis niloticus]	0.010982486	2.2407408	up
MPF_LOC101473328.2.4	XM_004574298.1 PREDICTED: Maylandia zebra reticulon-4-like (LOC101473328), mRNA	0.008428021	1.3025517	up
MPF_LOC101068490.2.3	XP_003971983.1 PREDICTED: C-type lectin domain family 4 member F-like [Takifugu rubripes]	0.027279796	-0.6927033	down
MPF_LOC101470609.1.1	XM_004552997.1 PREDICTED: Maylandia zebra mitochondrial glutamate carrier 1-like	0.02418725	3.0994995	up

	(LOC101470609), mRNA			
MPF_LOC100692258.2.2	XM_003445695.1 PREDICTED: Oreochromis niloticus ferritin, heavy subunit-like (LOC100692258), mRNA	0.00237142	-0.50986475	down
MPF_contig_020580		0.001609521	3.189059	up
MPF_CRE_07824.1.1	XP_003093184.1 hypothetical protein CRE_07824 [Caenorhabditis remanei]	0.003840653	3.2354248	up
MPF_LOC101471521.1.3	XM_004543486.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF128-like (LOC101471521), mRNA	3.83E-04	3.8493543	up
MPF_LOC101173449.1.1	XP_004086823.1 PREDICTED: renalase-like [Oryzias latipes]	0.03504605	-0.79485893	down
MPF_LOC101487444.1.1	XM_004547650.1 PREDICTED: Maylandia zebra alpha-1-syntrophin-like (LOC101487444), mRNA	0.013726315	2.3176448	up
MPF_contig_028949		0.013112701	2.081131	up
MPF_LOC101480440.1.1	XM_004541919.1 PREDICTED: Maylandia zebra deleted in malignant brain tumors 1 protein-like (LOC101480440), mRNA	0.004133615	0.9838447	up
MPF_LOC101486757.1.1	XM_004568817.1 PREDICTED: Maylandia zebra transmembrane protein 181-like (LOC101486757), mRNA	0.044378266	-0.47745985	down
MPF_CRE_23222.1.2	XP_003089877.1 hypothetical protein CRE_23222 [Caenorhabditis remanei]	0.012135304	1.5015712	up
MPF_LOC100174873.5.10	NM_001267638.1 Gasterosteus aculeatus beta globin (LOC100174873), mRNA gb|AY184355.1| Gasterosteus aculeatus beta globin mRNA, complete cds	0.017876474	2.2599387	up

MPF_LOC101480226.1.1	XM_004538168.1 PREDICTED: Maylandia zebra protein phosphatase PTC7 homolog (LOC101480226), mRNA	0.026052147	-0.71263885	down
MPF_B3AT.2.2	B3AT_ONCMY (sp|P32847) Band 3 anion exchange protein OS=Oncorhynchus mykiss GN=slc4a1 PE=2 SV=2	0.01238595	3.2205563	up
MPF_contig_047276	XM_004574499.1 PREDICTED: Maylandia zebra dedicator of cytokinesis protein 7-like (LOC101480191), transcript variant X3, mRNA	0.040898368	-0.95691437	down
MPF_LOC101465872.1.1	XM_004558783.1 PREDICTED: Maylandia zebra extended synaptotagmin-1-like (LOC101465872), mRNA	0.00237142	5.3062325	up
MPF_LOC101473918.1.1	XM_004552728.1 PREDICTED: Maylandia zebra histone-lysine N-methyltransferase, H3 lysine-79 specific-like (LOC101473918), transcript variant X1, mRNA	0.006095142	1.3064976	up
MPF_LOC101478190.2.2	XM_004571703.1 PREDICTED: Maylandia zebra platelet basic protein-like (LOC101478190), mRNA	0.001881666	3.7450702	up
MPF_contig_005973		0.028402865	2.2644835	up
MPF_LOC100690727.1.1	XM_003443255.1 PREDICTED: Oreochromis niloticus ribosomal RNA processing protein 1 homolog Blike (LOC100690727), mRNA	0.008823011	1.6279182	up
MPF_S18L2.2.2	S18L2_HUMAN (sp|Q9UHA2) SS18-like protein 2 OS=Homo sapiens GN=SS18L2 PE=2 SV=1	0.04598239	-0.8919725	down
MPF_LOC100693891.1.1	XM_003450511.1 PREDICTED: Oreochromis niloticus 28S ribosomal protein S15, mitochondrial-like (LOC100693891), mRNA	0.031395804	-0.7976909	down
MPF_LOC100710982.1.1	XM_003437658.1 PREDICTED: Oreochromis niloticus small EDRK-rich factor 2-like (LOC100710982), mRNA	0.03554348	-0.8659091	down
MPF_LOC101471935.1.1	XM_004545975.1 PREDICTED: Maylandia zebra transcription factor MafB-like (LOC101471935), mRNA	0.002285471	3.4772534	up
MPF_LOC100559296.1.1	XP_003228542.1 PREDICTED: zinc finger protein 229-like [Anolis carolinensis]	0.004220047	-0.54956627	down
MPF_RL18A.5.14	RL18A_DANRE (sp|Q7ZWJ4) 60S ribosomal protein L18a OS=Danio rerio GN=rpl18a PE=2 SV=1	0.041324485	1.3748708	up
MPF_LOC100700016.1.1	XM_003447883.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100700016 (LOC100700016), mRNA	6.00E-04	2.223293	up
MPF_LOC101475864.1.1	XM_004556346.1 PREDICTED: Maylandia zebra protein FAM83F-like (LOC101475864), mRNA	0.025755864	-0.7329073	down

MPF_contig_030045	XM_004538774.1 PREDICTED: Maylandia zebra regulatory-associated protein of mTOR-like (LOC101472178), transcript variant X1, mRNA	0.022762315	-0.5404177	down
MPF_LOC100702234.6.6	XM_003459254.1 PREDICTED: Oreochromis niloticus mamu class II histocompatibility antigen, DR alpha chain-like (LOC100702234), mRNA	0.008046914	2.1545954	up
MPF_LOC100708084.3.4	XM_003447339.1 PREDICTED: Oreochromis niloticus uridine phosphorylase 2-like (LOC100708084), mRNA	0.001872549	2.2884045	up
MPF_LOC100698172.1.3	XP_003455687.1 PREDICTED: beta-2-microglobulin-like [Oreochromis niloticus]	0.033488218	-0.73132086	down
MPF_LOC100695023.4.6	XM_003443439.1 PREDICTED: Oreochromis niloticus heterogeneous nuclear ribonucleoprotein A0like (LOC100695023), mRNA	0.025147038	-1.0561677	down
MPF_contig_016740	XM_004565584.1 PREDICTED: Maylandia zebra arf-GAP with GTPase, ANK repeat and PH domaincontaining protein 1-like (LOC101478076), transcript variant X6, mRNA	0.041065946	-0.8238763	down
MPF_LOC101467232.1.1	XM_004541226.1 PREDICTED: Maylandia zebra ceramide synthase 2-like (LOC101467232), mRNA	1.05E-04	3.8406622	up
MPF_LOC101481069.1.1	XM_004556635.1 PREDICTED: Maylandia zebra sideroflexin-2-like (LOC101481069), mRNA	0.044047236	-0.8239545	down
MPF_LOC100695240.1.2	XP_003452569.1 PREDICTED: calcium/calmodulin-dependent protein kinase type IV-like [Oreochromis niloticus]	0.03076677	2.069549	up
MPF_LOC100708802.1.1	XM_003447173.1 PREDICTED: Oreochromis niloticus prolyl endopeptidase-like (LOC100708802), mRNA	0.017319541	-0.53847694	down
MPF_LOC101484703.2.2	XM_004555446.1 PREDICTED: Maylandia zebra transmembrane protein 41A-A-like (LOC101484703), mRNA	1.87E-05	3.7771192	up
MPF_LOC101467113.4.4	XM_004559889.1 PREDICTED: Maylandia zebra nuclear ubiquitous casein and cyclin-dependent kinase substrate 1-like (LOC101467113), mRNA	0.038213134	-0.45785052	down
MPF_contig_012534		0.006727105	1.9206026	up
MPF_LOC100564008.1.1	XM_003223200.1 PREDICTED: Anolis carolinensis 40S ribosomal protein S26-like (LOC100564008), mRNA	0.04913947	1.8320454	up
MPF_LOC101464556.2.2	XM_004544100.1 PREDICTED: Maylandia zebra coxsackievirus and adenovirus receptor homolog (LOC101464556), transcript variant X2, mRNA	0.042507604	-0.5676985	down
MPF_contig_028362		0.015773721	-1.3174071	down
MPF_LOC100709741.1.1	XM_003456979.1 PREDICTED: Oreochromis niloticus macrophage colony-stimulating factor 1 receptor 2-like (LOC100709741), mRNA	0.007882108	3.6599865	up
MPF_DKC1.2.3	XM_003460212.1 PREDICTED: Oreochromis niloticus dyskeratosis congenita 1, dyskerin (DKC1), mRNA	0.026520038	-0.86193943	down
MPF_LOC100690793.1.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]	0.002822743	5.4909544	up
MPF_contig_023647		0.003151855	2.7250645	up
MPF_LOC100534480.2.2	XM_003447448.1 PREDICTED: Oreochromis niloticus inducible cAMP early repressor (LOC100534480), mRNA	0.04557982	1.4915929	up
MPF_LOC101476946.3.4	XM_004542655.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 5-like (LOC101476946), mRNA	0.004495184	2.1499486	up
MPF_contig_037007		0.007176654	3.0396175	up
MPF_contig_007811		0.03555063	-0.53768444	down
MPF_contig_034810		0.044378266	-0.7334127	down
MPF_RS13.7.9	RS13_XENLA (sp|P49393) 40S ribosomal protein S13 OS=Xenopus laevis GN=rps13 PE=3 SV=2	0.029624822	1.2353868	up
MPF_contig_040346		0.020825911	-0.8351579	down
MPF_LOC100701615.1.5	XM_003439975.1 PREDICTED: Oreochromis niloticus heterogeneous nuclear ribonucleoprotein Mlike (LOC100701615), mRNA	0.024380561	3.1149313	up
MPF_LOC100712420.1.5	XP_003456711.1 PREDICTED: adenine phosphoribosyltransferase-like [Oreochromis niloticus]	0.016616924	1.6373272	up

MPF_contig_048205	XM_004538853.1 PREDICTED: Maylandia zebra protocadherin-10-like (LOC101468123), transcript variant X2, mRNA	0.034163512	-0.823504	down

MPF_LOC101473612.4.5	XM_004550873.1 PREDICTED: Maylandia zebra sodium/potassium-transporting ATPase subunit alpha-3-like (LOC101473612), transcript variant X2, mRNA	8.47E-04	3.9584687	up
MPF_LOC101481619.2.2	XM_004546215.1 PREDICTED: Maylandia zebra RNA-binding protein 38-like (LOC101481619), mRNA	0.01041997	1.9678092	up
MPF_LOC101464956.1.1	XM_004545486.1 PREDICTED: Maylandia zebra large neutral amino acids transporter small subunit 3like (LOC101464956), mRNA	0.001031627	3.8219442	up
MPF_LOC100701242.9.9	XM_003459250.1 PREDICTED: Oreochromis niloticus h-2 class II histocompatibility antigen, I-A beta chain-like, transcript variant 1 (LOC100701242), mRNA	0.017475128	3.3089638	up
MPF_contig_047601		0.02468457	2.5536542	up
MPF_LOC100693091.2.2	XM_003450261.1 PREDICTED: Oreochromis niloticus fucolectin-7-like (LOC100693091), mRNA	0.00710018	3.8938656	up
MPF_LOC101482085.5.5	XM_004544079.1 PREDICTED: Maylandia zebra von Willebrand factor A domain-containing protein 5A-like (LOC101482085), mRNA	0.009977766	-0.55173826	down
MPF_LOC100703265.1.1	XP_003446695.1 PREDICTED: tRNA-specific adenosine deaminase 2-like [Oreochromis niloticus]	0.04716473	-0.9797268	down
MPF_LOC101464117.1.1	XM_004572292.1 PREDICTED: Maylandia zebra solute carrier family 12 member 7-like (LOC101464117), transcript variant X3, mRNA	0.002192435	2.5760393	up
MPF_LOC101072717.2.3	XP_003971444.1 PREDICTED: cytochrome c oxidase subunit 7A2, mitochondrial-like [Takifugu rubripes]	0.012072624	-0.6069708	down
MPF_LOC101482551.1.1	XM_004538177.1 PREDICTED: Maylandia zebra smoothelin-like (LOC101482551), mRNA	0.02568437	1.2929235	up
MPF_contig_005656		0.006138545	-0.91705513	down
MPF_contig_034320		0.035858028	1.3031478	up
MPF_LOC100702455.2.2	XP_003446860.1 PREDICTED: erythrocyte band 7 integral membrane protein-like [Oreochromis niloticus]	0.023639033	2.2601829	up
MPF_contig_048017		0.030648977	-1.0043812	down
MPF_LOC101477600.1.1	XM_004540339.1 PREDICTED: Maylandia zebra phospholipase B1, membrane-associated-like (LOC101477600), mRNA	0.031984054	-0.7612138	down
MPF_LOC100711618.1.1	XM_003458122.1 PREDICTED: Oreochromis niloticus armadillo repeat-containing protein 1-like (LOC100711618), mRNA	0.041065533	-1.761117	down
MPF_LOC100700642.2.2	XM_003445475.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100700642 (LOC100700642), mRNA	0.027302237	-1.344408	down
MPF_contig_005684		0.041035186	-0.64522743	down
MPF_LOC100703754.1.1	XM_003456632.1 PREDICTED: Oreochromis niloticus mannosyl-oligosaccharide 1,2-alphamannosidase IA-like (LOC100703754), mRNA	0.028302766	2.3887708	up
MPF_LOC101469362.1.1	XM_004549429.1 PREDICTED: Maylandia zebra integrator complex subunit 12-like (LOC101469362), transcript variant X1, mRNA	0.04490779	-0.8950596	down
MPF_COX3.3.3	[BBH] COX3_GADMO (sp|P55777) Cytochrome c oxidase subunit 3 OS=Gadus morhua GN=mt-co3 PE=3 SV=1	0.017300047	-1.4216002	down
MPF_LOC100174885.1.1	NM_001267644.1 Gasterosteus aculeatus ASPIP (LOC100174885), mRNA gb|DQ351706.1| Gasterosteus aculeatus cartilage acidic protein 2 (CRTAC-2) mRNA, complete cds	0.047274325	-0.7943601	down
MPF_LOC100697415.3.3	XP_003444759.1 PREDICTED: neuroblast differentiation-associated protein AHNAK-like [Oreochromis niloticus]	4.83E-04	5.33218	up
MPF_contig_011672	XM_004550791.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 6like (LOC101478586), transcript variant X1, mRNA	0.001881666	2.7749143	up
MPF_LOC101469667.2.2	XM_004557497.1 PREDICTED: Maylandia zebra V-set and transmembrane domain-containing protein	0.032700863	-0.79519266	down

	4-like (LOC101469667), mRNA			
MPF_GPX1.1.3	NM_001124525.1 Oncorhynchus mykiss glutathione peroxidase 1 (gpx1), mRNA gb|AY622862.1| Oncorhynchus mykiss glutathione peroxidase type 2 mRNA, complete cds	0.04242951	2.4655232	up
MPF_LOC101465129.13.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA	0.0432203	-0.7322951	down
MPF_LOC101068359.1.1	XP_003962600.1 PREDICTED: gap junction beta-4 protein-like [Takifugu rubripes]	0.03212826	-0.9304147	down
MPF_LOC101472402.1.1	XM_004568494.1 PREDICTED: Maylandia zebra 6-phosphofructokinase type C-like (LOC101472402), transcript variant X1, mRNA	0.003673072	1.8006572	up
MPF_LOC100706922.1.1	XP_003446211.1 PREDICTED: transcription initiation factor TFIID subunit 2-like [Oreochromis niloticus]	0.009382586	-1.2946887	down
MPF_contig_038752		0.0434344	-0.72535753	down
MPF_K1C18.1.2	K1C18_DANRE (sp|Q7ZTS4) Keratin, type I cytoskeletal 18 OS=Danio rerio GN=krt18 PE=1 SV=2	0.001464735	5.2155685	up
MPF_LOC100690604.1.1	XM_003456993.1 PREDICTED: Oreochromis niloticus rab proteins geranylgeranyltransferase component A 1-like (LOC100690604), mRNA	0.014991251	-0.6674823	down
MPF_LOC101483054.1.2	XM_004542678.1 PREDICTED: Maylandia zebra serotransferrin-like (LOC101483054), mRNA	0.002073439	3.3179283	up
MPF_LOC101161574.6.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.003768269	3.322744	up
MPF_contig_023176		0.006532356	2.8615553	up
MPF_contig_021996		0.026158698	-0.5693607	down
MPF_LOC100694868.1.2	XM_003446700.1 PREDICTED: Oreochromis niloticus c-C chemokine receptor type 6-like (LOC100694868), mRNA	0.005869763	1.839555	up
MPF_LOC101157253.1.2	XM_004080171.1 PREDICTED: Oryzias latipes homeobox protein Dlx4b-like (LOC101157253), mRNA	0.047293946	-0.6557684	down
MPF_LOC101471731.1.2	XM_004544422.1 PREDICTED: Maylandia zebra myocyte-specific enhancer factor 2C-like (LOC101471731), transcript variant X6, mRNA	6.01E-04	4.1781077	up
MPF_contig_014940		0.007176654	3.1287763	up
MPF_contig_036703		0.025734475	-0.60817146	down
MPF_SLC25A38.1.1	NM_001093190.1 Xenopus laevis solute carrier family 25, member 38 (slc25a38), nuclear gene encoding mitochondrial protein, mRNA	0.044047236	-0.7241253	down
MPF_LOC100692245.2.2	XM_003440351.1 PREDICTED: Oreochromis niloticus guanine nucleotide exchange factor for Rab-3Alike (LOC100692245), mRNA	0.012436931	0.9666672	up
MPF_LOC100698929.2.2	XM_003442472.1 PREDICTED: Oreochromis niloticus E3 ubiquitin-protein ligase RNF25-like (LOC100698929), mRNA	0.03571405	-0.9624853	down
MPF_contig_018142		0.004082234	2.1278262	up
MPF_LOC100701273.36.44	XM_003444228.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 12-like (LOC100701273), mRNA	0.020023411	-0.54696506	down
MPF_LOC101488106.1.1	XM_004550734.1 PREDICTED: Maylandia zebra adaptin ear-binding coat-associated protein 1-like (LOC101488106), mRNA	0.03502057	-0.9922504	down
MPF_LOC101472401.1.1	XM_004544882.1 PREDICTED: Maylandia zebra coiled-coil domain-containing protein 174-like (LOC101472401), transcript variant X2, mRNA	0.038813706	-0.6684732	down
MPF_LOC100692032.2.6	XP_003458104.1 PREDICTED: E3 ubiquitin/ISG15 ligase TRIM25-like [Oreochromis niloticus]	0.020129085	-0.8089981	down
MPF_GP91PHOX.2.2	NM_001032732.1 Takifugu rubripes gp91phox protein (gp91phox), mRNA	0.001454429	3.2590094	up
MPF_contig_011610		0.02104269	-0.8054037	down

MPF_LOC101463819.1.1	XM_004549502.1 PREDICTED: Maylandia zebra tetraspanin-5-like (LOC101463819), transcript variant X2, mRNA	0.01238595	3.716095	up
MPF_contig_023804		0.012368075	1.2377753	up
MPF_LOC101467224.1.2	XM_004563360.1 PREDICTED: Maylandia zebra pleckstrin homology-like domain family A member 2like (LOC101467224), mRNA	0.035139468	-0.8514013	down
MPF_MUCM.1.1	MUCM_MOUSE (sp|P01873) Ig mu chain C region membrane-bound form OS=Mus musculus GN=Igh-6 PE=2 SV=3	0.017475128	3.2919543	up
MPF_LOC101469314.1.1	XR_190849.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 44-like (LOC101469314), transcript variant X3, misc_RNA	0.003165984	-0.9124723	down
MPF_LOC100693203.3.4	XM_003457748.1 PREDICTED: Oreochromis niloticus tetraspanin-5-like (LOC100693203), mRNA	0.015026683	1.4039888	up
MPF_LOC101465015.1.1	XM_004562273.1 PREDICTED: Maylandia zebra MKL/myocardin-like protein 2-like (LOC101465015), transcript variant X4, mRNA	0.027443452	1.4604262	up
MPF_contig_036789		0.011377938	3.1454027	up
MPF_LOC101486284.2.3	XM_004546431.1 PREDICTED: Maylandia zebra transmembrane protein 189-like (LOC101486284), mRNA	0.00885032	-0.67591804	down
MPF_contig_037242		0.008872926	2.2562232	up
MPF_LOC101482854.4.4	XM_004540267.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(q) subunit alpha-like (LOC101482854), transcript variant X3, mRNA	0.011285475	-0.7915496	down
MPF_contig_038443		0.023471761	-0.6400004	down
MPF_contig_009797		0.038572192	-0.6858315	down
MPF_LOC100710548.3.4	XP_003459320.1 PREDICTED: major histocompatibility complex class I-related gene protein-like [Oreochromis niloticus]	0.002220721	4.23015	up
MPF_LOC101484947.1.1	XM_004546225.1 PREDICTED: Maylandia zebra acid-sensing ion channel 1-like (LOC101484947), mRNA	0.016257549	-0.70891905	down
MPF_LOC101072249.3.3	XP_003966663.1 PREDICTED: target of Nesh-SH3-like [Takifugu rubripes]	2.01E-04	3.9126093	up
MPF_contig_029562	XM_004575516.1 PREDICTED: Maylandia zebra protein FAM222B-like (LOC101485279), transcript variant X1, mRNA	0.039624773	-0.79320616	down
MPF_LOC100701568.2.2	XP_003450260.1 PREDICTED: copine-3-like [Oreochromis niloticus]	0.02418725	1.0528525	up
MPF_LOC100690883.1.2	XP_003458178.1 PREDICTED: zinc finger protein 84-like [Oreochromis niloticus]	0.03705777	-0.74482584	down
MPF_LOC100707087.2.2	XP_003446625.1 PREDICTED: major facilitator superfamily domain-containing protein 6-like [Oreochromis niloticus]	0.046008673	-0.7487168	down
MPF_LOC101169293.5.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.01829461	2.1770916	up
MPF_LOC100706800.1.1	XM_003439818.1 PREDICTED: Oreochromis niloticus retinoic acid receptor RXR-gamma-B-like, transcript variant 1 (LOC100706800), mRNA	0.003151855	2.961191	up
MPF_LOC101171201.3.6	XM_004080142.1 PREDICTED: Oryzias latipes hemoglobin subunit alpha-1-like (LOC101171201), mRNA	0.04069054	2.2733047	up
MPF_CFAH.14.15	CFAH_MOUSE (sp|P06909) Complement factor H OS=Mus musculus GN=Cfh PE=1 SV=2	0.001529747	3.5550563	up
MPF_LOC101474220.1.1	XM_004554937.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase NIM1-like (LOC101474220), mRNA	0.034740705	-0.569096	down
MPF_LOC101067754.3.3	XM_003961265.1 PREDICTED: Takifugu rubripes NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4-like (LOC101067754), mRNA	0.002760018	3.2085278	up
MPF_contig_017017		0.00834994	-0.7551971	down
MPF_LOC100704396.2.3	XP_003459961.1 PREDICTED: neoverrucotoxin subunit alpha-like [Oreochromis niloticus]	7.19E-04	4.1337285	up

MPF_LOC100694405.1.2	XM_003443693.1 PREDICTED: Oreochromis niloticus uncharacterized protein C8orf76-like (LOC100694405), mRNA	0.015684035	-1.055336	down
MPF_contig_044005		9.48E-04	3.1250434	up
MPF_LOC101481869.4.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA	0.004681449	1.5845823	up
MPF_LOC100711796.1.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA	0.001573924	2.6761518	up
MPF_LOC100705145.1.1	XM_003445077.1 PREDICTED: Oreochromis niloticus phenylserine dehydratase-like (LOC100705145), mRNA	0.03437004	-2.2145193	down
MPF_contig_004128		0.001348924	3.2660472	up
MPF_COX7R.2.3	COX7R_BOVIN (sp|Q3T061) Cytochrome c oxidase subunit 7A-related protein, mitochondrial OS=Bos taurus GN=COX7A2L PE=3 SV=1	0.025911832	-0.64052343	down
MPF_contig_004261		0.001531586	3.1599417	up
MPF_PFL1445W.1.1	XP_001350695.2 conserved Plasmodium protein [Plasmodium falciparum 3D7]	3.26E-04	3.1079955	up
MPF_LOC100703063.1.1	XM_003444398.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100703063 (LOC100703063), mRNA	0.039059788	-0.8343305	down
MPF_LOC100701392.1.1	XM_003452212.1 PREDICTED: Oreochromis niloticus protein phosphatase 1K, mitochondrial-like (LOC100701392), mRNA	0.03834614	2.03151	up
MPF_CD28.1.1	[BBH] CD28_HUMAN (sp|P10747) T-cell-specific surface glycoprotein CD28 OS=Homo sapiens GN=CD28 PE=1 SV=1	8.81E-04	2.9717345	up
MPF_contig_032061		0.02104948	1.2767043	up
MPF_RBBP5.1.1	XP_003447710.1 PREDICTED: retinoblastoma-binding protein 5 [Oreochromis niloticus]	0.014163161	-1.6067071	down
MPF_LOC101479192.1.1	XM_004541915.1 PREDICTED: Maylandia zebra lebercilin-like (LOC101479192), transcript variant X1, mRNA	8.81E-04	3.7814064	up
MPF_AHNK.22.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	7.93E-04	2.3680549	up
MPF_TNF6B.1.1	TNF6B_HUMAN (sp|O95407) Tumor necrosis factor receptor superfamily member 6B OS=Homo sapiens GN=TNFRSF6B PE=1 SV=1	0.005460658	5.4753942	up
MPF_LOC100705618.1.1	XP_003453815.1 PREDICTED: protogenin-like [Oreochromis niloticus]	0.002151374	3.1793706	up
MPF_LOC101479923.1.2	XM_004538167.1 PREDICTED: Maylandia zebra spidroin-2-like (LOC101479923), mRNA	0.044863876	-0.6470823	down
MPF_contig_040466		0.036862258	-0.43269736	down
MPF_LOC101471902.4.5	XM_004538867.1 PREDICTED: Maylandia zebra phosphatidylinositol 4-kinase type 2-beta-like (LOC101471902), mRNA	0.01958403	-0.40256023	down
MPF_LOC101467062.1.1	XM_004569816.1 PREDICTED: Maylandia zebra gamma-crystallin M1-like (LOC101467062), mRNA	0.035728484	2.4388022	up
MPF_LOC100701395.3.4	XM_003452701.1 PREDICTED: Oreochromis niloticus ig kappa chain V-III region MOPC 63-like (LOC100701395), mRNA	0.036837943	2.8524475	up
MPF_contig_017922		0.041065946	-0.4524054	down
MPF_contig_010158		0.04443673	1.1474271	up
MPF_contig_016560	XM_004571963.1 PREDICTED: Maylandia zebra neurofilament heavy polypeptide-like (LOC101475636), transcript variant X2, mRNA	0.023217764	-0.9783201	down
MPF_BT3A2.1.1	BT3A2_HUMAN (sp|P78410) Butyrophilin subfamily 3 member A2 OS=Homo sapiens GN=BTN3A2	0.022410905	-3.485649	down

	PE=1 SV=2			
MPF_LOC101474542.1.1	XM_004565746.1 PREDICTED: Maylandia zebra stathmin-4-like (LOC101474542), transcript variant X2, mRNA	0.039302945	-0.8044262	down
MPF_LOC101166011.1.1	XP_004080736.1 PREDICTED: disintegrin and metalloproteinase domain-containing protein 8-like [Oryzias latipes]	0.014309967	2.717012	up
MPF_FRIM.1.1	FRIM_SALSA (sp|P49947) Ferritin, middle subunit OS=Salmo salar PE=2 SV=1	0.043503962	-0.47674176	down
MPF_LOC101483611.1.1	XM_004563878.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF167-like (LOC101483611), transcript variant X4, mRNA	0.04269517	-0.6578207	down
MPF_MUC18.1.2	MUC18_RAT (sp|Q9EPF2) Cell surface glycoprotein MUC18 OS=Rattus norvegicus GN=Mcam PE=1 SV=2	0.041324485	0.8465499	up
MPF_contig_044606		0.001529747	4.236363	up
MPF_contig_033640	XM_004548336.1 PREDICTED: Maylandia zebra protein kinase C and casein kinase substrate in neurons protein 2-like (LOC101473402), transcript variant X1, mRNA	0.004962711	1.421164	up
MPF_contig_049016		0.049876817	-1.3624384	down
MPF_LOC101486434.1.2	XM_004560149.1 PREDICTED: Maylandia zebra cathepsin K-like (LOC101486434), mRNA	0.001766295	4.702138	up
MPF_contig_015596		0.035858028	2.2762358	up
MPF_contig_039397		0.021532089	1.14849	up
MPF_LOC101061752.1.1	XM_003975168.1 PREDICTED: Takifugu rubripes SEC14-like protein 2-like (LOC101061752), mRNA	0.001998473	3.6781378	up
MPF_LOC100702817.3.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.001348924	5.904471	up
MPF_LOC100488485.5.10	XP_002941723.1 PREDICTED: hypothetical protein LOC100488485 [Xenopus (Silurana) tropicalis]	0.009382586	3.8559165	up
MPF_LOC100701544.18.20	XM_003444229.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 3-like (LOC100701544), mRNA	0.008833091	2.8870335	up
MPF_LOC101472640.3.4	XM_004574391.1 PREDICTED: Maylandia zebra microtubule-associated serine/threonine-protein kinase 3-like (LOC101472640), transcript variant X2, mRNA	0.008325805	1.8328891	up
MPF_LOC101076756.1.1	XM_003972767.1 PREDICTED: Takifugu rubripes histone-lysine N-methyltransferase MLL5-like (LOC101076756), mRNA	1.57E-04	3.2896016	up
MPF_LOC100712517.2.2	XM_003459650.1 PREDICTED: Oreochromis niloticus RNA (guanine-9-)-methyltransferase domaincontaining protein 2-like (LOC100712517), mRNA	0.008823011	2.2135458	up
MPF_FCGR1.1.1	FCGR1_MOUSE (sp|P26151) High affinity immunoglobulin gamma Fc receptor I OS=Mus musculus GN=Fcgr1 PE=1 SV=1	0.007640657	4.199449	up
MPF_contig_004326		7.34E-04	2.52957	up
MPF_LOC101480609.1.2	XM_004539422.1 PREDICTED: Maylandia zebra homeodomain-interacting protein kinase 3-like (LOC101480609), transcript variant X2, mRNA	5.89E-04	4.2730393	up
MPF_LOC100708213.1.1	XP_003457845.1 PREDICTED: hypothetical protein LOC100708213 [Oreochromis niloticus]	0.047641937	3.7080085	up
MPF_LOC101483514.1.1	XM_004539709.1 PREDICTED: Maylandia zebra glucose-6-phosphate isomerase-like (LOC101483514), mRNA	0.044378266	-1.0791149	down
MPF_LOC101465129.6.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA	0.003156557	2.3084435	up
MPF_LOC101481809.13.19	XM_004569424.1 PREDICTED: Maylandia zebra tripartite motif-containing protein 16-like (LOC101481809), mRNA	0.021008566	-0.6273718	down
MPF_contig_029673		0.001555588	2.6035385	up

MPF_LOC101473936.1.1	XM_004559270.1 PREDICTED: Maylandia zebra PQ-loop repeat-containing protein 3-like (LOC101473936), mRNA	0.028377142	-0.5815392	down
MPF_LOC101487373.23.24	XM_004576282.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101487373), mRNA	0.002251516	1.2641149	up
MPF_contig_044368		0.01412041	-0.7052745	down
MPF_LOC101062709.2.3	XM_003972629.1 PREDICTED: Takifugu rubripes beta-2-microglobulin-like (LOC101062709), mRNA	0.049350053	2.0200424	up
MPF_LOC100710921.1.1	XM_003442353.1 PREDICTED: Oreochromis niloticus protein FAM63B-like (LOC100710921), mRNA	0.037003025	-1.1680278	down
MPF_LOC100704053.3.12	XM_003440652.1 PREDICTED: Oreochromis niloticus ubiquitin-like protein FUBI-like (LOC100704053), mRNA	0.002963641	1.6503099	up
MPF_contig_043890		0.032868147	1.8016679	up
MPF_LOC100699618.1.3	XM_003458706.1 PREDICTED: Oreochromis niloticus macrophage-capping protein-like (LOC100699618), mRNA	0.002620848	3.8118968	up

MPF_LOC101475177.1.1	XM_004562132.1 PREDICTED: Maylandia zebra protein CYR61-like (LOC101475177), mRNA	0.017583612	3.238129	up
MPF_LOC101480149.1.1	XM_004542668.1 PREDICTED: Maylandia zebra serine--pyruvate aminotransferase, mitochondriallike (LOC101480149), mRNA	0.044863876	-0.8707242	down
MPF_contig_025370	XM_004558558.1 PREDICTED: Maylandia zebra autism susceptibility gene 2 protein-like (LOC101480020), transcript variant X7, mRNA	3.41E-04	3.4160354	up
MPF_LOC101077329.1.1	XP_003965511.1 PREDICTED: glycerol-3-phosphate acyltransferase 3-like [Takifugu rubripes]	0.021234617	-0.6570882	down
MPF_contig_037677		0.004449121	-2.7641551	down
MPF_LOC100694934.2.2	XP_003442506.1 PREDICTED: putative N-acetylglucosamine-6-phosphate deacetylase-like [Oreochromis niloticus]	0.047976848	-0.7977814	down
MPF_LOC101479518.3.5	XM_004570668.1 PREDICTED: Maylandia zebra alpha-actinin-3-like (LOC101479518), mRNA	0.005706875	2.4731374	up
MPF_LOC101483522.1.1	XM_004564699.1 PREDICTED: Maylandia zebra adipocyte enhancer-binding protein 1-like (LOC101483522), mRNA	0.026520215	2.9159656	up
MPF_LOC101464125.1.1	XM_004573638.1 PREDICTED: Maylandia zebra DNA-directed RNA polymerase I subunit RPA12-like (LOC101464125), transcript variant X4, mRNA	0.016444676	-0.77478975	down
MPF_LOC100705343.3.3	XM_003450141.1 PREDICTED: Oreochromis niloticus claudin-8-like (LOC100705343), mRNA	0.002951977	4.4718795	up
MPF_LOC101171771.2.2	XM_004077345.1 PREDICTED: Oryzias latipes uncharacterized LOC101171771 (LOC101171771), mRNA	0.014529526	2.3613925	up
MPF_LOC101167345.13.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA	1.57E-04	3.6370053	up
MPF_LOC100701823.2.2	XM_003446064.1 PREDICTED: Oreochromis niloticus protamine-like protein-like (LOC100701823), mRNA	0.04242951	2.177722	up
MPF_contig_017955		0.003097902	2.189281	up
MPF_contig_009977		0.006238447	1.9186492	up
MPF_LOC101475629.1.1	XM_004570493.1 PREDICTED: Maylandia zebra lactosylceramide 1,3-N-acetyl-beta-Dglucosaminyltransferase A-like (LOC101475629), transcript variant X2, mRNA	0.001017018	2.684533	up
MPF_LOC101465998.2.3	XM_004541412.1 PREDICTED: Maylandia zebra serum amyloid P-component-like (LOC101465998), mRNA	0.018205103	2.6507237	up
MPF_LOC101487936.1.3	XM_004552317.1 PREDICTED: Maylandia zebra F-box/LRR-repeat protein 20-like (LOC101487936), transcript variant X2, mRNA	0.00738922	-1.3030987	down
MPF_LOC101466772.1.2	XM_004542617.1 PREDICTED: Maylandia zebra glypican-5-like (LOC101466772), transcript variant X2, mRNA	0.001244554	-0.51403904	down

MPF_LOC101484083.3.3	XM_004539190.1 PREDICTED: Maylandia zebra ATP-binding cassette sub-family A member 1-like (LOC101484083), transcript variant X2, mRNA	0.015427726	1.9631357	up
MPF_contig_026589		0.006380456	-1.5683646	down
MPF_LOC101480505.1.1	XM_004557175.1 PREDICTED: Maylandia zebra ankyrin repeat domain-containing protein 29-like (LOC101480505), transcript variant X3, mRNA	0.002667826	-0.6039267	down
MPF_LOC101161574.12.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.002710021	3.230505	up
MPF_TSP_02148.1.1	XP_003377890.1 7 transmembrane receptor [Trichinella spiralis]	0.006238447	1.0607533	up
MPF_LOC101483933.1.1	XM_004547257.1 PREDICTED: Maylandia zebra coiled-coil domain-containing protein 112-like (LOC101483933), transcript variant X2, mRNA	0.030766957	-0.8054361	down
MPF_contig_035224	XM_004568483.1 PREDICTED: Maylandia zebra copine-3-like (LOC101469901), transcript variant X1, mRNA	0.030273842	1.0316687	up
MPF_contig_013979	XM_004551640.1 PREDICTED: Maylandia zebra 40S ribosomal protein S24-like (LOC101482129), transcript variant X1, mRNA	1.57E-04	4.3073773	up
MPF_ACTBA.4.4	XM_003964421.1 PREDICTED: Takifugu rubripes actin, cytoplasmic 1-like (LOC101073736), mRNA	0.038213134	-0.49763587	down
MPF_LOC100707856.1.1	XP_003458866.1 PREDICTED: transforming growth factor beta-2-like [Oreochromis niloticus]	0.011725964	1.2003403	up
MPF_contig_023437		0.010092718	1.8718486	up
MPF_LOC101475675.1.1	XM_004558632.1 PREDICTED: Maylandia zebra Golgi phosphoprotein 3-like (LOC101475675), mRNA	0.041324485	-0.9103307	down
MPF_LOC100692490.2.4	XM_003457423.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L37a-like (LOC100692490), mRNA	0.002746439	3.20583	up
MPF_LOC101480380.1.2	XM_004573988.1 PREDICTED: Maylandia zebra ras-related protein Rab-2A-like (LOC101480380), mRNA	0.017501377	0.9917702	up
MPF_LOC101486063.1.1	XM_004563250.1 PREDICTED: Maylandia zebra highly divergent homeobox-like (LOC101486063), mRNA	0.044378266	-0.98210144	down
MPF_LOC100692657.1.1	XM_003456343.1 PREDICTED: Oreochromis niloticus chromobox protein homolog 8-like (LOC100692657), mRNA	0.037868377	-0.78449297	down
MPF_LOC100706186.1.2	XM_003460059.1 PREDICTED: Oreochromis niloticus calpain-2 catalytic subunit-like (LOC100706186), mRNA	0.001733547	2.908043	up
MPF_LOC100705620.1.1	XM_003454184.1 PREDICTED: Oreochromis niloticus gamma-crystallin M2-like (LOC100705620), mRNA	0.035858028	2.3217056	up
MPF_LOC101466612.1.2	XM_004549597.1 PREDICTED: Maylandia zebra zinc finger protein 462-like (LOC101466612), transcript variant X1, mRNA	0.00209402	2.710652	up
MPF_LOC100700325.1.1	XP_003457974.1 PREDICTED: hypothetical protein LOC100700325 [Oreochromis niloticus]	0.008195538	2.7560387	up
MPF_LOC100536809.2.2	XP_003198537.1 PREDICTED: zinc finger protein 850-like [Danio rerio]	0.01113301	-0.89054435	down
MPF_contig_009137		0.026436092	1.8821425	up
MPF_LOC101473441.1.1	XM_004558810.1 PREDICTED: Maylandia zebra transcription factor NF-E2 45 kDa subunit-like (LOC101473441), transcript variant X2, mRNA	0.00209402	1.4817522	up
MPF_LOC100698649.10.10	XP_003460222.1 PREDICTED: complement C1q tumor necrosis factor-related protein 3-like [Oreochromis niloticus]	0.007256765	4.622731	up
MPF_LOC100707046.4.12	XM_003454686.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100707046), mRNA	0.008823011	2.722301	up
MPF_NEMVEDRAFT_V1G118504.1.1	XP_001628905.1 predicted protein [Nematostella vectensis]	0.009199617	2.9823308	up
MPF_LOC101475483.1.1	XM_004539773.1 PREDICTED: Maylandia zebra bifunctional glutamate/proline--tRNA ligase-like (LOC101475483), transcript variant X2, mRNA	0.049584605	-0.41137883	down
MPF_contig_046542	XP_003443377.1 PREDICTED: myosin-Ib isoform 1 [Oreochromis niloticus]	0.0434344	-0.61329937	down

MPF_contig_024386		0.001417114	3.6115708	up
MPF_SI_DKEY-222H21.2.1.2	XP_001334961.3 PREDICTED: NACHT, LRR and PYD domains-containing protein 3 [Danio rerio]	0.02104948	2.5704312	up
MPF_LOC100693180.1.1	XP_003452227.1 PREDICTED: hypothetical protein LOC100693180 [Oreochromis niloticus]	0.027302237	-0.52621937	down
MPF_contig_024721		0.04557982	2.5753741	up
MPF_LOC100706211.1.2	XM_003445662.1 PREDICTED: Oreochromis niloticus piwi-like protein 2-like (LOC100706211), mRNA	0.019017402	1.5586476	up
MPF_HACE1.1.3	HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2	3.59E-04	5.7351723	up
MPF_LOC101482220.1.3	XM_004571715.1 PREDICTED: Maylandia zebra h-2 class II histocompatibility antigen gamma chainlike (LOC101482220), mRNA	0.00558936	4.074065	up
MPF_OSTC.2.3	OSTC_DANRE (sp|Q7ZWJ3) Oligosaccharyltransferase complex subunit ostc OS=Danio rerio GN=ostc PE=2 SV=1	0.016034812	1.9090185	up
MPF_LOC100174873.7.10	NM_001267638.1 Gasterosteus aculeatus beta globin (LOC100174873), mRNA gb|AY184355.1| Gasterosteus aculeatus beta globin mRNA, complete cds	0.010548602	2.5230482	up
MPF_LOC100700237.2.3	XM_003457452.1 PREDICTED: Oreochromis niloticus collagen alpha-1(VI) chain-like (LOC100700237), mRNA	0.012094057	4.1958704	up
MPF_LOC101480115.2.2	XM_004555427.1 PREDICTED: Maylandia zebra pituitary tumor-transforming gene 1 proteininteracting protein-like (LOC101480115), mRNA	0.047854975	1.0265874	up
MPF_LOC101465466.1.1	XM_004553276.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily A member 2-like (LOC101465466), mRNA	0.022986831	-0.59552383	down
MPF_LOC100696180.1.1	XR_134816.1 PREDICTED: Oreochromis niloticus fibronectin-like (LOC100696180), miscRNA	0.006532356	5.8268046	up
MPF_LOC100701242.7.9	XM_003459250.1 PREDICTED: Oreochromis niloticus h-2 class II histocompatibility antigen, I-A beta chain-like, transcript variant 1 (LOC100701242), mRNA	0.03322063	2.0662413	up
MPF_LOC101476819.7.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0.003369483	2.7969096	up
MPF_contig_032849		0.013368727	1.9468672	up
MPF_LOC100702379.1.2	XP_003451673.1 PREDICTED: probable peptide chain release factor C12orf65 homolog, mitochondrial-like [Oreochromis niloticus]	0.04281975	-0.5632496	down
MPF_LOC101162897.2.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]	0.001031627	4.064746	up
MPF_LOC100694557.11.24	XM_003458536.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100694557), mRNA	0.023794947	2.4047732	up
MPF_LOC100700407.1.1	XM_003454414.1 PREDICTED: Oreochromis niloticus IGF-like family receptor 1-like (LOC100700407), mRNA	6.10E-04	4.423212	up
MPF_LOC101482440.1.2	XM_004553601.1 PREDICTED: Maylandia zebra macrophage erythroblast attacher-like (LOC101482440), mRNA	0.044869024	-0.6738868	down
MPF_contig_031665		0.009509102	3.0796235	up
MPF_LOC101168228.1.1	XP_004076087.1 PREDICTED: T-cell immunoglobulin and mucin domain-containing protein 4-like [Oryzias latipes]	0.003420229	3.8765574	up
MPF_LOC101466143.1.18	XM_004574840.1 PREDICTED: Maylandia zebra 40S ribosomal protein S18-like (LOC101466143), mRNA	0.012320424	2.106595	up
MPF_ZC2HC1C.1.1	XP_003924603.1 PREDICTED: zinc finger C2HC domain-containing protein 1C homolog isoform 1 [Saimiri boliviensis boliviensis]	0.046479017	-0.6405425	down
MPF_LOC101473055.1.4	XM_004560375.1 PREDICTED: Maylandia zebra basement membrane-specific heparan sulfate proteoglycan core protein-like (LOC101473055), transcript variant X2, mRNA	0.014363623	2.2799954	up
MPF_LOC101468488.7.7	XM_004552241.1 PREDICTED: Maylandia zebra 40S ribosomal protein S11-like (LOC101468488), mRNA	0.043486074	-0.68802595	down
MPF_LOC100634711.1.2	XP_003391247.1 PREDICTED: hypothetical protein LOC100634711 [Amphimedon queenslandica]	0.0107549	2.1992989	up

MPF_contig_009740		0.034256127	1.0481232	up
MPF_LOC101171771.1.2	XM_004077345.1 PREDICTED: Oryzias latipes uncharacterized LOC101171771 (LOC101171771), mRNA	0.009977766	2.4040556	up
MPF_PSV.1.1	PSV_DICDI (sp|P08798) Prespore vesicle protein OS=Dictyostelium discoideum GN=psvA PE=2 SV=3	0.008381675	2.7016747	up
MPF_LOC101161574.4.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.001454429	3.49221	up
MPF_contig_032895		0.001942287	1.8080368	up
MPF_LOC101469930.1.1	XM_004551309.1 PREDICTED: Maylandia zebra inosine-uridine preferring nucleoside hydrolase-like (LOC101469930), transcript variant X2, mRNA	0.037279557	-1.0652319	down
MPF_contig_015435		0.001083207	3.454259	up
MPF_LOC101467796.9.9	XM_004554825.1 PREDICTED: Maylandia zebra nesprin-2-like (LOC101467796), mRNA	0.02424857	1.6562428	up
MPF_LOC101476604.1.1	XM_004548900.1 PREDICTED: Maylandia zebra MAP7 domain-containing protein 1-like (LOC101476604), transcript variant X4, mRNA	0.046732556	0.91148376	up
MPF_contig_015699		0.029445808	1.3373599	up
MPF_LOC101488070.1.1	XM_004543546.1 PREDICTED: Maylandia zebra neprilysin-like (LOC101488070), transcript variant X1, mRNA	0.013368727	5.9836783	up
MPF_LOC101166970.1.1	XP_004073985.1 PREDICTED: uncharacterized protein LOC101166970 [Oryzias latipes]	3.59E-04	4.4760637	up
MPF_LOC101487484.1.1	XM_004560337.1 PREDICTED: Maylandia zebra pleckstrin homology domain-containing family G member 5-like (LOC101487484), transcript variant X1, mRNA	0.002963641	-0.88971514	down
MPF_LOC100693952.1.2	XP_003442761.1 PREDICTED: hypothetical protein LOC100693952 [Oreochromis niloticus]	0.017089954	-0.63916206	down
MPF_LOC100704190.2.2	XR_134884.1 PREDICTED: Oreochromis niloticus complement C4-like (LOC100704190), miscRNA	0.019503621	3.505732	up
MPF_C1QC.1.1	NP_001135251.1 complement C1q subcomponent subunit C precursor [Salmo salar]	0.003106062	2.4166975	up
MPF_LOC100710050.4.6	XM_003446256.1 PREDICTED: Oreochromis niloticus 6.8 kDa mitochondrial proteolipid-like (LOC100710050), mRNA	0.02104948	-0.9722185	down
MPF_LOC100690282.1.1	XP_003445069.1 PREDICTED: tripartite motif-containing protein 39-like [Oreochromis niloticus]	0.027641093	1.5062995	up

MPF_contig_037761		0.01161333	3.1815372	up
MPF_contig_003837		0.002963641	4.426024	up
MPF_LOC100494438.1.4	XP_002935169.1 PREDICTED: putative nuclease HARBI1-like [Xenopus (Silurana) tropicalis]	0.010982486	3.073871	up
MPF_LOC101472300.1.1	XM_004568586.1 PREDICTED: Maylandia zebra uncharacterized LOC101472300 (LOC101472300), mRNA	2.11E-04	4.8405204	up
MPF_PRS6B.1.1	[BBH] PRS6B_RAT (sp|Q63570) 26S protease regulatory subunit 6B OS=Rattus norvegicus GN=Psmc4 PE=1 SV=1	0.004876332	-0.62929624	down
MPF_LOC100933241.7.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.042700395	-0.46835333	down
MPF_LOC100709648.6.13	XM_003457730.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S4-like (LOC100709648), mRNA	0.023434808	-0.87403727	down
MPF_contig_037247		0.001739613	2.7688417	up
MPF_LOC100690809.1.1	XM_003441690.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100690809 (LOC100690809), mRNA	0.011362375	-0.78103113	down
MPF_LOC100700823.1.2	XP_003446356.1 PREDICTED: hypothetical protein LOC100700823 [Oreochromis niloticus]	0.048314296	-0.7531709	down

MPF_contig_020110		0.026052788	1.1471109	up
MPF_contig_044670		0.03554348	-1.5908837	down
MPF_ZO71.4.10	ZO71_XENLA (sp|P18751) Oocyte zinc finger protein XlCOF7.1 (Fragment) OS=Xenopus laevis PE=2 SV=1	0.045249682	-1.0104613	down
MPF_contig_015500		0.001031627	4.060633	up
MPF_LOC100710569.1.1	XP_003443715.1 PREDICTED: WASH complex subunit strumpellin-like [Oreochromis niloticus]	0.049222965	-0.66738707	down
MPF_LOC100695937.1.1	XM_003449613.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100695937 (LOC100695937), mRNA	0.036345366	2.055462	up
MPF_COX42.2.2	[BBH] COX42_THUOB (sp|P80971) Cytochrome c oxidase subunit 4 isoform 2, mitochondrial OS=Thunnus obesus PE=1 SV=2	0.049889382	-0.67383814	down
MPF_LOC100703657.7.12	XM_003456466.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100703657), mRNA	0.045249682	0.95436716	up
MPF_LOC101475042.1.1	XM_004549634.1 PREDICTED: Maylandia zebra dymeclin-like (LOC101475042), transcript variant X1, mRNA	0.021473808	-0.66725534	down
MPF_LOC100697471.2.2	XP_003458746.1 PREDICTED: PWWP domain-containing protein 2B-like [Oreochromis niloticus]	0.036879085	-0.71018225	down
MPF_LOC101162094.3.3	XP_004084518.1 PREDICTED: putative nuclease HARBI1-like [Oryzias latipes]	0.007866101	3.3281853	up
MPF_LOC100699750.3.3	XP_003447686.1 PREDICTED: hypothetical protein LOC100699750 [Oreochromis niloticus]	0.012885527	2.0832999	up
MPF_contig_006727		0.031001762	-0.66779804	down
MPF_LOC101166152.1.2	XM_004075096.1 PREDICTED: Oryzias latipes mixed lineage kinase domain-like protein-like (LOC101166152), mRNA	0.016968872	1.6036196	up
MPF_LOC100488659.3.10	XP_002933173.1 PREDICTED: hypothetical protein LOC100488659 [Xenopus (Silurana) tropicalis]	0.001531586	3.1038747	up
MPF_LOC101485929.2.2	XM_004560148.1 PREDICTED: Maylandia zebra cathepsin S-like (LOC101485929), transcript variant X2, mRNA	0.013368727	3.3811927	up
MPF_FBX38.1.1	[BBH] FBX38_HUMAN (sp|Q6PIJ6) F-box only protein 38 OS=Homo sapiens GN=FBXO38 PE=1 SV=3	0.02861339	-0.82747364	down
MPF_BT2A1.1.1	BT2A1_HUMAN (sp|Q7KYR7) Butyrophilin subfamily 2 member A1 OS=Homo sapiens GN=BTN2A1 PE=1 SV=3	0.008637839	2.7784886	up
MPF_LOC101483727.1.1	XM_004541387.1 PREDICTED: Maylandia zebra nuclear receptor subfamily 4 group A member 3-like (LOC101483727), transcript variant X2, mRNA	0.017876474	2.5085177	up
MPF_LOC101477280.6.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.001998473	3.8617678	up
MPF_contig_027996		0.03554348	2.4008002	up
MPF_contig_028860		0.001564096	4.292222	up
MPF_LYG.3.3	[BBH] LYG_EPICO (sp|Q90X99) Lysozyme g OS=Epinephelus coioides PE=1 SV=1	0.02551738	-0.4571233	down
MPF_LOC100703120.2.3	XP_003458215.1 PREDICTED: hypothetical protein LOC100703120 [Oreochromis niloticus]	0.028586214	2.1020617	up
MPF_LOC101471741.1.1	XM_004546374.1 PREDICTED: Maylandia zebra G patch domain and KOW motifs-containing proteinlike (LOC101471741), mRNA	0.04406637	-0.84416777	down
MPF_LOC100698625.10.22	XM_003456694.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100698625), mRNA	0.007984483	1.6371012	up
MPF_LOC101076460.1.1	XP_003978301.1 PREDICTED: homeobox protein CDX-1-like [Takifugu rubripes]	0.022749815	-0.59091663	down
MPF_LOC100703536.1.1	XP_003447455.1 PREDICTED: interferon-induced helicase C domain-containing protein 1-like [Oreochromis niloticus]	0.037952468	2.0838952	up
MPF_PCGF1.2.2	PCGF1_DANRE (sp|Q7ZYZ7) Polycomb group RING finger protein 1 OS=Danio rerio GN=pcgf1 PE=3 SV=1	0.023778697	2.8605056	up

MPF_contig_002686		0.043455426	-0.83471394	down
MPF_RTBS.12.36	RTBS_DROME (sp|Q95SX7) Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1	0.002112055	4.040797	up
MPF_LOC100695830.1.2	XM_003445456.1 PREDICTED: Oreochromis niloticus serine/arginine-rich splicing factor 4-like, transcript variant 1 (LOC100695830), mRNA	1.57E-04	4.191743	up
MPF_LOC101484994.2.2	XM_004555447.1 PREDICTED: Maylandia zebra UPF0524 protein C3orf70 homolog A-like (LOC101484994), mRNA	0.005308218	3.2371638	up
MPF_RPS7.1.12	XM_003971400.1 PREDICTED: Takifugu rubripes 40S ribosomal protein S7-like (LOC101073757), mRNA	0.03864389	1.7893925	up
MPF_LOC101486993.1.1	XM_004554270.1 PREDICTED: Maylandia zebra sodium-dependent neutral amino acid transporter SLC6A17-like (LOC101486993), mRNA	0.003720693	2.3862784	up
MPF_contig_028605		1.81E-04	4.714762	up
MPF_LOC101464712.2.5	XM_004554817.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2Blike (LOC101464712), transcript variant X2, mRNA	0.028094104	1.6708791	up
MPF_contig_015464		6.43E-04	4.0762377	up

MPF_LOC100703239.1.1	XP_003440200.1 PREDICTED: hypothetical protein LOC100703239 [Oreochromis niloticus]	0.008637839	3.5354636	up
MPF_LOC101471012.1.1	XM_004556045.1 PREDICTED: Maylandia zebra golgin subfamily A member 4-like (LOC101471012), transcript variant X2, mRNA	0.046203203	-0.7833013	down
MPF_LOC101471575.1.1	XM_004554485.1 PREDICTED: Maylandia zebra uncharacterized LOC101471575 (LOC101471575), mRNA	0.044635	-1.2045393	down
MPF_LOC101486623.1.3	XM_004556475.1 PREDICTED: Maylandia zebra nuclear protein 1-like (LOC101486623), transcript variant X2, mRNA	0.036862258	3.3999653	up
MPF_contig_026772	XM_004569431.1 PREDICTED: Maylandia zebra nucleolar protein 7-like (LOC101483852), transcript variant X1, mRNA	0.02654446	-0.66963434	down
MPF_LOC101479424.1.1	XM_004550242.1 PREDICTED: Maylandia zebra fatty aldehyde dehydrogenase-like (LOC101479424), transcript variant X2, mRNA	0.012136511	2.1453023	up
MPF_LOC101474121.7.17	XM_004575391.1 PREDICTED: Maylandia zebra stonustoxin subunit beta-like (LOC101474121), mRNA	0.006576244	2.35325	up
MPF_LOC101076840.1.1	XM_003974902.1 PREDICTED: Takifugu rubripes chemokine-like receptor 1-like (LOC101076840), mRNA	0.002288654	3.5250745	up
MPF_contig_022962		7.08E-04	3.3233538	up
MPF_LOC101488089.1.1	XM_004570084.1 PREDICTED: Maylandia zebra uncharacterized LOC101488089 (LOC101488089), transcript variant X3, mRNA	0.002746439	3.9035773	up
MPF_DDB_G0283527.1.1	XM_633998.1 Dictyostelium discoideum AX4 hypothetical protein (DDB_G0283527) mRNA, complete cds	0.028021984	3.9374151	up
MPF_contig_027052		0.001719659	3.0178752	up
MPF_contig_024051		0.026912019	-0.765904	down
MPF_LOC100490320.1.3	XP_002938353.1 PREDICTED: hypothetical protein LOC100490320 [Xenopus (Silurana) tropicalis]	0.044863876	-0.7826886	down
MPF_LOC101063580.1.1	XP_003966085.1 PREDICTED: syndecan-2-like [Takifugu rubripes]	0.004120294	2.1589828	up
MPF_LOC101466301.1.1	XM_004543748.1 PREDICTED: Maylandia zebra glutamate receptor ionotropic, kainate 4-like (LOC101466301), mRNA	0.049222965	-0.83196163	down
MPF_LOC100702906.1.1	XP_003448860.1 PREDICTED: putative transporter SVOPL-like [Oreochromis niloticus]	0.02127427	-1.3003539	down
MPF_LOC101465173.1.1	XM_004550838.1 PREDICTED: Maylandia zebra COP9 signalosome complex subunit 7a-like (LOC101465173), transcript variant X2, mRNA	0.026520038	-0.76156753	down
MPF_UBB.1.11	UBB_PONPY (sp|P0CG60) Polyubiquitin-B OS=Pongo pygmaeus GN=UBB PE=3 SV=1	0.01605041	-0.74842256	down

MPF_LOC100703560.1.2	XM_003453596.1 PREDICTED: Oreochromis niloticus BRCA1-A complex subunit Abraxas-like (LOC100703560), mRNA	0.03555063	-0.7269511	down
MPF_LOC101464848.5.5	XM_004545232.1 PREDICTED: Maylandia zebra bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]like (LOC101464848), transcript variant X2, mRNA	0.028586214	1.9209476	up
MPF_LOC101468563.1.2	XM_004572588.1 PREDICTED: Maylandia zebra alkaline nuclease-like (LOC101468563), transcript variant X6, mRNA	1.57E-04	2.1571417	up
MPF_SPT5H.1.1	[BBH] SPT5H_DANRE (sp|Q9DDT5) Transcription elongation factor SPT5 OS=Danio rerio GN=supt5h PE=1 SV=1	0.014827	-1.3654675	down
MPF_LOC101478889.2.3	XM_004561424.1 PREDICTED: Maylandia zebra protein yippee-like 2-like (LOC101478889), transcript variant X2, mRNA	0.03917634	-0.47251037	down
MPF_LOC101071185.4.4	XM_003961280.1 PREDICTED: Takifugu rubripes fructose-bisphosphate aldolase A-like (LOC101071185), mRNA	0.005917009	3.0712285	up
MPF_contig_014816		0.009509102	2.5805821	up
MPF_LOC100698625.3.22	XM_003456694.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100698625), mRNA	0.010470707	2.7707486	up
MPF_LOC101068301.2.3	XM_003966217.1 PREDICTED: Takifugu rubripes protein S100-A11-like (LOC101068301), mRNA	8.33E-04	4.5121613	up
MPF_contig_043801		0.026520215	-0.9706607	down
MPF_contig_037637		0.006576244	0.7730336	up
MPF_contig_022315		0.043805894	1.7199068	up
MPF_contig_042931		0.008877138	2.3580186	up
MPF_B2MG.10.10	NM_001198574.1 Salmo salar Beta-2-microglobulin precursor (b2mg), mRNA gb|BT049278.1| Salmo salar clone ssal-rgb2-510-275 Beta-2-microglobulin precursor putative mRNA, complete cds	0.046665516	2.0193796	up
MPF_WDR78.1.3	NP_001018595.1 WD repeat-containing protein 78 [Danio rerio]	0.017876474	-1.7302599	down
MPF_LOC100005864.2.2	XP_001921726.1 PREDICTED: GTPase IMAP family member 8-like [Danio rerio]	0.002516571	3.0094738	up
MPF_contig_032148		0.019035574	-0.74081045	down
MPF_LOC101470306.1.1	XM_004574119.1 PREDICTED: Maylandia zebra uncharacterized LOC101470306 (LOC101470306), mRNA	0.006755633	3.3139195	up
MPF_contig_001047	XM_004559756.1 PREDICTED: Maylandia zebra vitrin-like (LOC101482458), transcript variant X1, mRNA	0.041324485	-1.1133507	down
MPF_LOC101487734.1.2	XM_004571292.1 PREDICTED: Maylandia zebra cytohesin-4-like (LOC101487734), mRNA	7.08E-04	3.7484539	up
MPF_LOC101473855.10.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA	0.004591258	2.2160082	up
MPF_LOC101482854.3.4	XM_004540267.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(q) subunit alpha-like (LOC101482854), transcript variant X3, mRNA	0.014529526	-0.73786116	down
MPF_contig_019388		8.62E-04	2.8861358	up
MPF_LOC101471890.1.1	XM_004559351.1 PREDICTED: Maylandia zebra nuclear GTPase SLIP-GC-like (LOC101471890), mRNA	1.57E-04	3.3782074	up
MPF_LOC100703437.1.1	XP_003446449.1 PREDICTED: homeobox protein Dlx4a-like [Oreochromis niloticus]	0.03405019	-0.80949974	down
MPF_LOC100699821.2.2	XP_003443423.1 PREDICTED: ATP-binding cassette sub-family A member 1-like [Oreochromis niloticus]	0.026101131	-0.75788164	down
MPF_LOC101480162.2.2	XM_004568522.1 PREDICTED: Maylandia zebra ubiquitin-conjugating enzyme E2 E1-like (LOC101480162), mRNA	0.037327815	-0.9594092	down
MPF_LOC101485437.2.2	XM_004573081.1 PREDICTED: Maylandia zebra beta-2-microglobulin-like (LOC101485437), mRNA	0.04817197	2.0253248	up
MPF_RPL18.3.13	XM_003450907.1 PREDICTED: Oreochromis niloticus ribosomal protein L18 (rpl18), mRNA	0.012941425	4.5622234	up

MPF_RTXE.3.6	RTXE_DROME (sp|Q9NBX4) Probable RNA-directed DNA polymerase from transposon X-element OS=Drosophila melanogaster GN=X-elementORF2 PE=3 SV=1	1.57E-04	2.7214346	up
MPF_LOC100696821.1.2	XP_003452493.1 PREDICTED: ictacalcin-like [Oreochromis niloticus]	0.01036082	4.932419	up
MPF_LOC101477439.1.1	XM_004545735.1 PREDICTED: Maylandia zebra mid1-interacting protein 1-like (LOC101477439), mRNA	0.019503621	-0.6718878	down
MPF_LOC101473980.1.1	XM_004546842.1 PREDICTED: Maylandia zebra leucine-rich repeat-containing protein 14-like (LOC101473980), transcript variant X1, mRNA	0.029624822	-0.61812884	down
MPF_CR2.1.1	CR2_MOUSE (sp|P19070) Complement receptor type 2 OS=Mus musculus GN=Cr2 PE=2 SV=1	0.003110101	2.8134403	up
MPF_LOC101156534.1.3	XR_177556.1 PREDICTED: Oryzias latipes synaptotagmin-1-like (LOC101156534), misc_RNA	8.81E-04	2.1600995	up
MPF_LOC100699007.2.2	XM_003442225.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100699007, transcript variant 2 (LOC100699007), mRNA	0.004128271	4.840722	up
MPF_contig_025924	XM_004574349.1 PREDICTED: Maylandia zebra protein FAM49A-like (LOC101486310), transcript variant X2, mRNA	0.001417114	3.3506558	up
MPF_LOC100706983.1.11	XP_003460110.1 PREDICTED: 28S ribosomal protein S28, mitochondrial-like [Oreochromis niloticus]	0.01856408	1.8591332	up
MPF_LOC100695504.1.1	XM_003452685.1 PREDICTED: Oreochromis niloticus ig kappa chain V-I region Walker-like (LOC100695504), mRNA	0.017876474	2.2720017	up
MPF_BLCAP.2.2	[BBH] BLCAP_DANRE (sp|Q9IB61) Bladder cancer-associated protein OS=Danio rerio GN=blcap PE=3 SV=1	0.004188448	-0.67495203	down
MPF_contig_026907		0.003364038	4.2392354	up
MPF_contig_004895		0.041949626	-0.6684904	down
MPF_LOC100695591.1.1	XM_003453256.1 PREDICTED: Oreochromis niloticus tonsoku-like protein-like (LOC100695591), mRNA	0.03734247	-0.70742124	down
MPF_LOC101482705.1.1	XM_004551359.1 PREDICTED: Maylandia zebra insulin receptor substrate 2-like (LOC101482705), mRNA	0.003644931	2.5607934	up
MPF_LOC101469089.4.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA	0.041324485	1.1104635	up
MPF_LOC100694896.1.11	XP_003455674.1 PREDICTED: NACHT, LRR and PYD domains-containing protein 12-like [Oreochromis niloticus]	0.026052147	-0.61572266	down
MPF_LOC101474190.1.1	XM_004547121.1 PREDICTED: Maylandia zebra RING finger protein 122-like (LOC101474190), transcript variant X1, mRNA	0.040712327	-0.7203617	down
MPF_LOC101483324.1.1	XM_004541004.1 PREDICTED: Maylandia zebra regulator of cell cycle RGCC-like (LOC101483324), mRNA	0.032308754	-0.7130999	down
MPF_contig_032259		9.65E-04	3.9432948	up
MPF_contig_023989		0.039703995	2.4273527	up
MPF_contig_031639		0.022260072	3.0127606	up
MPF_LOC101475621.1.1	XM_004568862.1 PREDICTED: Maylandia zebra cytochrome c oxidase assembly factor 6 homolog (LOC101475621), mRNA	0.03571405	-0.6623554	down
MPF_contig_021432		0.001366893	2.809019	up
MPF_LOC100694383.1.2	XP_003458505.1 PREDICTED: protein artemis-like [Oreochromis niloticus]	0.016743813	-0.6296272	down
MPF_LOC100698283.1.1	XP_003438995.1 PREDICTED: NEDD8-activating enzyme E1 catalytic subunit-like isoform 2 [Oreochromis niloticus]	0.028402865	-0.61053276	down
MPF_LOC101160141.1.1	XR_177319.1 PREDICTED: Oryzias latipes keratin, type I cytoskeletal 13-like (LOC101160141), misc_RNA	0.002468569	4.618202	up
MPF_LOC101470738.8.20	XM_004560737.1 PREDICTED: Maylandia zebra actin, cytoplasmic 1-like (LOC101470738), mRNA	0.04242951	0.50362307	up
MPF_LOC101467183.1.2	XM_004550296.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like	3.98E-04	3.1678567	up

	(LOC101467183), transcript variant X7, mRNA			
MPF_LOC100709634.2.3	XM_003455185.1 PREDICTED: Oreochromis niloticus h-2 class II histocompatibility antigen gamma chain-like (LOC100709634), mRNA	0.010453924	4.224257	up
MPF_contig_048319		0.031001762	1.5460396	up
MPF_LOC101468196.2.2	XM_004575285.1 PREDICTED: Maylandia zebra caspase-12-like (LOC101468196), mRNA	4.12E-05	4.3002977	up
MPF_contig_012573		0.007640657	3.6854663	up
MPF_contig_042898		0.049688037	-0.49427038	down
MPF_LOC101486001.1.1	XM_004549577.1 PREDICTED: Maylandia zebra protein C9orf69-like (LOC101486001), mRNA	0.025911832	-0.9490316	down
MPF_contig_021708		3.33E-04	2.3161268	up
MPF_LOC100694351.1.1	XM_003450430.1 PREDICTED: Oreochromis niloticus aryl hydrocarbon receptor nuclear translocator 2-like, transcript variant 1 (LOC100694351), mRNA	0.030171083	3.4403663	up
MPF_LOC101479766.4.5	XM_004565587.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101479766), mRNA	0.015160592	2.4070067	up
MPF_LOC101465192.1.6	XM_004554818.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2Blike (LOC101465192), mRNA	0.041324485	2.6953068	up
MPF_C1QT3.4.4	C1QT3_MOUSE (sp|Q9ES30) Complement C1q tumor necrosis factor-related protein 3 OS=Mus musculus GN=C1qtnf3 PE=2 SV=1	0.013368727	4.3229413	up
MPF_contig_047945		0.021014832	-0.7194433	down
MPF_contig_016136		0.036390092	1.6129441	up
MPF_LOC101475415.1.1	XM_004568342.1 PREDICTED: Maylandia zebra protein FAM83G-like (LOC101475415), transcript variant X2, mRNA	0.007866101	1.9369649	up
MPF_LOC101481996.3.6	XM_004569599.1 PREDICTED: Maylandia zebra interferon regulatory factor 2-binding protein 1-like (LOC101481996), mRNA	0.039518435	1.7149384	up
MPF_LOC100698649.3.10	XP_003460222.1 PREDICTED: complement C1q tumor necrosis factor-related protein 3-like [Oreochromis niloticus]	0.020464122	4.558934	up
MPF_LOC101481376.3.4	XM_004557456.1 PREDICTED: Maylandia zebra heat shock protein beta-1-like (LOC101481376), mRNA	0.008471099	3.9724758	up
MPF_contig_018259		0.0434344	-0.77562803	down
MPF_LOC101476137.1.1	XM_004574406.1 PREDICTED: Maylandia zebra baculoviral IAP repeat-containing protein 6-like (LOC101476137), transcript variant X5, mRNA	9.48E-04	-0.5455651	down
MPF_LOC101485279.3.4	XM_004575517.1 PREDICTED: Maylandia zebra protein FAM222B-like (LOC101485279), transcript variant X2, mRNA	0.026436092	-0.9610648	down
MPF_LOC101477938.4.9	XM_004574058.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101477938), mRNA	4.17E-04	3.496052	up
MPF_LOC100697579.1.2	XP_003439236.1 PREDICTED: cystatin-A1-like [Oreochromis niloticus]	0.011350054	4.888118	up
MPF_LOC101486605.3.3	XM_004551948.1 PREDICTED: Maylandia zebra protein CDV3 homolog (LOC101486605), transcript variant X2, mRNA	0.023639033	-0.65783685	down
MPF_contig_028903		0.021307992	2.2449374	up
MPF_contig_002474		0.02580533	-2.238884	down
MPF_LOC101477850.6.10	XM_004575562.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12like (LOC101477850), mRNA	0.007988929	4.0062656	up
MPF_LOC101464804.1.1	XM_004556769.1 PREDICTED: Maylandia zebra ankyrin-3-like (LOC101464804), transcript variant X1, mRNA	0.02788023	1.9551246	up

MPF_LOC100695137.3.3	XP_003447509.1 PREDICTED: high affinity immunoglobulin epsilon receptor subunit gamma-like [Oreochromis niloticus]	0.002473002	5.126222	up
MPF_LOC101476292.1.1	XM_004567039.1 PREDICTED: Maylandia zebra transgelin-like (LOC101476292), transcript variant X2, mRNA	0.005752388	5.920392	up
MPF_LOC100708025.2.2	XM_003456564.1 PREDICTED: Oreochromis niloticus cytohesin-4-like (LOC100708025), mRNA	0.002546	3.4362655	up
MPF_AHNK.20.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.012997934	1.4106114	up
MPF_LOC100702843.2.2	XP_003455945.1 PREDICTED: protein-tyrosine kinase 2-beta-like [Oreochromis niloticus]	0.00246914	2.7245374	up
MPF_contig_026973	XM_004553863.1 PREDICTED: Maylandia zebra poly [ADP-ribose] polymerase 12-like (LOC101480887), transcript variant X1, mRNA	0.002468569	3.3518472	up
MPF_LOC101474461.1.1	XM_004546190.1 PREDICTED: Maylandia zebra ataxin-1-like (LOC101474461), transcript variant X2, mRNA	0.002546	2.8729162	up
MPF_IGSF3.1.1	IGSF3_HUMAN (sp|O75054) Immunoglobulin superfamily member 3 OS=Homo sapiens GN=IGSF3 PE=2 SV=3	0.015684035	-1.1363858	down
MPF_LOC100707133.1.12	XP_003457606.1 PREDICTED: hypothetical protein LOC100707133 [Oreochromis niloticus]	0.04242951	1.6218619	up
MPF_CD276.6.9	CD276_XENLA (sp|Q68EV1) CD276 antigen homolog OS=Xenopus laevis GN=cd276 PE=2 SV=1	0.002302039	3.0436468	up
MPF_contig_011996		0.026015801	1.437252	up
MPF_LOC101478373.2.2	XM_004545374.1 PREDICTED: Maylandia zebra neurofilament heavy polypeptide-like (LOC101478373), mRNA	0.044863876	-1.3006372	down
MPF_LOC101166773.1.1	XP_004085184.1 PREDICTED: uncharacterized protein LOC101166773, partial [Oryzias latipes]	0.016444676	1.3986475	up
MPF_LOC101468908.1.1	XM_004539040.1 PREDICTED: Maylandia zebra tuberin-like (LOC101468908), transcript variant X5, mRNA	0.044512663	-0.7060547	down
MPF_LOC100697337.2.4	XP_003446015.1 PREDICTED: hypothetical protein LOC100697337 [Oreochromis niloticus]	0.013970896	1.7816718	up
MPF_LOC101470529.3.3	XM_004558267.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 16-Alike (LOC101470529), mRNA	0.034387197	-0.721622	down
MPF_BHWA1_01395.1.1	YP_002721575.1 hypothetical protein BHWA1_01395 [Brachyspira hyodysenteriae WA1]	0.044269416	2.1781483	up
MPF_FA7.2.2	FA7_HUMAN (sp|P08709) Coagulation factor VII OS=Homo sapiens GN=F7 PE=1 SV=1	0.046607666	-0.9655409	down
MPF_contig_023611		0.013970896	3.109242	up
MPF_CD4.1.1	NP_001072091.1 T-cell surface glycoprotein CD4 [Takifugu rubripes]	0.003840653	-0.8835148	down
MPF_LOC100703126.6.7	XM_003459102.1 PREDICTED: Oreochromis niloticus tripartite motif-containing protein 16-like (LOC100703126), mRNA	0.048359927	-0.6031322	down
MPF_contig_020862		0.022185378	1.2708092	up
MPF_LOC101482458.1.3	XM_004559758.1 PREDICTED: Maylandia zebra vitrin-like (LOC101482458), transcript variant X3, mRNA	0.037279557	-0.7092447	down
MPF_LOC100695994.5.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.027893681	-1.1237612	down
MPF_contig_006498		6.83E-04	3.5317407	up
MPF_contig_031891		0.006663353	3.7915459	up
MPF_LOC101487485.1.1	XM_004560899.1 PREDICTED: Maylandia zebra fibroleukin-like (LOC101487485), mRNA	8.62E-04	2.9514308	up
MPF_CD48.2.4	CD48_MOUSE (sp|P18181) CD48 antigen OS=Mus musculus GN=Cd48 PE=1 SV=1	0.001032533	3.777067	up
MPF_LOC100706287.1.1	XP_003448039.1 PREDICTED: CD209 antigen-like [Oreochromis niloticus]	0.012001276	3.876192	up
MPF_contig_011517		0.009831676	-0.58088547	down

MPF_LOC101163417.1.1	XM_004073013.1 PREDICTED: Oryzias latipes heterogeneous nuclear ribonucleoprotein A0-like (LOC101163417), mRNA	0.025561532	-1.0831537	down
MPF_contig_023735		0.016207457	1.3512261	up
MPF_contig_043323		0.028616454	1.5978842	up
MPF_contig_042687		0.002200209	3.0769415	up
MPF_LOC100697522.1.1	XM_003447958.1 PREDICTED: Oreochromis niloticus N-acetylmuramoyl-L-alanine amidase-like (LOC100697522), mRNA	0.015053061	2.5931659	up
MPF_LOC101466869.3.3	XM_004570894.1 PREDICTED: Maylandia zebra KRR1 small subunit processome component homolog (LOC101466869), mRNA	0.01662978	-0.44289783	down
MPF_LOC101485929.1.2	XM_004560148.1 PREDICTED: Maylandia zebra cathepsin S-like (LOC101485929), transcript variant X2, mRNA	0.016257549	3.4417548	up
MPF_LOC101173415.2.3	XP_004079889.1 PREDICTED: thioredoxin-like [Oryzias latipes]	0.031357706	-0.8581829	down
MPF_contig_035115		0.00237142	3.5078335	up
MPF_contig_023056		0.01989737	2.8476663	up

MPF_LOC101168710.1.1	XP_004070984.1 PREDICTED: CD27 antigen-like [Oryzias latipes]	0.007585581	3.927644	up
MPF_LOC100700653.1.1	XP_003448440.1 PREDICTED: REM2- and Rab-like small GTPase 1-like [Oreochromis niloticus]	0.011032867	-0.95182514	down
MPF_LOC101486821.3.3	XM_004562174.1 PREDICTED: Maylandia zebra vacuolar protein sorting-associated protein 54-like (LOC101486821), transcript variant X4, mRNA	0.028497541	-0.6852722	down
MPF_LOC101473901.1.2	XM_004572233.1 PREDICTED: Maylandia zebra CDC42 small effector protein 1-like (LOC101473901), transcript variant X2, mRNA	6.00E-04	4.611373	up
MPF_LOC101471998.1.1	XM_004540134.1 PREDICTED: Maylandia zebra MFS-type transporter SLC18B1-like (LOC101471998), mRNA	0.03554348	-1.7630835	down
MPF_LOC101471898.1.1	XM_004561201.1 PREDICTED: Maylandia zebra short/branched chain specific acyl-CoA dehydrogenase, mitochondrial-like (LOC101471898), mRNA	0.02922682	-0.8239479	down
MPF_LOC100697907.1.2	XP_003456249.1 PREDICTED: NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial-like [Oreochromis niloticus]	0.031447295	-0.9539251	down
MPF_LOC101479241.1.1	XM_004574967.1 PREDICTED: Maylandia zebra transforming growth factor beta-1-induced transcript 1 protein-like (LOC101479241), mRNA	0.034740705	2.2547724	up
MPF_LOC101167218.1.1	XP_004074111.1 PREDICTED: major histocompatibility complex class I-related gene protein-like [Oryzias latipes]	0.048853412	1.1277237	up
MPF_LOC101478250.3.3	XM_004538353.1 PREDICTED: Maylandia zebra flocculation protein FLO11-like (LOC101478250), transcript variant X3, mRNA	0.010192382	4.583131	up
MPF_LOC101484489.9.10	XM_004548851.1 PREDICTED: Maylandia zebra 14-3-3 protein beta/alpha-A-like (LOC101484489), mRNA	0.03420694	0.5837612	up
MPF_LOC100692406.1.1	XP_003439388.1 PREDICTED: nucleolar MIF4G domain-containing protein 1-like [Oreochromis niloticus]	0.027375028	-1.150958	down
MPF_LOC100707640.2.2	XP_003451524.1 PREDICTED: hypothetical protein LOC100707640 [Oreochromis niloticus]	0.03776411	1.4791398	up
MPF_LECG.42.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.03776411	4.1281343	up
MPF_LOC100690203.1.1	XP_003448147.1 PREDICTED: 3'-5' exoribonuclease 1-like [Oreochromis niloticus]	0.04330966	-0.6175346	down
MPF_LOC101486194.1.1	XM_004547649.1 PREDICTED: Maylandia zebra protein CBFA2T2-like (LOC101486194), transcript variant X6, mRNA	0.027153343	-1.882883	down

MPF_LOC101476819.6.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0.004853593	2.7991982	up
MPF_contig_020212		0.04488326	3.9848986	up
MPF_LOC101162274.1.1	XR_177692.1 PREDICTED: Oryzias latipes uncharacterized LOC101162274 (LOC101162274), misc_RNA	0.0429224	-0.57835954	down
MPF_LOC101075983.1.1	XP_003971539.1 PREDICTED: DNA-binding protein RFX6-like [Takifugu rubripes]	0.02788023	-0.8757753	down
MPF_LOC100696796.2.2	XM_003445884.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100696796 (LOC100696796), mRNA	0.002440055	2.9276361	up
MPF_LOC101470011.1.1	XM_004572767.1 PREDICTED: Maylandia zebra agrin-like (LOC101470011), transcript variant X5, mRNA	0.006574786	3.0234823	up
MPF_LOC101477684.2.4	XM_004539594.1 PREDICTED: Maylandia zebra small EDRK-rich factor 2-like (LOC101477684), mRNA	0.043133523	-0.77772427	down
MPF_LOC100710874.10.12	XP_003453997.1 PREDICTED: hypothetical protein LOC100710874 [Oreochromis niloticus]	0.034387197	2.0718992	up
MPF_LOC100698701.1.2	XM_003455230.1 PREDICTED: Oreochromis niloticus protein S100-A13-like (LOC100698701), mRNA	7.00E-04	4.123232	up
MPF_contig_046735		0.042345475	-0.9054565	down
MPF_LOC101476924.2.2	XM_004539957.1 PREDICTED: Maylandia zebra RNA polymerase-associated protein RTF1 homolog (LOC101476924), mRNA	0.032160897	-0.5304003	down
MPF_LOC101467030.1.1	XM_004563996.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 31-like (LOC101467030), mRNA	0.003227499	2.384986	up
MPF_LOC100710313.1.1	XP_003445472.1 PREDICTED: pleckstrin-2-like [Oreochromis niloticus]	0.02797111	-1.1381869	down
MPF_LOC101167345.25.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA	0.034774322	1.5525117	up
MPF_LOC100699882.3.4	XM_003437783.1 PREDICTED: Oreochromis niloticus gelsolin-like (LOC100699882), mRNA	0.009991773	2.5046384	up
MPF_RL23.2.9	RL23_RAT (sp|P62832) 60S ribosomal protein L23 OS=Rattus norvegicus GN=Rpl23 PE=2 SV=1	0.016433666	2.185503	up
MPF_LOC445921.1.1	XP_003979513.1 PREDICTED: Ig mu chain C region membrane-bound form [Takifugu rubripes]	0.00113283	4.200001	up
MPF_LOC101477280.1.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	7.08E-04	3.698094	up
MPF_LOC101160373.1.1	XP_004083232.1 PREDICTED: DNA damage-regulated autophagy modulator protein 1-like [Oryzias latipes]	0.002468569	2.5756078	up
MPF_LOC101474504.4.5	XM_004557613.1 PREDICTED: Maylandia zebra anthrax toxin receptor 1-like (LOC101474504), mRNA	0.001881666	4.0300612	up
MPF_contig_026208		0.002457504	2.621745	up
MPF_LOC101175629.2.2	XM_004086349.1 PREDICTED: Oryzias latipes proteasomal ubiquitin receptor ADRM1-like (LOC101175629), mRNA	0.013726315	-0.726531	down
MPF_contig_009872		0.03168701	1.3900508	up
MPF_LOC100711395.2.3	XM_003449838.1 PREDICTED: Oreochromis niloticus collagenase 3-like (LOC100711395), mRNA	0.026912019	2.0869765	up
MPF_contig_009643		0.022046478	1.191511	up
MPF_LOC101470738.15.20	XM_004560737.1 PREDICTED: Maylandia zebra actin, cytoplasmic 1-like (LOC101470738), mRNA	0.036526952	4.2968884	up
MPF_contig_009454		0.032422595	2.9621983	up
MPF_contig_022672		0.042345475	3.0940938	up
MPF_APOC1.1.1	NP_001134834.1 Apolipoprotein C-I precursor [Salmo salar]	0.009171961	3.6299038	up
MPF_LOC101475513.1.1	XM_004545621.1 PREDICTED: Maylandia zebra EGF-containing fibulin-like extracellular matrix protein 2-like (LOC101475513), mRNA	1.57E-04	4.3323913	up

MPF_LOC100694733.1.1	XP_003438312.1 PREDICTED: pleckstrin-like [Oreochromis niloticus]	0.017144402	2.806075	up

MPF_GTF2H4.1.1	XP_003458568.1 PREDICTED: general transcription factor IIH subunit 4 [Oreochromis niloticus]	0.025474494	-0.9031573	down
MPF_RS7.7.10	RS7_TAKRU (sp|P50894) 40S ribosomal protein S7 OS=Takifugu rubripes GN=rps7 PE=3 SV=1	0.010192382	2.2051504	up
MPF_FHOD3.2.2	XP_003437785.1 PREDICTED: FH1/FH2 domain-containing protein 3 [Oreochromis niloticus]	0.042317577	-0.6562443	down
MPF_LOC101473946.1.3	XM_004540042.1 PREDICTED: Maylandia zebra protein salvador homolog 1-like (LOC101473946), mRNA	0.035858028	-0.5310325	down
MPF_contig_014416		0.029997513	-0.7655639	down
MPF_LOC101464981.1.1	XM_004574536.1 PREDICTED: Maylandia zebra cyclic AMP-dependent transcription factor ATF-4-like (LOC101464981), mRNA	0.0497115	2.6300066	up
MPF_contig_026183	XM_004548669.1 PREDICTED: Maylandia zebra uncharacterized LOC101485992 (LOC101485992), transcript variant X3, mRNA	0.002103607	-1.1466475	down
MPF_contig_027568		3.57E-04	3.9647753	up
MPF_LOC101172433.1.1	XP_004077062.1 PREDICTED: uncharacterized protein LOC101172433 [Oryzias latipes]	0.046479017	-1.290534	down
MPF_contig_022844		0.03884524	-0.440979	down
MPF_contig_035547		0.041035186	2.9646533	up
MPF_RTJK.7.23	RTJK_DROME (sp|P21328) RNA-directed DNA polymerase from mobile element jockey OS=Drosophila melanogaster GN=pol PE=1 SV=1	0.018141897	1.7995453	up
MPF_LOC100712186.1.1	XM_003444184.1 PREDICTED: Oreochromis niloticus glyoxylate reductase-like (LOC100712186), mRNA	0.042419747	-0.6668635	down
MPF_LOC101064915.1.1	XM_003967542.1 PREDICTED: Takifugu rubripes thromboxane-A synthase-like (LOC101064915), mRNA	9.81E-04	3.4125743	up
MPF_LOC101061096.1.1	XM_003962598.1 PREDICTED: Takifugu rubripes ryanodine receptor 3-like (LOC101061096), mRNA	0.047441483	-1.3127612	down
MPF_LOC100691990.2.2	XM_003445526.1 PREDICTED: Oreochromis niloticus annexin A1-like (LOC100691990), mRNA	0.001348924	2.166544	up
MPF_LOC100708289.2.2	XM_003455519.1 PREDICTED: Oreochromis niloticus serine/threonine-protein kinase Chk2-like (LOC100708289), mRNA	0.03917634	-0.9767027	down
MPF_LOC101464899.2.4	XM_004553991.1 PREDICTED: Maylandia zebra protein bassoon-like (LOC101464899), transcript variant X2, mRNA	1.57E-04	2.9259949	up
MPF_LOC101475778.1.1	XM_004563120.1 PREDICTED: Maylandia zebra histamine N-methyltransferase-like (LOC101475778), transcript variant X4, mRNA	0.035689894	-0.9180917	down
MPF_LOC101479507.2.2	XM_004568789.1 PREDICTED: Maylandia zebra T-complex protein 1 subunit alpha-like (LOC101479507), mRNA	8.81E-04	-0.40870434	down
MPF_LOC101065219.1.3	XM_003969289.1 PREDICTED: Takifugu rubripes protein S100-A1-like (LOC101065219), mRNA	1.57E-04	3.6838677	up
MPF_contig_032267		0.0434344	3.436575	up
MPF_FZD6.7.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440 IMAGE:6971142), complete cds	0.022970537	1.1178765	up
MPF_LOC100711484.7.8	XM_003448843.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100711484), mRNA	0.004764388	-0.53337526	down
MPF_LOC101155558.1.1	XM_004082371.1 PREDICTED: Oryzias latipes interferon alpha-inducible protein 27-like protein 2-like (LOC101155558), mRNA	0.010825883	3.4806643	up
MPF_C-MYB.1.1	NM_001104689.2 Oryzias latipes transcription factor C-MYB (c-myb), mRNA	0.048455328	-0.8692322	down

MPF_LOC100708028.2.8	XM_003457397.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 12-like (LOC100708028), mRNA	0.044378266	2.3896585	up
MPF_LOC101484746.1.1	XM_004544275.1 PREDICTED: Maylandia zebra DNA-directed RNA polymerase III subunit RPC4-like (LOC101484746), mRNA	0.024760202	-0.76887083	down
MPF_LOC101073669.1.1	XM_003964261.1 PREDICTED: Takifugu rubripes coatomer subunit zeta-2-like (LOC101073669), mRNA	0.029445808	-1.1966848	down
MPF_DMBT1.5.9	DMBT1_RABIT (sp|Q95218) Deleted in malignant brain tumors 1 protein OS=Oryctolagus cuniculus GN=Dmbt1 PE=1 SV=2	0.012072624	2.4205117	up
MPF_KRA43.1.2	KRA43_HUMAN (sp|Q9BYR4) Keratin-associated protein 4-3 OS=Homo sapiens GN=KRTAP4-3 PE=2 SV=2	0.016444676	2.7739522	up
MPF_LOC100691896.1.1	XM_003445111.1 PREDICTED: Oreochromis niloticus tetratricopeptide repeat protein 4-like (LOC100691896), mRNA	0.01606265	-0.90360737	down
MPF_LOC101479404.3.4	XM_004570313.1 PREDICTED: Maylandia zebra prolactin-1-like (LOC101479404), mRNA	0.005514357	2.722774	up
MPF_LOC100706378.2.2	XM_003444576.1 PREDICTED: Oreochromis niloticus thioredoxin-related transmembrane protein 2-Blike (LOC100706378), mRNA	0.035858028	-0.85424805	down
MPF_contig_008885		0.04342777	-0.7083373	down
MPF_LOC101476071.1.1	XM_004541164.1 PREDICTED: Maylandia zebra uncharacterized LOC101476071 (LOC101476071), mRNA	8.38E-06	3.9349985	up
MPF_LOC100711190.10.17	XM_003443585.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L21-like (LOC100711190), mRNA	0.043623883	-0.4726229	down
MPF_LOC100695915.1.1	XP_003443746.1 PREDICTED: zinc finger protein ZFAT-like [Oreochromis niloticus]	0.034740705	-0.78857327	down
MPF_contig_015676		0.032200683	3.8265045	up
MPF_LOC101486169.4.4	XM_004566076.1 PREDICTED: Maylandia zebra cyclin-T2-like (LOC101486169), mRNA	0.001881666	6.5849495	up
MPF_LOC100708198.1.1	XP_003453989.1 PREDICTED: wiskott-Aldrich syndrome protein family member 3-like [Oreochromis niloticus]	0.022986831	-0.5207739	down
MPF_LOC101487377.1.3	XM_004555180.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 30-like (LOC101487377), transcript variant X2, mRNA	0.008416634	2.9691749	up
MPF_LOC100709967.1.1	XM_003444841.1 PREDICTED: Oreochromis niloticus acylamino-acid-releasing enzyme-like (LOC100709967), mRNA	0.044094026	-0.9977307	down
MPF_contig_014120		0.00834583	4.344848	up
MPF_LOC101471082.1.1	XM_004551978.1 PREDICTED: Maylandia zebra SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 3-like (LOC101471082), transcript variant X3, mRNA	0.023313882	2.6847823	up
MPF_LOC100701489.3.4	XM_003454000.1 PREDICTED: Oreochromis niloticus ATP synthase mitochondrial F1 complex assembly factor 1-like, transcript variant 1 (LOC100701489), mRNA	0.013721257	-0.5253086	down
MPF_contig_023216		0.005421654	2.3416483	up
MPF_LOC101483438.1.1	XM_004543718.1 PREDICTED: Maylandia zebra serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform-like (LOC101483438), transcript variant X1, mRNA	0.049876817	-0.70099926	down
MPF_contig_031514		0.002760018	-0.94868135	down
MPF_LOC101469505.1.1	XM_004563094.1 PREDICTED: Maylandia zebra ephrin-B2a-like (LOC101469505), transcript variant X2, mRNA	2.92E-04	3.810545	up
MPF_LOC100704656.4.4	XM_003438303.1 PREDICTED: Oreochromis niloticus histidine triad nucleotide-binding protein 1-like (LOC100704656), mRNA	0.047009382	-0.9692421	down
MPF_contig_043487		0.006517754	1.7815833	up

MPF_contig_016882		3.34E-04	2.2951689	up
MPF_LOC100710612.1.1	XM_003454616.1 PREDICTED: Oreochromis niloticus macrophage mannose receptor 1-like (LOC100710612), mRNA	0.00451757	3.2127872	up
MPF_ACBD5.1.1	ACBD5_PONAB (sp|Q5R7V3) Acyl-CoA-binding domain-containing protein 5 OS=Pongo abelii GN=ACBD5 PE=2 SV=1	8.81E-04	2.473514	up
MPF_contig_003009	XM_003449656.1 PREDICTED: Oreochromis niloticus transcription factor BTF3-like, transcript variant 1 (LOC100707467), mRNA	0.025755864	-0.80737066	down
MPF_LOC101464848.2.5	XM_004545232.1 PREDICTED: Maylandia zebra bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]like (LOC101464848), transcript variant X2, mRNA	0.0402451	0.854569	up
MPF_contig_020194		1.36E-04	4.7262993	up
MPF_contig_044487		0.009065297	2.610356	up
MPF_contig_014060		0.040898368	0.39253333	up
MPF_LOC101465099.1.1	XM_004557394.1 PREDICTED: Maylandia zebra moesin-like (LOC101465099), mRNA	0.009046079	4.503078	up
MPF_LOC101487032.1.1	XM_004543159.1 PREDICTED: Maylandia zebra ADM-like (LOC101487032), transcript variant X1, mRNA	0.012076636	3.9123912	up
MPF_LOC101487338.1.2	XM_004546896.1 PREDICTED: Maylandia zebra protein AF-10-like (LOC101487338), mRNA	0.0494809	-0.745758	down
MPF_contig_018996		0.04817197	1.3940735	up
MPF_LOC101482256.1.1	XM_004537985.1 PREDICTED: Maylandia zebra breast carcinoma-amplified sequence 3-like (LOC101482256), transcript variant X3, mRNA	0.04450626	-0.96930593	down
MPF_LOC101476871.1.3	XM_004569314.1 PREDICTED: Maylandia zebra nuclear factor 1 C-type-like (LOC101476871), transcript variant X2, mRNA	0.001700591	3.0432134	up
MPF_LOC101475468.3.3	XM_004560663.1 PREDICTED: Maylandia zebra Na(+)/H(+) exchange regulatory cofactor NHE-RF1like (LOC101475468), mRNA	0.038876574	-0.621231	down
MPF_AHNK.11.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.002112055	5.075597	up
MPF_LOC101486277.2.2	XM_004568460.1 PREDICTED: Maylandia zebra uncharacterized LOC101486277 (LOC101486277), mRNA	0.03832713	2.0811899	up
MPF_contig_041104		0.02746211	-0.8854451	down
MPF_LOC101476415.1.1	XM_004548724.1 PREDICTED: Maylandia zebra prostacyclin synthase-like (LOC101476415), mRNA	0.016840367	1.3099527	up
MPF_GUN4.1.5	GUN4_BACS5 (sp|P28622) Endoglucanase 4 OS=Bacillus sp. (strain KSM-522) PE=3 SV=2	0.046134368	-0.7133946	down
MPF_LOC100709179.1.1	XM_003450238.1 PREDICTED: Oreochromis niloticus neuropilin-1a-like (LOC100709179), mRNA	0.043133523	-0.92917585	down
MPF_LOC101487074.1.1	XM_004574997.1 PREDICTED: Maylandia zebra cGMP-specific 3',5'-cyclic phosphodiesterase-like (LOC101487074), transcript variant X3, mRNA	0.016214738	1.2697053	up
MPF_LOC101071508.1.2	XP_003966119.1 PREDICTED: chemokine-like receptor 1-like [Takifugu rubripes]	0.008091031	3.3232062	up
MPF_LOC101464911.1.1	XM_004560530.1 PREDICTED: Maylandia zebra protein FAM181B-like (LOC101464911), mRNA	0.019358166	-1.7489728	down
MPF_LOC101468511.1.1	XM_004558339.1 PREDICTED: Maylandia zebra sodium/myo-inositol cotransporter 2-like (LOC101468511), mRNA	0.034387197	-0.5035959	down
MPF_LOC100691661.1.1	XM_003451671.1 PREDICTED: Oreochromis niloticus THO complex subunit 5 homolog (LOC100691661), mRNA	0.017876474	-0.38352105	down
MPF_NU5M.1.5	NU5M_SALSA (sp|Q9ZZM3) NADH-ubiquinone oxidoreductase chain 5 OS=Salmo salar GN=MT-ND5 PE=3 SV=1	0.035007354	-1.4207883	down

MPF_contig_021336		6.10E-04	2.1705694	up
MPF_LOC101467829.1.2	XM_004565458.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase pim-1-like (LOC101467829), mRNA	0.002094106	2.9882936	up
MPF_LOC101073703.1.1	XP_003974064.1 PREDICTED: DNA-directed RNA polymerases I, II, and III subunit RPABC1-like [Takifugu rubripes]	0.036705527	-0.5559225	down
MPF_LOC101173666.1.1	XP_004082016.1 PREDICTED: poliovirus receptor-related protein 2-like [Oryzias latipes]	0.003303301	2.7866678	up
MPF_LOC101172475.2.2	XM_004086336.1 PREDICTED: Oryzias latipes serine/threonine-protein kinase pim-2-like (LOC101172475), mRNA	0.0499995	-0.6954293	down
MPF_LOC101487208.1.1	XM_004564346.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase ZFP91-like (LOC101487208), transcript variant X3, mRNA	1.57E-04	3.7473211	up
MPF_LOC100699469.2.2	XM_003444301.1 PREDICTED: Oreochromis niloticus mediator of RNA polymerase II transcription subunit 8-like (LOC100699469), mRNA	0.010144662	-0.7103214	down
MPF_LOC101156189.1.1	XM_004076645.1 PREDICTED: Oryzias latipes tetratricopeptide repeat protein 1-like (LOC101156189), mRNA	0.011377938	-0.7527093	down
MPF_LOC100705934.1.1	XM_003443819.1 PREDICTED: Oreochromis niloticus iroquois-class homeodomain protein irx-1-A-like (LOC100705934), mRNA	0.044269416	-0.7169061	down
MPF_LOC101172867.1.1	XP_004083993.1 PREDICTED: transcription factor E2F2-like [Oryzias latipes]	0.020078404	-0.5722361	down
MPF_LOC101478927.1.1	XM_004545195.1 PREDICTED: Maylandia zebra transforming acidic coiled-coil-containing protein 1like (LOC101478927), transcript variant X4, mRNA	0.010470707	1.6514492	up
MPF_LOC101165175.3.3	XM_004078345.1 PREDICTED: Oryzias latipes cathepsin S-like (LOC101165175), mRNA	0.008428021	3.26854	up
MPF_LOC101475700.1.3	XM_004564763.1 PREDICTED: Maylandia zebra phosphate carrier protein, mitochondrial-like (LOC101475700), transcript variant X2, mRNA	0.007230636	2.7160304	up
MPF_LOC101061229.1.1	XM_003976974.1 PREDICTED: Takifugu rubripes tudor and KH domain-containing protein-like (LOC101061229), mRNA	0.017681202	-0.6316471	down
MPF_contig_011938		0.047316227	1.7878132	up
MPF_LOC101484400.4.5	XM_004572910.1 PREDICTED: Maylandia zebra 60S ribosomal protein L22-like 1-like (LOC101484400), mRNA	0.0434344	1.9027481	up
MPF_LOC101065219.2.3	XM_003969289.1 PREDICTED: Takifugu rubripes protein S100-A1-like (LOC101065219), mRNA	2.46E-04	3.8248	up
MPF_LOC101479628.3.3	XM_004554593.1 PREDICTED: Maylandia zebra proto-oncogene c-Rel-like (LOC101479628), mRNA	0.002486534	1.9476233	up
MPF_LOC101170497.4.8	XP_004086004.1 PREDICTED: oocyte zinc finger protein XlCOF6-like [Oryzias latipes]	0.03936484	-1.0255319	down
MPF_LOC101472935.1.1	XM_004576185.1 PREDICTED: Maylandia zebra prestin-like (LOC101472935), mRNA	0.03785587	-1.0292132	down
MPF_RPS7.5.12	XM_003971400.1 PREDICTED: Takifugu rubripes 40S ribosomal protein S7-like (LOC101073757), mRNA	0.043359183	2.5427866	up
MPF_LOC100699721.1.2	XP_003460016.1 PREDICTED: bifunctional protein NCOAT-like, partial [Oreochromis niloticus]	0.043747965	3.0368958	up
MPF_LOC100708289.1.2	XP_003455567.1 PREDICTED: serine/threonine-protein kinase Chk2-like [Oreochromis niloticus]	0.01412041	-1.1176825	down
MPF_LOC100707639.2.2	XP_003451269.1 PREDICTED: membrane-spanning 4-domains subfamily A member 5-like [Oreochromis niloticus]	0.02788023	3.0675333	up
MPF_LOC101481500.3.3	XM_004542966.1 PREDICTED: Maylandia zebra macrophage mannose receptor 1-like (LOC101481500), transcript variant X4, mRNA	0.03168701	3.524352	up
MPF_contig_011981		0.003573118	4.659707	up
MPF_LOC101156484.2.2	XM_004067491.1 PREDICTED: Oryzias latipes CD81 antigen-like (LOC101156484), mRNA	0.001065316	3.2077875	up

MPF_LOC101478816.1.1	XM_004541641.1 PREDICTED: Maylandia zebra ubiquitin carboxyl-terminal hydrolase 45-like (LOC101478816), transcript variant X1, mRNA	0.001719659	2.8760319	up
MPF_contig_021826		0.02104948	2.1785493	up
MPF_CFAH.6.15	CFAH_HUMAN (sp|P08603) Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	8.47E-04	3.2932303	up
MPF_LOC101473855.2.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA	0.003323905	2.4980478	up
MPF_LOC101469207.1.1	XM_004560645.1 PREDICTED: Maylandia zebra c-Jun-amino-terminal kinase-interacting protein 3like (LOC101469207), transcript variant X10, mRNA	0.002614762	2.8966904	up
MPF_contig_011239	XM_004562318.1 PREDICTED: Maylandia zebra TOM1-like protein 2-like (LOC101476649), transcript variant X2, mRNA	0.04683513	-0.5285625	down
MPF_contig_036887		0.03620729	-0.42515415	down
MPF_LOC101483649.1.3	XM_004547734.1 PREDICTED: Maylandia zebra integrin alpha-7-like (LOC101483649), transcript variant X2, mRNA	0.049350053	-0.8084147	down
MPF_LOC100710078.2.2	XM_003453451.1 PREDICTED: Oreochromis niloticus FCH and double SH3 domains protein 2-like (LOC100710078), mRNA	0.023882385	2.872311	up
MPF_ZO22.1.2	ZO22_XENLA (sp|P18745) Oocyte zinc finger protein XlCOF22 OS=Xenopus laevis PE=3 SV=1	0.045051187	-0.68553257	down
MPF_LOC101471773.1.3	XM_004553653.1 PREDICTED: Maylandia zebra dihydropteridine reductase-like (LOC101471773), mRNA	0.007191924	-0.92257166	down
MPF_LOC101464155.1.2	XM_004561739.1 PREDICTED: Maylandia zebra solute carrier family 22 member 5-like (LOC101464155), mRNA	0.017331399	-1.0142454	down
MPF_contig_032910		0.004567914	3.6962607	up
MPF_LOC100690836.1.1	XP_003447492.1 PREDICTED: presequence protease, mitochondrial-like [Oreochromis niloticus]	0.046732556	-0.50099087	down
MPF_LOC101482347.1.1	XR_191458.1 PREDICTED: Maylandia zebra TBC1 domain family member 13-like (LOC101482347), transcript variant X2, misc_RNA	0.015427726	2.0531657	up
MPF_contig_018845		0.021671582	-0.47244927	down
MPF_LOC100712330.1.2	XM_003438072.1 PREDICTED: Oreochromis niloticus ATP synthase subunit g, mitochondrial-like (LOC100712330), mRNA	0.00535355	-1.2139411	down
MPF_LOC100331403.3.3	XM_003200790.1 PREDICTED: Danio rerio hypothetical protein LOC100331403 (LOC100331403), mRNA	0.019503621	1.5760193	up
MPF_LOC101168049.1.1	XM_004072873.1 PREDICTED: Oryzias latipes sushi domain-containing protein 1-like (LOC101168049), mRNA	4.51E-04	2.7465043	up
MPF_LOC100701956.6.6	XM_003456056.1 PREDICTED: Oreochromis niloticus cytochrome c oxidase subunit 7C, mitochondriallike (LOC100701956), mRNA	0.015558531	-0.64856243	down
MPF_LOC101474870.3.3	XM_004556428.1 PREDICTED: Maylandia zebra RNA-binding protein FUS-like (LOC101474870), mRNA	0.044378266	-0.5665126	down
MPF_LOC101468137.1.1	XM_004540589.1 PREDICTED: Maylandia zebra charged multivesicular body protein 3-like (LOC101468137), mRNA	0.034958396	-0.7479163	down
MPF_LOC100706740.1.1	XP_003445045.1 PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein C12orf26 homolog [Oreochromis niloticus]	0.027563581	-0.7016268	down
MPF_LOC101480552.1.1	XM_004544820.1 PREDICTED: Maylandia zebra protein polybromo-1-like (LOC101480552), transcript variant X3, mRNA	0.0434344	-0.6929035	down
MPF_contig_010970		0.022970537	-0.79807425	down
MPF_AHNK.7.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.03715651	-0.6723075	down
MPF_LOC101486284.3.3	XM_004546431.1 PREDICTED: Maylandia zebra transmembrane protein 189-like (LOC101486284), mRNA	0.010982486	-0.5636968	down

MPF_LOC101159641.5.35	XM_004085298.1 PREDICTED: Oryzias latipes tenascin-like (LOC101159641), mRNA	0.002963641	2.3866792	up
MPF_LOC101072145.1.1	XM_003976150.1 PREDICTED: Takifugu rubripes glutathione S-transferase kappa 1-like (LOC101072145), mRNA	0.047854975	-0.4170732	down
MPF_contig_028837		0.030171083	-0.71193933	down
MPF_LOC101479481.1.1	XM_004563952.1 PREDICTED: Maylandia zebra latent-transforming growth factor beta-binding protein 3-like (LOC101479481), transcript variant X2, mRNA	0.001715593	2.7085924	up

MPF_LOC100701242.3.9	XM_003459250.1 PREDICTED: Oreochromis niloticus h-2 class II histocompatibility antigen, I-A beta chain-like, transcript variant 1 (LOC100701242), mRNA	0.009338709	3.8526583	up
MPF_LOC100705878.1.2	XP_003451853.1 PREDICTED: protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha-like [Oreochromis niloticus]	0.01812699	-0.6570864	down
MPF_LOC100707166.2.2	XM_003442172.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100707166 (LOC100707166), mRNA	0.0015351	3.007449	up
MPF_CFAH.11.15	CFAH_BOVIN (sp|Q28085) Complement factor H OS=Bos taurus GN=CFH PE=1 SV=3	0.005904248	1.6917307	up
MPF_contig_000382	XM_004569524.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 29-like (LOC101484386), transcript variant X1, mRNA	0.019029807	-0.9955931	down
MPF_LOC100705415.2.5	XM_003445578.1 PREDICTED: Oreochromis niloticus cytochrome c oxidase subunit 6A, mitochondrial-like (LOC100705415), mRNA	0.046496723	-0.9380331	down
MPF_LOC101077496.1.1	XM_003968940.1 PREDICTED: Takifugu rubripes gamma-glutamylcyclotransferase-like (LOC101077496), mRNA	0.02358756	3.035171	up
MPF_LOC101063002.1.1	XP_003971894.1 PREDICTED: LOW QUALITY PROTEIN: T-cell activation Rho GTPase-activating proteinlike [Takifugu rubripes]	8.81E-04	2.969264	up
MPF_LOC101476773.2.2	XM_004543216.1 PREDICTED: Maylandia zebra serum amyloid A protein-like (LOC101476773), mRNA	0.020375086	-0.68093926	down
MPF_LOC101474649.1.2	XM_004569663.1 PREDICTED: Maylandia zebra zinc finger protein 729-like (LOC101474649), mRNA	0.00209402	2.1420984	up
MPF_LOC101469758.1.3	XM_004558073.1 PREDICTED: Maylandia zebra estradiol 17-beta-dehydrogenase 12-B-like (LOC101469758), mRNA	0.024502428	0.54988956	up
MPF_contig_043823		0.009004667	2.9398503	up
MPF_LOC100693750.1.3	XM_003438089.1 PREDICTED: Oreochromis niloticus 7-alpha-hydroxycholest-4-en-3-one 12-alphahydroxylase-like (LOC100693750), mRNA	0.03994847	-0.6511541	down
MPF_contig_028990		0.01662978	2.7731109	up
MPF_LOC101483994.1.1	XM_004562444.1 PREDICTED: Maylandia zebra zinc finger protein 646-like (LOC101483994), transcript variant X4, mRNA	0.028843079	-0.5293031	down
MPF_contig_017190		6.98E-04	3.5979717	up
MPF_RS7.10.10	RS7_TAKRU (sp|P50894) 40S ribosomal protein S7 OS=Takifugu rubripes GN=rps7 PE=3 SV=1	3.98E-04	2.1745827	up
MPF_IKBKB.2.2	XM_003451030.1 PREDICTED: Oreochromis niloticus inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta (IKBKB), mRNA	9.48E-04	2.7921405	up
MPF_LOC100709019.1.2	XM_003458034.1 PREDICTED: Oreochromis niloticus ATP synthase subunit g, mitochondrial-like (LOC100709019), mRNA	0.047641937	-0.61375046	down
MPF_LOC100700912.1.1	XP_003447360.1 PREDICTED: nuclear pore glycoprotein p62-like [Oreochromis niloticus]	0.024760202	-0.7883392	down
MPF_LOC101466731.1.2	XM_004553632.1 PREDICTED: Maylandia zebra glutamate receptor 2-like (LOC101466731), transcript variant X2, mRNA	0.012072624	2.5108392	up
MPF_contig_043196		0.044612322	-1.0660529	down
MPF_LOC101161674.2.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA	0.00289221	3.2277021	up

MPF_LOC101483532.1.2	XM_004543245.1 PREDICTED: Maylandia zebra transcription factor PU.1-like (LOC101483532), transcript variant X2, mRNA	0.008802448	2.3058743	up
MPF_RS6.6.11	RS6_PROMA (sp|Q7V9F9) 30S ribosomal protein S6 OS=Prochlorococcus marinus (strain SARG / CCMP1375 / SS120) GN=rpsF PE=3 SV=1	0.001733547	3.9648004	up
MPF_contig_048512		0.043133523	-0.5717554	down
MPF_LOC101484929.2.3	XM_004542976.1 PREDICTED: Maylandia zebra CMP-N-acetylneuraminate-beta-1,4-galactoside alpha-2,3-sialyltransferase-like (LOC101484929), mRNA	0.006115756	3.5361981	up
MPF_contig_020972		0.035626214	-0.83609533	down
MPF_LOC101172990.2.36	XM_004073898.1 PREDICTED: Oryzias latipes uncharacterized LOC101172990 (LOC101172990), mRNA	0.015485545	2.9006023	up
MPF_LOC101071928.1.1	XP_003978669.1 PREDICTED: uncharacterized protein LOC101071928 [Takifugu rubripes]	3.28E-06	4.09557	up
MPF_LOC101484322.2.2	XM_004549391.1 PREDICTED: Maylandia zebra zinc finger protein basonuclin-2-like (LOC101484322), transcript variant X3, mRNA	0.02413602	2.3427873	up
MPF_LOC101478201.3.4	XM_004573511.1 PREDICTED: Maylandia zebra laminin subunit gamma-1-like (LOC101478201), transcript variant X2, mRNA	0.047641937	1.9852142	up
MPF_LOC101474357.1.1	XM_004566124.1 PREDICTED: Maylandia zebra anamorsin-like (LOC101474357), mRNA	0.015773721	-0.55460936	down
MPF_LOC100697793.2.2	XM_003447553.1 PREDICTED: Oreochromis niloticus DNA polymerase III polC-type-like (LOC100697793), mRNA	0.028021984	3.4068706	up
MPF_LOC101487772.1.2	XM_004559324.1 PREDICTED: Maylandia zebra alcohol dehydrogenase 1-like (LOC101487772), mRNA	0.002516571	-0.9317198	down
MPF_LOC100698929.1.2	XM_003442472.1 PREDICTED: Oreochromis niloticus E3 ubiquitin-protein ligase RNF25-like (LOC100698929), mRNA	0.02418725	-0.9837408	down
MPF_contig_001934		0.049350053	-0.76647186	down
MPF_LOC101170719.1.1	XM_004081257.1 PREDICTED: Oryzias latipes extracellular sulfatase Sulf-1-like (LOC101170719), mRNA	0.022966782	-0.8871979	down
MPF_contig_022673		0.046004508	-0.97791004	down
MPF_contig_017562		0.017306602	-0.7559537	down
MPF_LOC101482854.1.4	XM_004540267.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(q) subunit alpha-like (LOC101482854), transcript variant X3, mRNA	0.040741388	-0.6182417	down

2. Supplementary table 3

Common genes in (SR24_80+ vs. SR24_45-) ∩ (SR48_80+ vs. SR48_45-):	
Phylofish gene ID	Gene description
MPF_LOC101474419.1.1	XM_004554493.1 PREDICTED: Maylandia zebra sperm-associated antigen 17-like (LOC101474419), mRNA
MPF_contig_016882	
Common genes in (SR48_80+ vs. SR48_45-) ∩ (SR48_80+ vs. SR48_30-):	
Phylofish gene ID	Gene description

MPF_LOC100698998.2.7	XM_003439446.1 PREDICTED: Oreochromis niloticus myosin heavy chain, fast skeletal muscle-like (LOC100698998), mRNA
MPF_LOC101472355.1.1	XM_004556700.1 PREDICTED: Maylandia zebra peripheral myelin protein 22-like (LOC101472355), mRNA
MPF_LOC101476572.2.2	XM_004541074.1 PREDICTED: Maylandia zebra tetraspanin-17-like (LOC101476572), mRNA
MPF_AHNAK.3.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]
MPF_LOC101483521.1.1	XM_004540909.1 PREDICTED: Maylandia zebra early growth response protein 1-like (LOC101483521), mRNA
MPF_LOC100690512.1.1	XP_003438469.1 PREDICTED: hypothetical protein LOC100690512 [Oreochromis niloticus]
MPF_contig_022617	
MPF_RL17.5.5	RL17_RAT (sp|P24049) 60S ribosomal protein L17 OS=Rattus norvegicus GN=Rpl17 PE=2 SV=3
MPF_LOC100702817.2.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA
MPF_LOC101156898.4.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]
MPF_LOC100690258.1.1	XP_003440479.1 PREDICTED: annexin A2-A-like [Oreochromis niloticus]
MPF_LOC101075367.4.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]
MPF_LOC101477280.2.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_LOC101156898.1.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]
MPF_contig_035424	
MPF_LOC101474121.17.17	XM_004575391.1 PREDICTED: Maylandia zebra stonustoxin subunit beta-like (LOC101474121), mRNA
MPF_LOC100933241.9.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA
MPF_LOC101162897.1.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]
MPF_LOC100698096.4.4	XM_003457021.1 PREDICTED: Oreochromis niloticus H/ACA ribonucleoprotein complex subunit 2-like protein-like (LOC100698096), mRNA
MPF_RL37P.1.1	RL37P_RAT (sp|P61515) Putative 60S ribosomal protein L37a OS=Rattus norvegicus GN=Rpl37a-ps1 PE=5 SV=2
MPF_MIR142A.1.1	NR_030090.1 Danio rerio microRNA 142a (mir142a), microRNA
MPF_LOC101477280.5.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_LOC100711796.2.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA
MPF_contig_032146	
MPF_contig_020082	
MPF_contig_024224	
MPF_LOC100933241.11.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA
MPF_LOC101477280.4.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_LOC101161674.1.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA
MPF_contig_018948	WP_006047458.1 hypothetical protein [Burkholderia graminis]
MPF_LOC101161574.14.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA
MPF_LOC100702318.5.5	XP_003458375.1 PREDICTED: galectin-9-like [Oreochromis niloticus]
MPF_LOC101075367.1.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]
MPF_contig_008714	
MPF_contig_043137	
MPF_LOC101155699.2.2	XM_004073699.1 PREDICTED: Oryzias latipes protein S100-A10-like (LOC101155699), mRNA
MPF_LOC100699721.2.2	XP_003460016.1 PREDICTED: bifunctional protein NCOAT-like, partial [Oreochromis niloticus]
MPF_AHNAK.4.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]

MPF_LOC100707140.3.4	XP_003458392.1 PREDICTED: hypothetical protein LOC100707140 [Oreochromis niloticus]
MPF_AHNK.16.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_LY9.3.3	LY9_HUMAN (sp|Q9HBG7) T-lymphocyte surface antigen Ly-9 OS=Homo sapiens GN=LY9 PE=1 SV=3
MPF_LOC101156898.3.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]
MPF_LOC100695691.2.2	XM_003455952.1 PREDICTED: Oreochromis niloticus actin-related protein 2/3 complex subunit 1B-like (LOC100695691), mRNA
MPF_LOC101475950.3.3	XM_004553845.1 PREDICTED: Maylandia zebra cAMP-specific 3',5'-cyclic phosphodiesterase 4B-like (LOC101475950), transcript variant X3, mRNA
MPF_C1QA.2.2	[BBH] C1QA_PIG (sp|Q69DL0) Complement C1q subcomponent subunit A OS=Sus scrofa GN=C1QA PE=2 SV=1
MPF_contig_032442	
MPF_RL37A.1.1	RL37A_XENLA (sp|Q7SZB4) 60S ribosomal protein L37a OS=Xenopus laevis GN=rpl37a PE=3 SV=3
MPF_contig_026335	
MPF_LOC101486559.2.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA
MPF_contig_020945	XM_004542601.1 PREDICTED: Maylandia zebra muscleblind-like protein 1-like (LOC101483053), transcript variant X16, mRNA
MPF_LOC100696784.1.1	XP_003441680.1 PREDICTED: HHIP-like protein 1-like [Oreochromis niloticus]
MPF_LOC101170487.4.4	XM_004085086.1 PREDICTED: Oryzias latipes low-density lipoprotein receptor 2-like (LOC101170487), mRNA
MPF_contig_017097	
MPF_LOC100690793.2.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]
MPF_contig_033424	
MPF_ANXA1.1.2	NP_001098295.1 annexin max3 [Oryzias latipes]
MPF_LOC101477695.1.9	XM_004564867.1 PREDICTED: Maylandia zebra 60S ribosomal protein L18a-like (LOC101477695), transcript variant X2, mRNA
MPF_LOC101169293.6.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA
MPF_ENPP1.1.2	XM_003446358.1 PREDICTED: Oreochromis niloticus ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA
MPF_contig_030749	
MPF_LOC101465148.1.1	XM_004569455.1 PREDICTED: Maylandia zebra brain acid soluble protein 1-like (LOC101465148), transcript variant X1, mRNA
MPF_LOC101465079.2.2	XM_004551108.1 PREDICTED: Maylandia zebra basal cell adhesion molecule-like (LOC101465079), mRNA
MPF_LOC100697750.1.3	XM_003459604.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 14-like (LOC100697750), mRNA
MPF_LOC101471553.1.1	XM_004572678.1 PREDICTED: Maylandia zebra protein capicua homolog (LOC101471553), transcript variant X4, mRNA
MPF_LOC100691105.1.2	XP_003449231.1 PREDICTED: cytochrome c oxidase subunit 8B, mitochondrial-like [Oreochromis niloticus]
MPF_CFAH.8.15	CFAH_BOVIN (sp|Q28085) Complement factor H OS=Bos taurus GN=CFH PE=1 SV=3
MPF_MXAN_5876.1.1	YP_634013.1 hypothetical protein MXAN_5876 [Myxococcus xanthus DK 1622]
MPF_contig_011640	
MPF_LOC101476475.1.1	XM_004562669.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 3-like (LOC101476475), mRNA
MPF_LOC101472370.1.1	XM_004538428.1 PREDICTED: Maylandia zebra gelsolin-like (LOC101472370), transcript variant X2, mRNA
MPF_contig_002650	XM_004079020.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 1 (LOC101161674), mRNA

MPF_LOC100696287.1.2	XP_003450735.1 PREDICTED: C-type lectin domain family 9 member A-like isoform 1 [Oreochromis niloticus]
MPF_LOC101169293.1.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA
MPF_contig_034792	
MPF_LOC100702519.1.1	XM_003441393.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702519), mRNA
MPF_LOC100702817.1.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA
MPF_LOC101486209.1.4	XM_004551098.1 PREDICTED: Maylandia zebra uncharacterized LOC101486209 (LOC101486209), mRNA
MPF_LOC101487243.1.3	XM_004570967.1 PREDICTED: Maylandia zebra pleckstrin homology domain-containing family M member 2-like (LOC101487243), transcript variant X2, mRNA
MPF_LOC101156352.1.1	XP_004077953.1 PREDICTED: ictacalcin-like [Oryzias latipes]
MPF_LOC101480831.3.3	XM_004565417.1 PREDICTED: Maylandia zebra putative 60S ribosomal protein L37a-like (LOC101480831), mRNA
MPF_LOC101078462.1.1	XP_003965271.1 PREDICTED: lysosome membrane protein 2-like [Takifugu rubripes]
MPF_LOC100711510.1.8	XM_003455849.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100711510), mRNA
MPF_LOC101485244.1.1	XM_004568719.1 PREDICTED: Maylandia zebra zinc transporter 1-like (LOC101485244), mRNA
MPF_LOC101477091.1.3	XM_004574318.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101477091), transcript variant X5, mRNA
MPF_LOC100690401.1.3	XP_003454006.1 PREDICTED: hypothetical protein LOC100690401 [Oreochromis niloticus]
MPF_LOC100703589.1.1	XM_003460117.1 PREDICTED: Oreochromis niloticus plasminogen activator inhibitor 1-like (LOC100703589), mRNA
MPF_AHNK.21.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_LOC101075004.1.1	XM_003964966.1 PREDICTED: Takifugu rubripes uncharacterized LOC101075004 (LOC101075004), mRNA
MPF_LOC100696821.2.2	XM_003452445.1 PREDICTED: Oreochromis niloticus ictacalcin-like (LOC100696821), mRNA
MPF_contig_028541	
MPF_HEPHL1.1.1	XM_003446729.1 PREDICTED: Oreochromis niloticus hephaestin-like 1 (HEPHL1), mRNA
MPF_LOC100689711.4.6	XP_003459483.1 PREDICTED: h-2 class I histocompatibility antigen, L-D alpha chain-like [Oreochromis niloticus]
MPF_LOC101465872.1.1	XM_004558783.1 PREDICTED: Maylandia zebra extended synaptotagmin-1-like (LOC101465872), mRNA
MPF_LOC101471935.1.1	XM_004545975.1 PREDICTED: Maylandia zebra transcription factor MafB-like (LOC101471935), mRNA
MPF_LOC100690793.1.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]
MPF_LOC101473612.4.5	XM_004550873.1 PREDICTED: Maylandia zebra sodium/potassium-transporting ATPase subunit alpha-3-like (LOC101473612), transcript variant X2, mRNA
MPF_LOC101464956.1.1	XM_004545486.1 PREDICTED: Maylandia zebra large neutral amino acids transporter small subunit 3-like (LOC101464956), mRNA
MPF_LOC100697415.3.3	XP_003444759.1 PREDICTED: neuroblast differentiation-associated protein AHNAK-like [Oreochromis niloticus]
MPF_K1C18.1.2	K1C18_DANRE (sp|Q7ZTS4) Keratin, type I cytoskeletal 18 OS=Danio rerio GN=krt18 PE=1 SV=2
MPF_contig_036789	
MPF_LOC100710548.3.4	XP_003459320.1 PREDICTED: major histocompatibility complex class I-related gene protein-like [Oreochromis niloticus]
MPF_LOC101481869.4.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA
MPF_LOC100711796.1.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA
MPF_contig_023721	
MPF_TNF6B.1.1	TNF6B_HUMAN (sp|O95407) Tumor necrosis factor receptor superfamily member 6B OS=Homo sapiens GN=TNFRSF6B PE=1 SV=1
MPF_LOC100705618.1.1	XP_003453815.1 PREDICTED: protogenin-like [Oreochromis niloticus]

MPF_LOC101486434.1.2	XM_004560149.1 PREDICTED: Maylandia zebra cathepsin K-like (LOC101486434), mRNA
MPF_LOC100702817.3.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA
MPF_LOC101482128.1.2	XM_004574739.1 PREDICTED: Maylandia zebra MARCKS-related protein-like (LOC101482128), mRNA
MPF_LOC100712517.2.2	XM_003459650.1 PREDICTED: Oreochromis niloticus RNA (guanine-9-)-methyltransferase domain-containing protein 2-like (LOC100712517), mRNA
MPF_LOC101480609.1.2	XM_004539422.1 PREDICTED: Maylandia zebra homeodomain-interacting protein kinase 3-like (LOC101480609), transcript variant X2, mRNA
MPF_LOC101465129.6.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA
MPF_contig_043890	
MPF_LOC100705343.3.3	XM_003450141.1 PREDICTED: Oreochromis niloticus claudin-8-like (LOC100705343), mRNA
MPF_LOC101487936.1.3	XM_004552317.1 PREDICTED: Maylandia zebra F-box/LRR-repeat protein 20-like (LOC101487936), transcript variant X2, mRNA
MPF_contig_026589	
MPF_LOC100692490.2.4	XM_003457423.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L37a-like (LOC100692490), mRNA

MPF_LOC100706186.1.2	XM_003460059.1 PREDICTED: Oreochromis niloticus calpain-2 catalytic subunit-like (LOC100706186), mRNA
MPF_HACE1.1.3	HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2
MPF_LOC101162897.2.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]
MPF_LOC100700407.1.1	XM_003454414.1 PREDICTED: Oreochromis niloticus IGF-like family receptor 1-like (LOC100700407), mRNA
MPF_LOC101161574.4.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA
MPF_LOC101488070.1.1	XM_004543546.1 PREDICTED: Maylandia zebra neprilysin-like (LOC101488070), transcript variant X1, mRNA
MPF_contig_003837	
MPF_contig_015500	
MPF_LOC101477280.6.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_contig_022962	
MPF_LOC101488089.1.1	XM_004570084.1 PREDICTED: Maylandia zebra uncharacterized LOC101488089 (LOC101488089), transcript variant X3, mRNA
MPF_contig_027052	
MPF_LOC101468563.1.2	XM_004572588.1 PREDICTED: Maylandia zebra alkaline nuclease-like (LOC101468563), transcript variant X6, mRNA
MPF_LOC101068301.2.3	XM_003966217.1 PREDICTED: Takifugu rubripes protein S100-A11-like (LOC101068301), mRNA
MPF_LOC101473855.10.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA
MPF_LOC101481486.1.2	XM_004563678.1 PREDICTED: Maylandia zebra MARCKS-related protein-like (LOC101481486), mRNA
MPF_LOC100699007.2.2	XM_003442225.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100699007, transcript variant 2 (LOC100699007), mRNA
MPF_contig_026907	
MPF_contig_032259	
MPF_contig_031639	
MPF_contig_012573	
MPF_contig_021708	

MPF_LOC100695137.3.3	XP_003447509.1 PREDICTED: high affinity immunoglobulin epsilon receptor subunit gamma-like [Oreochromis niloticus]
MPF_LOC101476292.1.1	XM_004567039.1 PREDICTED: Maylandia zebra transgelin-like (LOC101476292), transcript variant X2, mRNA
MPF_LOC100697337.2.4	XP_003446015.1 PREDICTED: hypothetical protein LOC100697337 [Oreochromis niloticus]
MPF_contig_031891	
MPF_CD48.2.4	CD48_MOUSE (sp|P18181) CD48 antigen OS=Mus musculus GN=Cd48 PE=1 SV=1
MPF_LOC101168710.1.1	XP_004070984.1 PREDICTED: CD27 antigen-like [Oryzias latipes]
MPF_LOC101473901.1.2	XM_004572233.1 PREDICTED: Maylandia zebra CDC42 small effector protein 1-like (LOC101473901), transcript variant X2, mRNA
MPF_LOC101478250.3.3	XM_004538353.1 PREDICTED: Maylandia zebra flocculation protein FLO11-like (LOC101478250), transcript variant X3, mRNA
MPF_LOC100698701.1.2	XM_003455230.1 PREDICTED: Oreochromis niloticus protein S100-A13-like (LOC100698701), mRNA
MPF_LOC101477280.1.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_LOC101160373.1.1	XP_004083232.1 PREDICTED: DNA damage-regulated autophagy modulator protein 1-like [Oryzias latipes]
MPF_LOC101475513.1.1	XM_004545621.1 PREDICTED: Maylandia zebra EGF-containing fibulin-like extracellular matrix protein 2-like (LOC101475513), mRNA
MPF_LOC100691990.2.2	XM_003445526.1 PREDICTED: Oreochromis niloticus annexin A1-like (LOC100691990), mRNA
MPF_LOC101486169.4.4	XM_004566076.1 PREDICTED: Maylandia zebra cyclin-T2-like (LOC101486169), mRNA
MPF_contig_014120	
MPF_contig_043487	
MPF_contig_016882	
MPF_ACBD5.1.1	ACBD5_PONAB (sp|Q5R7V3) Acyl-CoA-binding domain-containing protein 5 OS=Pongo abelii GN=ACBD5 PE=2 SV=1
MPF_contig_020194	
MPF_LOC101465099.1.1	XM_004557394.1 PREDICTED: Maylandia zebra moesin-like (LOC101465099), mRNA
MPF_AHNK.11.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_LOC101467829.1.2	XM_004565458.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase pim-1-like (LOC101467829), mRNA
MPF_contig_011981	
MPF_LOC101156484.2.2	XM_004067491.1 PREDICTED: Oryzias latipes CD81 antigen-like (LOC101156484), mRNA
MPF_LOC101473855.2.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA
MPF_LOC101159641.5.35	XM_004085298.1 PREDICTED: Oryzias latipes tenascin-like (LOC101159641), mRNA
MPF_LOC101161674.2.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA
Common genes in (SR48_70+ vs. SR48_45-) ∩ (SR48_70+ vs. SR48_30-):	
Phylofish gene ID	Gene description
MPF_LOC101472355.1.1	XM_004556700.1 PREDICTED: Maylandia zebra peripheral myelin protein 22-like (LOC101472355), mRNA
MPF_LOC101476572.2.2	XM_004541074.1 PREDICTED: Maylandia zebra tetraspanin-17-like (LOC101476572), mRNA
MPF_AHNAK.3.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]
MPF_LOC101475665.1.3	XM_004554127.1 PREDICTED: Maylandia zebra mucin-2-like (LOC101475665), transcript variant X2, mRNA

MPF_contig_020534	
MPF_LOC101483521.1.1	XM_004540909.1 PREDICTED: Maylandia zebra early growth response protein 1-like (LOC101483521), mRNA
MPF_LOC101476812.1.3	XM_004575484.1 PREDICTED: Maylandia zebra DNA-directed RNA polymerase III subunit RPC8-like (LOC101476812), mRNA
MPF_LOC100711025.1.1	XP_003444057.1 PREDICTED: putative helicase Mov10l1-like [Oreochromis niloticus]
MPF_LOC100702817.2.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA
MPF_LOC101156898.4.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]
MPF_ZN214.3.8	ZN214_HUMAN (sp|Q9UL59) Zinc finger protein 214 OS=Homo sapiens GN=ZNF214 PE=2 SV=2
MPF_LOC100690258.1.1	XP_003440479.1 PREDICTED: annexin A2-A-like [Oreochromis niloticus]
MPF_LOC101477280.2.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_LOC101156898.1.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]

MPF_LOC101480875.1.1	XM_004574330.1 PREDICTED: Maylandia zebra proline-, glutamic acid- and leucine-rich protein 1-like (LOC101480875), transcript variant X2, mRNA
MPF_contig_044643	
MPF_contig_013399	
MPF_LOC100703477.2.2	XM_003456383.1 PREDICTED: Oreochromis niloticus DCN1-like protein 5-like (LOC100703477), mRNA
MPF_LOC100933241.9.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA
MPF_SELMODRAFT_443953.1.1	XP_002978779.1 hypothetical protein SELMODRAFT_443953 [Selaginella moellendorffii]
MPF_LOC100698096.4.4	XM_003457021.1 PREDICTED: Oreochromis niloticus H/ACA ribonucleoprotein complex subunit 2-like protein-like (LOC100698096), mRNA
MPF_LOC101477280.5.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_contig_032146	
MPF_contig_020082	
MPF_LOC101466982.1.2	XM_004574455.1 PREDICTED: Maylandia zebra pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial-like (LOC101466982), mRNA
MPF_LOC101480826.9.9	XM_004564784.1 PREDICTED: Maylandia zebra ubiquitin-60S ribosomal protein L40-like (LOC101480826), mRNA
MPF_LOC100933241.11.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA
MPF_LOC101477280.4.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_HACE1.3.3	[BBH] HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2
MPF_LOC101161674.1.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA
MPF_contig_018948	WP_006047458.1 hypothetical protein [Burkholderia graminis]
MPF_LOC101161574.14.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA
MPF_LOC101467885.1.2	XM_004574029.1 PREDICTED: Maylandia zebra calpain-1 catalytic subunit-like (LOC101467885), transcript variant X1, mRNA
MPF_LOC100702318.5.5	XP_003458375.1 PREDICTED: galectin-9-like [Oreochromis niloticus]
MPF_contig_008714	
MPF_contig_043137	
MPF_CJ032.1.1	CJ032_DANRE (sp|Q4V8S9) UPF0693 protein C10orf32 homolog OS=Danio rerio GN=si:ch211-67n3.3 PE=3 SV=1
MPF_contig_038580	

MPF_LOC101468983.2.2	XR_191999.1 PREDICTED: Maylandia zebra uncharacterized LOC101468983 (LOC101468983), misc_RNA
MPF_AHNAK.4.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]
MPF_contig_037980	
MPF_AHNK.16.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_LOC101467642.1.1	XM_004565102.1 PREDICTED: Maylandia zebra ubiquitin-like-conjugating enzyme ATG10-like (LOC101467642), transcript variant X3, mRNA
MPF_LOC101156898.3.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]
MPF_LOC100695691.2.2	XM_003455952.1 PREDICTED: Oreochromis niloticus actin-related protein 2/3 complex subunit 1B-like (LOC100695691), mRNA
MPF_contig_036627	
MPF_LOC100699383.1.6	XM_003445310.1 PREDICTED: Oreochromis niloticus translationally-controlled tumor protein homolog (LOC100699383), mRNA
MPF_LOC101486559.2.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA
MPF_contig_020945	XM_004542601.1 PREDICTED: Maylandia zebra muscleblind-like protein 1-like (LOC101483053), transcript variant X16, mRNA
MPF_contig_001265	XM_004544289.1 PREDICTED: Maylandia zebra rab11 family-interacting protein 1-like (LOC101463597), transcript variant X1, mRNA
MPF_MYO1B.1.2	XP_003443378.1 PREDICTED: myosin-Ib isoform 2 [Oreochromis niloticus]
MPF_contig_023403	
MPF_LOC100696784.1.1	XP_003441680.1 PREDICTED: HHIP-like protein 1-like [Oreochromis niloticus]
MPF_LOC101170487.4.4	XM_004085086.1 PREDICTED: Oryzias latipes low-density lipoprotein receptor 2-like (LOC101170487), mRNA
MPF_contig_017097	
MPF_LOC100690793.2.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]
MPF_LOC101468488.3.7	XM_004552241.1 PREDICTED: Maylandia zebra 40S ribosomal protein S11-like (LOC101468488), mRNA
MPF_LOC101167402.1.2	XM_004080364.1 PREDICTED: Oryzias latipes uncharacterized LOC101167402 (LOC101167402), mRNA
MPF_contig_033424	
MPF_LOC101477532.1.1	XM_004569581.1 PREDICTED: Maylandia zebra claudin-4-like (LOC101477532), mRNA
MPF_LOC100685053.1.1	XP_003434657.1 PREDICTED: polyubiquitin-like [Canis lupus familiaris]
MPF_LOC100769042.1.1	XP_003512927.1 PREDICTED: hypothetical protein LOC100769042 [Cricetulus griseus]
MPF_LOC100697017.2.2	XM_003455478.1 PREDICTED: Oreochromis niloticus ubiquitin-40S ribosomal protein S27a-like (LOC100697017), mRNA
MPF_LOC101481611.1.2	XM_004544911.1 PREDICTED: Maylandia zebra elongation factor Ts, mitochondrial-like (LOC101481611), mRNA
MPF_ENPP1.1.2	XM_003446358.1 PREDICTED: Oreochromis niloticus ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA
MPF_LOC101468606.1.3	XM_004561834.1 PREDICTED: Maylandia zebra protein PBDC1-like (LOC101468606), transcript variant X2, mRNA
MPF_contig_030749	
MPF_UBC.1.5	UBC_RAT (sp|Q63429) Polyubiquitin-C OS=Rattus norvegicus GN=Ubc PE=1 SV=1
MPF_LOC101465148.1.1	XM_004569455.1 PREDICTED: Maylandia zebra brain acid soluble protein 1-like (LOC101465148), transcript variant X1, mRNA
MPF_LOC100698764.2.2	XM_003449126.1 PREDICTED: Oreochromis niloticus probable cation-transporting ATPase 13A2-like (LOC100698764), mRNA
MPF_LOC101465079.2.2	XM_004551108.1 PREDICTED: Maylandia zebra basal cell adhesion molecule-like (LOC101465079), mRNA
MPF_LOC100695799.6.7	XM_003460096.1 PREDICTED: Oreochromis niloticus leukocyte elastase inhibitor-like (LOC100695799), mRNA

MPF_LOC100697750.1.3	XM_003459604.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 14-like (LOC100697750), mRNA
MPF_contig_037474	
MPF_contig_024281	

MPF_MXAN_5876.1.1	YP_634013.1 hypothetical protein MXAN_5876 [Myxococcus xanthus DK 1622]
MPF_contig_011640	
MPF_LOC101062526.1.1	XP_003962815.1 PREDICTED: d-2-hydroxyglutarate dehydrogenase, mitochondrial-like [Takifugu rubripes]
MPF_LOC101476475.1.1	XM_004562669.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 3-like (LOC101476475), mRNA
MPF_contig_002650	XM_004079020.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 1 (LOC101161674), mRNA
MPF_LOC101485532.1.1	XM_004573748.1 PREDICTED: Maylandia zebra nuclear receptor-interacting protein 2-like (LOC101485532), mRNA
MPF_contig_032831	
MPF_LOC100702817.1.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA
MPF_LOC101486209.1.4	XM_004551098.1 PREDICTED: Maylandia zebra uncharacterized LOC101486209 (LOC101486209), mRNA
MPF_LOC100698399.1.1	XM_003444297.1 PREDICTED: Oreochromis niloticus non-specific lipid-transfer protein-like (LOC100698399), mRNA
MPF_LOC101078462.1.1	XP_003965271.1 PREDICTED: lysosome membrane protein 2-like [Takifugu rubripes]
MPF_LOC100711510.1.8	XM_003455849.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100711510), mRNA
MPF_contig_023699	
MPF_LOC101477091.1.3	XM_004574318.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101477091), transcript variant X5, mRNA
MPF_LOC100690401.1.3	XP_003454006.1 PREDICTED: hypothetical protein LOC100690401 [Oreochromis niloticus]
MPF_LOC100703589.1.1	XM_003460117.1 PREDICTED: Oreochromis niloticus plasminogen activator inhibitor 1-like (LOC100703589), mRNA
MPF_AHNK.21.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_contig_024444	
MPF_LOC101075004.1.1	XM_003964966.1 PREDICTED: Takifugu rubripes uncharacterized LOC101075004 (LOC101075004), mRNA
MPF_LOC100696821.2.2	XM_003452445.1 PREDICTED: Oreochromis niloticus ictacalcin-like (LOC100696821), mRNA
MPF_LOC101172863.1.1	XP_004082959.1 PREDICTED: splicing factor 45-like [Oryzias latipes]
MPF_contig_028541	
MPF_contig_014987	
MPF_LOC101464487.2.5	XM_004571832.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase BRSK2-like (LOC101464487), transcript variant X8, mRNA
MPF_B3AT.2.2	B3AT_ONCMY (sp|P32847) Band 3 anion exchange protein OS=Oncorhynchus mykiss GN=slc4a1 PE=2 SV=2
MPF_LOC101465872.1.1	XM_004558783.1 PREDICTED: Maylandia zebra extended synaptotagmin-1-like (LOC101465872), mRNA
MPF_LOC100708802.1.1	XM_003447173.1 PREDICTED: Oreochromis niloticus prolyl endopeptidase-like (LOC100708802), mRNA
MPF_LOC101467113.4.4	XM_004559889.1 PREDICTED: Maylandia zebra nuclear ubiquitous casein and cyclin-dependent kinase substrate 1-like (LOC101467113), mRNA
MPF_LOC100690793.1.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]
MPF_contig_034810	

MPF_contig_040346	
MPF_LOC101473612.4.5	XM_004550873.1 PREDICTED: Maylandia zebra sodium/potassium-transporting ATPase subunit alpha-3-like (LOC101473612), transcript variant X2, mRNA
MPF_contig_048017	
MPF_contig_005684	
MPF_LOC100697415.3.3	XP_003444759.1 PREDICTED: neuroblast differentiation-associated protein AHNAK-like [Oreochromis niloticus]
MPF_LOC101068359.1.1	XP_003962600.1 PREDICTED: gap junction beta-4 protein-like [Takifugu rubripes]
MPF_K1C18.1.2	K1C18_DANRE (sp|Q7ZTS4) Keratin, type I cytoskeletal 18 OS=Danio rerio GN=krt18 PE=1 SV=2
MPF_contig_021996	
MPF_LOC101472401.1.1	XM_004544882.1 PREDICTED: Maylandia zebra coiled-coil domain-containing protein 174-like (LOC101472401), transcript variant X2, mRNA
MPF_LOC100692032.2.6	XP_003458104.1 PREDICTED: E3 ubiquitin/ISG15 ligase TRIM25-like [Oreochromis niloticus]
MPF_contig_036789	
MPF_LOC101482854.4.4	XM_004540267.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(q) subunit alpha-like (LOC101482854), transcript variant X3, mRNA
MPF_contig_017017	
MPF_LOC101481869.4.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA
MPF_RBBP5.1.1	XP_003447710.1 PREDICTED: retinoblastoma-binding protein 5 [Oreochromis niloticus]
MPF_TNF6B.1.1	TNF6B_HUMAN (sp|O95407) Tumor necrosis factor receptor superfamily member 6B OS=Homo sapiens GN=TNFRSF6B PE=1 SV=1
MPF_LOC100705618.1.1	XP_003453815.1 PREDICTED: protogenin-like [Oreochromis niloticus]
MPF_LOC100702817.3.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA
MPF_LOC100712517.2.2	XM_003459650.1 PREDICTED: Oreochromis niloticus RNA (guanine-9-)-methyltransferase domain-containing protein 2-like (LOC100712517), mRNA
MPF_LOC101480609.1.2	XM_004539422.1 PREDICTED: Maylandia zebra homeodomain-interacting protein kinase 3-like (LOC101480609), transcript variant X2, mRNA
MPF_LOC101465129.6.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA
MPF_LOC100710921.1.1	XM_003442353.1 PREDICTED: Oreochromis niloticus protein FAM63B-like (LOC100710921), mRNA
MPF_contig_026589	
MPF_LOC101483933.1.1	XM_004547257.1 PREDICTED: Maylandia zebra coiled-coil domain-containing protein 112-like (LOC101483933), transcript variant X2, mRNA
MPF_LOC100707046.4.12	XM_003454686.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100707046), mRNA
MPF_contig_046542	XP_003443377.1 PREDICTED: myosin-Ib isoform 1 [Oreochromis niloticus]
MPF_HACE1.1.3	HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2
MPF_LOC100696180.1.1	XR_134816.1 PREDICTED: Oreochromis niloticus fibronectin-like (LOC100696180), miscRNA
MPF_LOC100700407.1.1	XM_003454414.1 PREDICTED: Oreochromis niloticus IGF-like family receptor 1-like (LOC100700407), mRNA
MPF_PSV.1.1	PSV_DICDI (sp|P08798) Prespore vesicle protein OS=Dictyostelium discoideum GN=psvA PE=2 SV=3
MPF_LOC101161574.4.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA
MPF_LOC101487484.1.1	XM_004560337.1 PREDICTED: Maylandia zebra pleckstrin homology domain-containing family G member 5-like (LOC101487484), transcript variant X1, mRNA

MPF_contig_003837	
MPF_LOC100690809.1.1	XM_003441690.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100690809 (LOC100690809), mRNA

MPF_contig_015500	
MPF_LOC101477280.6.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_contig_022962	
MPF_contig_027052	
MPF_contig_032148	
MPF_LOC101482854.3.4	XM_004540267.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(q) subunit alpha-like (LOC101482854), transcript variant X3, mRNA
MPF_contig_026907	
MPF_LOC101469089.4.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA
MPF_contig_032259	
MPF_LOC100694383.1.2	XP_003458505.1 PREDICTED: protein artemis-like [Oreochromis niloticus]
MPF_contig_021708	
MPF_LOC101465192.1.6	XM_004554818.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2B-like (LOC101465192), mRNA
MPF_LOC101476137.1.1	XM_004574406.1 PREDICTED: Maylandia zebra baculoviral IAP repeat-containing protein 6-like (LOC101476137), transcript variant X5, mRNA
MPF_LOC101486605.3.3	XM_004551948.1 PREDICTED: Maylandia zebra protein CDV3 homolog (LOC101486605), transcript variant X2, mRNA
MPF_contig_026973	XM_004553863.1 PREDICTED: Maylandia zebra poly [ADP-ribose] polymerase 12-like (LOC101480887), transcript variant X1, mRNA
MPF_LOC101166773.1.1	XP_004085184.1 PREDICTED: uncharacterized protein LOC101166773, partial [Oryzias latipes]
MPF_LOC101468908.1.1	XM_004539040.1 PREDICTED: Maylandia zebra tuberin-like (LOC101468908), transcript variant X5, mRNA
MPF_CD4.1.1	NP_001072091.1 T-cell surface glycoprotein CD4 [Takifugu rubripes]
MPF_contig_031891	
MPF_LOC101473901.1.2	XM_004572233.1 PREDICTED: Maylandia zebra CDC42 small effector protein 1-like (LOC101473901), transcript variant X2, mRNA
MPF_LOC101471998.1.1	XM_004540134.1 PREDICTED: Maylandia zebra MFS-type transporter SLC18B1-like (LOC101471998), mRNA
MPF_LOC101471898.1.1	XM_004561201.1 PREDICTED: Maylandia zebra short/branched chain specific acyl-CoA dehydrogenase, mitochondrial-like (LOC101471898), mRNA
MPF_LOC100692406.1.1	XP_003439388.1 PREDICTED: nucleolar MIF4G domain-containing protein 1-like [Oreochromis niloticus]
MPF_LOC101477280.1.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_LOC101475513.1.1	XM_004545621.1 PREDICTED: Maylandia zebra EGF-containing fibulin-like extracellular matrix protein 2-like (LOC101475513), mRNA
MPF_LOC101073669.1.1	XM_003964261.1 PREDICTED: Takifugu rubripes coatomer subunit zeta-2-like (LOC101073669), mRNA
MPF_LOC100691896.1.1	XM_003445111.1 PREDICTED: Oreochromis niloticus tetratricopeptide repeat protein 4-like (LOC100691896), mRNA
MPF_LOC101486169.4.4	XM_004566076.1 PREDICTED: Maylandia zebra cyclin-T2-like (LOC101486169), mRNA
MPF_contig_016882	
MPF_contig_020194	
MPF_LOC101475468.3.3	XM_004560663.1 PREDICTED: Maylandia zebra Na(+)/H(+) exchange regulatory cofactor NHE-RF1-like (LOC101475468), mRNA
MPF_AHNK.11.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_LOC100691661.1.1	XM_003451671.1 PREDICTED: Oreochromis niloticus THO complex subunit 5 homolog (LOC100691661), mRNA

MPF_LOC101165175.3.3	XM_004078345.1 PREDICTED: Oryzias latipes cathepsin S-like (LOC101165175), mRNA
MPF_LOC101156484.2.2	XM_004067491.1 PREDICTED: Oryzias latipes CD81 antigen-like (LOC101156484), mRNA
MPF_contig_000382	XM_004569524.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 29-like (LOC101484386), transcript variant X1, mRNA
MPF_LOC101484929.2.3	XM_004542976.1 PREDICTED: Maylandia zebra CMP-N-acetylneuraminate-beta-1,4-galactoside alpha-2,3sialyltransferase-like (LOC101484929), mRNA
MPF_LOC101487772.1.2	XM_004559324.1 PREDICTED: Maylandia zebra alcohol dehydrogenase 1-like (LOC101487772), mRNA
MPF_contig_022673	
MPF_LOC101482854.1.4	XM_004540267.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(q) subunit alpha-like (LOC101482854), transcript variant X3, mRNA
Common genes in (SR24_90+ vs. SR24_45-) ∩ (SR24_80+ vs. SR24_45-):	
Phylofish gene ID	Gene description
MPF_LOC101474419.1.1	XM_004554493.1 PREDICTED: Maylandia zebra sperm-associated antigen 17-like (LOC101474419), mRNA
MPF_contig_008230	
MPF_LOC101072249.3.3	XP_003966663.1 PREDICTED: target of Nesh-SH3-like [Takifugu rubripes]
MPF_LOC100708211.3.3	XM_003457561.1 PREDICTED: Oreochromis niloticus GON-4-like protein-like (LOC100708211), mRNA
MPF_contig_015464	
MPF_contig_016882	
Common genes in (SR48_80+ vs. SR48_45-) ∩ (SR48_70+ vs. SR48_45-):	
Phylofish gene ID	Gene description
MPF_LOC101472355.1.1	XM_004556700.1 PREDICTED: Maylandia zebra peripheral myelin protein 22-like (LOC101472355), mRNA
MPF_LOC101476572.2.2	XM_004541074.1 PREDICTED: Maylandia zebra tetraspanin-17-like (LOC101476572), mRNA
MPF_AHNAK.3.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]
MPF_contig_020534	
MPF_LOC101483521.1.1	XM_004540909.1 PREDICTED: Maylandia zebra early growth response protein 1-like (LOC101483521), mRNA
MPF_LOC100702817.2.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA
MPF_LOC101156898.4.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]
MPF_LOC100690258.1.1	XP_003440479.1 PREDICTED: annexin A2-A-like [Oreochromis niloticus]
MPF_LOC101477280.2.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_LOC101156898.1.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]
MPF_contig_002534	
MPF_LOC100933241.9.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA
MPF_LOC100698096.4.4	XM_003457021.1 PREDICTED: Oreochromis niloticus H/ACA ribonucleoprotein complex subunit 2-like protein-like (LOC100698096), mRNA
MPF_LOC101477280.5.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA

MPF_contig_032146	
MPF_contig_020082	
MPF_LOC100933241.11.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA
MPF_LOC101477280.4.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_HACE1.3.3	[BBH] HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2
MPF_LOC101161674.1.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA
MPF_contig_018948	WP_006047458.1 hypothetical protein [Burkholderia graminis]
MPF_LOC101161574.14.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA
MPF_LAMP2.1.1	NP_001133282.1 lysosomal membrane glycoprotein 2 precursor [Salmo salar]
MPF_LOC100702318.5.5	XP_003458375.1 PREDICTED: galectin-9-like [Oreochromis niloticus]
MPF_contig_008714	
MPF_contig_043137	
MPF_contig_038580	
MPF_LOC101468983.2.2	XR_191999.1 PREDICTED: Maylandia zebra uncharacterized LOC101468983 (LOC101468983), misc_RNA
MPF_AHNAK.4.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]
MPF_contig_037980	
MPF_AHNK.16.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_LOC101156898.3.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]
MPF_LOC100695691.2.2	XM_003455952.1 PREDICTED: Oreochromis niloticus actin-related protein 2/3 complex subunit 1B-like (LOC100695691), mRNA
MPF_LOC100699383.1.6	XM_003445310.1 PREDICTED: Oreochromis niloticus translationally-controlled tumor protein homolog (LOC100699383), mRNA
MPF_LOC101486559.2.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA
MPF_contig_020945	XM_004542601.1 PREDICTED: Maylandia zebra muscleblind-like protein 1-like (LOC101483053), transcript variant X16, mRNA
MPF_contig_023403	
MPF_LOC100696784.1.1	XP_003441680.1 PREDICTED: HHIP-like protein 1-like [Oreochromis niloticus]
MPF_LOC101170487.4.4	XM_004085086.1 PREDICTED: Oryzias latipes low-density lipoprotein receptor 2-like (LOC101170487), mRNA
MPF_contig_017097	
MPF_LOC100690793.2.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]
MPF_contig_033424	
MPF_ENPP1.1.2	XM_003446358.1 PREDICTED: Oreochromis niloticus ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA
MPF_contig_030749	
MPF_LOC101465148.1.1	XM_004569455.1 PREDICTED: Maylandia zebra brain acid soluble protein 1-like (LOC101465148), transcript variant X1, mRNA
MPF_LOC101465079.2.2	XM_004551108.1 PREDICTED: Maylandia zebra basal cell adhesion molecule-like (LOC101465079), mRNA
MPF_LOC100695799.6.7	XM_003460096.1 PREDICTED: Oreochromis niloticus leukocyte elastase inhibitor-like (LOC100695799), mRNA
MPF_LOC100697750.1.3	XM_003459604.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 14-like (LOC100697750), mRNA

MPF_MXAN_5876.1.1	YP_634013.1 hypothetical protein MXAN_5876 [Myxococcus xanthus DK 1622]
MPF_contig_011640	
MPF_LOC101476475.1.1	XM_004562669.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 3-like (LOC101476475), mRNA
MPF_contig_002650	XM_004079020.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 1 (LOC101161674), mRNA
MPF_LOC101485532.1.1	XM_004573748.1 PREDICTED: Maylandia zebra nuclear receptor-interacting protein 2-like (LOC101485532), mRNA
MPF_contig_032831	
MPF_LOC100702817.1.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA
MPF_LOC101486209.1.4	XM_004551098.1 PREDICTED: Maylandia zebra uncharacterized LOC101486209 (LOC101486209), mRNA
MPF_LOC101078462.1.1	XP_003965271.1 PREDICTED: lysosome membrane protein 2-like [Takifugu rubripes]
MPF_LOC100711510.1.8	XM_003455849.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100711510), mRNA
MPF_contig_023699	
MPF_LOC100712435.2.2	XP_003459327.1 PREDICTED: major histocompatibility complex class I-related gene protein-like [Oreochromis niloticus]
MPF_LOC101477091.1.3	XM_004574318.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101477091), transcript variant X5, mRNA
MPF_LOC100690401.1.3	XP_003454006.1 PREDICTED: hypothetical protein LOC100690401 [Oreochromis niloticus]
MPF_LOC100703589.1.1	XM_003460117.1 PREDICTED: Oreochromis niloticus plasminogen activator inhibitor 1-like (LOC100703589), mRNA
MPF_AHNK.21.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_contig_024444	
MPF_LOC101075004.1.1	XM_003964966.1 PREDICTED: Takifugu rubripes uncharacterized LOC101075004 (LOC101075004), mRNA
MPF_LOC100696821.2.2	XM_003452445.1 PREDICTED: Oreochromis niloticus ictacalcin-like (LOC100696821), mRNA
MPF_LOC100693306.9.13	XP_003458501.1 PREDICTED: protein NLRC3-like [Oreochromis niloticus]
MPF_contig_028541	
MPF_B3AT.2.2	B3AT_ONCMY (sp|P32847) Band 3 anion exchange protein OS=Oncorhynchus mykiss GN=slc4a1 PE=2 SV=2
MPF_LOC101465872.1.1	XM_004558783.1 PREDICTED: Maylandia zebra extended synaptotagmin-1-like (LOC101465872), mRNA
MPF_LOC100690793.1.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]

MPF_LOC101473612.4.5	XM_004550873.1 PREDICTED: Maylandia zebra sodium/potassium-transporting ATPase subunit alpha-3-like (LOC101473612), transcript variant X2, mRNA
MPF_LOC100697415.3.3	XP_003444759.1 PREDICTED: neuroblast differentiation-associated protein AHNAK-like [Oreochromis niloticus]
MPF_K1C18.1.2	K1C18_DANRE (sp|Q7ZTS4) Keratin, type I cytoskeletal 18 OS=Danio rerio GN=krt18 PE=1 SV=2
MPF_MYH11.1.2	MYH11_MOUSE (sp|O08638) Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1
MPF_contig_036789	
MPF_LOC101481869.4.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA
MPF_RBBP5.1.1	XP_003447710.1 PREDICTED: retinoblastoma-binding protein 5 [Oreochromis niloticus]
MPF_TNF6B.1.1	TNF6B_HUMAN (sp|O95407) Tumor necrosis factor receptor superfamily member 6B OS=Homo sapiens GN=TNFRSF6B PE=1 SV=1
MPF_LOC100705618.1.1	XP_003453815.1 PREDICTED: protogenin-like [Oreochromis niloticus]
MPF_LOC100702817.3.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA

MPF_LOC100712517.2.2	XM_003459650.1 PREDICTED: Oreochromis niloticus RNA (guanine-9-)-methyltransferase domain-containing protein 2-like (LOC100712517), mRNA
MPF_LOC101480609.1.2	XM_004539422.1 PREDICTED: Maylandia zebra homeodomain-interacting protein kinase 3-like (LOC101480609), transcript variant X2, mRNA
MPF_LOC101465129.6.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA
MPF_contig_026589	
MPF_LOC100707046.4.12	XM_003454686.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100707046), mRNA
MPF_HACE1.1.3	HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2
MPF_LOC100696180.1.1	XR_134816.1 PREDICTED: Oreochromis niloticus fibronectin-like (LOC100696180), miscRNA
MPF_LOC100700407.1.1	XM_003454414.1 PREDICTED: Oreochromis niloticus IGF-like family receptor 1-like (LOC100700407), mRNA
MPF_PSV.1.1	PSV_DICDI (sp|P08798) Prespore vesicle protein OS=Dictyostelium discoideum GN=psvA PE=2 SV=3
MPF_LOC101161574.4.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA
MPF_contig_003837	
MPF_LOC101161574.3.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA
MPF_contig_015500	
MPF_LOC101477280.6.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_contig_022962	
MPF_contig_027052	
MPF_contig_019111	
MPF_contig_026907	
MPF_LOC101469089.4.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA
MPF_contig_032259	
MPF_contig_021708	
MPF_LOC101465192.1.6	XM_004554818.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2B-like (LOC101465192), mRNA
MPF_contig_026973	XM_004553863.1 PREDICTED: Maylandia zebra poly [ADP-ribose] polymerase 12-like (LOC101480887), transcript variant X1, mRNA
MPF_LOC101166773.1.1	XP_004085184.1 PREDICTED: uncharacterized protein LOC101166773, partial [Oryzias latipes]
MPF_contig_031891	
MPF_LOC101473901.1.2	XM_004572233.1 PREDICTED: Maylandia zebra CDC42 small effector protein 1-like (LOC101473901), transcript variant X2, mRNA
MPF_LOC101471998.1.1	XM_004540134.1 PREDICTED: Maylandia zebra MFS-type transporter SLC18B1-like (LOC101471998), mRNA
MPF_LOC101477280.1.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_LOC101475513.1.1	XM_004545621.1 PREDICTED: Maylandia zebra EGF-containing fibulin-like extracellular matrix protein 2-like (LOC101475513), mRNA
MPF_LOC101073669.1.1	XM_003964261.1 PREDICTED: Takifugu rubripes coatomer subunit zeta-2-like (LOC101073669), mRNA
MPF_LOC101486169.4.4	XM_004566076.1 PREDICTED: Maylandia zebra cyclin-T2-like (LOC101486169), mRNA
MPF_contig_016882	
MPF_contig_020194	
MPF_AHNK.11.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2

MPF_LOC101165175.3.3	XM_004078345.1 PREDICTED: Oryzias latipes cathepsin S-like (LOC101165175), mRNA
MPF_LOC101156484.2.2	XM_004067491.1 PREDICTED: Oryzias latipes CD81 antigen-like (LOC101156484), mRNA
MPF_LOC101482619.1.3	XM_004556458.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase TAO2-like (LOC101482619), transcript variant X2, mRNA
MPF_LOC101484929.2.3	XM_004542976.1 PREDICTED: Maylandia zebra CMP-N-acetylneuraminate-beta-1,4-galactoside alpha-2,3sialyltransferase-like (LOC101484929), mRNA
Common genes in (SR48_80+ vs. SR48_30-) ∩ (SR48_70+ vs. SR48_30-):	
Phylofish gene ID	Gene description
MPF_contig_034181	
MPF_CD68.2.2	NP_001158857.1 Macrosialin precursor [Salmo salar]
MPF_LOC100696676.4.4	XP_003459127.1 PREDICTED: zinc finger protein 235-like [Oreochromis niloticus]
MPF_LOC100698998.2.7	XM_003439446.1 PREDICTED: Oreochromis niloticus myosin heavy chain, fast skeletal muscle-like (LOC100698998), mRNA
MPF_LOC100706528.4.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA
MPF_LOC101157594.1.1	XP_004065840.1 PREDICTED: uncharacterized protein LOC101157594 [Oryzias latipes]
MPF_LOC101472355.1.1	XM_004556700.1 PREDICTED: Maylandia zebra peripheral myelin protein 22-like (LOC101472355), mRNA
MPF_contig_045041	
MPF_LOC100135188.1.5	NP_001107363.1 uncharacterized protein LOC100135188 [Xenopus (Silurana) tropicalis]
MPF_LOC100702375.2.2	XM_003450215.1 PREDICTED: Oreochromis niloticus 6-phosphofructokinase type C-like (LOC100702375), mRNA
MPF_contig_003522	XM_004551014.1 PREDICTED: Maylandia zebra akirin-1-like (LOC101486208), transcript variant X1, mRNA
MPF_LOC101473402.1.1	XM_004548338.1 PREDICTED: Maylandia zebra protein kinase C and casein kinase substrate in neurons protein 2-like (LOC101473402), transcript variant X3, mRNA
MPF_contig_045446	
MPF_LOC101472043.4.14	XM_004573789.1 PREDICTED: Maylandia zebra tight junction-associated protein 1-like (LOC101472043), transcript variant X4, mRNA
MPF_contig_044599	
MPF_contig_023930	
MPF_contig_040368	
MPF_contig_038379	
MPF_SSL-2.1.2	NP_001117194.1 serum lectin 2 precursor [Salmo salar]
MPF_LOC101470583.3.3	XM_004571226.1 PREDICTED: Maylandia zebra TSC22 domain family protein 1-like (LOC101470583), mRNA
MPF_TTC9B.1.1	NM_001078791.2 Xenopus (Silurana) tropicalis tetratricopeptide repeat domain 9B (ttc9b), mRNA
MPF_LOC101172154.1.1	XP_004068682.1 PREDICTED: epithelial membrane protein 3-like [Oryzias latipes]
MPF_LOC100700496.3.3	XM_003453022.1 PREDICTED: Oreochromis niloticus probable ribonuclease ZC3H12D-like (LOC100700496), mRNA
MPF_LOC101476572.2.2	XM_004541074.1 PREDICTED: Maylandia zebra tetraspanin-17-like (LOC101476572), mRNA
MPF_LOC101155471.2.2	XM_004080809.1 PREDICTED: Oryzias latipes cullin-1-like (LOC101155471), mRNA
MPF_contig_045323	
MPF_LOC101474911.1.1	XM_004566844.1 PREDICTED: Maylandia zebra B-cell receptor CD22-like (LOC101474911), transcript variant X3, mRNA

MPF_AHNAK.3.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]
MPF_LOC101472002.1.2	XM_004541243.1 PREDICTED: Maylandia zebra histone-lysine N-methyltransferase ASH1L-like (LOC101472002), transcript variant X1, mRNA
MPF_THAP9.1.1	[BBH] THAP9_HUMAN (sp|Q9H5L6) DNA transposase THAP9 OS=Homo sapiens GN=THAP9 PE=1 SV=2
MPF_LOC101470829.1.1	XM_004557598.1 PREDICTED: Maylandia zebra desumoylating isopeptidase 1-like (LOC101470829), mRNA
MPF_contig_026757	
MPF_LOC101483521.1.1	XM_004540909.1 PREDICTED: Maylandia zebra early growth response protein 1-like (LOC101483521), mRNA
MPF_LOC100690512.1.1	XP_003438469.1 PREDICTED: hypothetical protein LOC100690512 [Oreochromis niloticus]
MPF_LOC101170712.1.1	XM_004080140.1 PREDICTED: Oryzias latipes hemoglobin subunit beta-1-like (LOC101170712), mRNA
MPF_LOC101476936.1.1	XM_004565493.1 PREDICTED: Maylandia zebra peptidyl-prolyl cis-trans isomerase FKBP1A-like (LOC101476936), mRNA
MPF_LOC101464855.1.1	XM_004546244.1 PREDICTED: Maylandia zebra signal peptide, CUB and EGF-like domain-containing protein 3like (LOC101464855), transcript variant X1, mRNA
MPF_LOC100711025.1.1	XP_003444057.1 PREDICTED: putative helicase Mov10l1-like [Oreochromis niloticus]
MPF_LOC100693993.1.1	XM_003453809.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693993 (LOC100693993), mRNA
MPF_LOC101479407.1.1	XM_004547238.1 PREDICTED: Maylandia zebra macrophage-expressed gene 1 protein-like (LOC101479407), mRNA
MPF_LOC101487734.2.2	XM_004571292.1 PREDICTED: Maylandia zebra cytohesin-4-like (LOC101487734), mRNA
MPF_contig_038012	
MPF_LOC100708275.1.1	XM_003449495.1 PREDICTED: Oreochromis niloticus alpha-aspartyl dipeptidase-like (LOC100708275), mRNA
MPF_LOC101464789.7.10	XM_004574915.1 PREDICTED: Maylandia zebra heat shock cognate 71 kDa protein-like (LOC101464789), mRNA
MPF_LOC101486244.2.2	XM_004539011.1 PREDICTED: Maylandia zebra transcription factor MafG-like (LOC101486244), transcript variant X3, mRNA
MPF_LOC100706528.6.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA
MPF_contig_022617	
MPF_RL17.5.5	RL17_RAT (sp|P24049) 60S ribosomal protein L17 OS=Rattus norvegicus GN=Rpl17 PE=2 SV=3
MPF_LOC100702817.2.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA
MPF_LOC101486439.1.1	XM_004561632.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 21-like (LOC101486439), mRNA
MPF_LOC101156898.4.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]
MPF_LOC100690258.1.1	XP_003440479.1 PREDICTED: annexin A2-A-like [Oreochromis niloticus]
MPF_LOC101075367.4.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]
MPF_ZG57.7.12	ZG57_XENLA (sp|P18729) Gastrula zinc finger protein XlCGF57.1 (Fragment) OS=Xenopus laevis PE=3 SV=1
MPF_LOC101477280.2.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_contig_044194	
MPF_MOR1A.1.1	[BBH] MOR1A_CHICK (sp|Q2YHT7) Cell surface glycoprotein CD200 receptor 1-A OS=Gallus gallus GN=CD200R1A PE=1 SV=1
MPF_LOC101156898.1.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]
MPF_contig_036689	
MPF_contig_035424	
MPF_contig_013399	
MPF_LOC101474121.17.17	XM_004575391.1 PREDICTED: Maylandia zebra stonustoxin subunit beta-like (LOC101474121), mRNA

MPF_LOC101477399.1.1	XM_004538348.1 PREDICTED: Maylandia zebra uncharacterized LOC101477399 (LOC101477399), mRNA
MPF_LOC100933241.9.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA
MPF_LOC101472694.2.4	XM_004542457.1 PREDICTED: Maylandia zebra ephrin type-A receptor 3-like (LOC101472694), transcript variant X2, mRNA
MPF_contig_015342	
MPF_LOC101162897.1.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]
MPF_LOC101485932.1.1	XM_004538480.1 PREDICTED: Maylandia zebra phosphatidylinositol 4-phosphate 5-kinase type-1 beta-like (LOC101485932), transcript variant X2, mRNA
MPF_LOC100698096.4.4	XM_003457021.1 PREDICTED: Oreochromis niloticus H/ACA ribonucleoprotein complex subunit 2-like protein-like (LOC100698096), mRNA
MPF_contig_016131	
MPF_RL37P.1.1	RL37P_RAT (sp|P61515) Putative 60S ribosomal protein L37a OS=Rattus norvegicus GN=Rpl37a-ps1 PE=5 SV=2
MPF_MIR142A.1.1	NR_030090.1 Danio rerio microRNA 142a (mir142a), microRNA
MPF_LOC101477280.5.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_AHNK.17.22	[BBH] AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_LOC101062855.1.1	XM_003970797.1 PREDICTED: Takifugu rubripes polyubiquitin-B-like, transcript variant 2 (LOC101062855), mRNA
MPF_LOC101474370.1.1	XM_004568239.1 PREDICTED: Maylandia zebra mitochondrial glutamate carrier 1-like (LOC101474370), transcript variant X3, mRNA
MPF_LOC100706657.3.3	XP_003447550.1 PREDICTED: CD48 antigen-like [Oreochromis niloticus]

MPF_LOC100711796.2.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA
MPF_contig_032146	
MPF_LOC101485578.1.1	XM_004539623.1 PREDICTED: Maylandia zebra CD276 antigen-like (LOC101485578), mRNA
MPF_contig_020082	
MPF_contig_024224	
MPF_MYHM2126-2.1.3	XP_003975582.1 PREDICTED: myosin-7 [Takifugu rubripes]
MPF_LOC101480826.9.9	XM_004564784.1 PREDICTED: Maylandia zebra ubiquitin-60S ribosomal protein L40-like (LOC101480826), mRNA
MPF_LOC100933241.11.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA
MPF_B2MG.3.10	B2MG_CYPCA (sp|Q03422) Beta-2-microglobulin OS=Cyprinus carpio GN=b2m PE=3 SV=1
MPF_LOC101069906.1.1	XP_003969359.1 PREDICTED: tissue factor pathway inhibitor-like [Takifugu rubripes]
MPF_LOC101477280.4.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_LOC101161674.1.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA
MPF_contig_018948	WP_006047458.1 hypothetical protein [Burkholderia graminis]
MPF_LOC101161574.14.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA
MPF_LOC101481543.7.7	XM_004550249.1 PREDICTED: Maylandia zebra zinc finger BED domain-containing protein 1-like (LOC101481543), mRNA
MPF_contig_021317	
MPF_LOC101481234.4.12	XM_004569866.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2B-like (LOC101481234), mRNA
MPF_contig_029207	
MPF_LOC100702318.5.5	XP_003458375.1 PREDICTED: galectin-9-like [Oreochromis niloticus]

MPF_CAL6303_1855.1.3	YP_007136861.1 hypothetical protein Cal6303_1855 [Calothrix sp. PCC 6303]
MPF_LOC101065219.3.3	XM_003969289.1 PREDICTED: Takifugu rubripes protein S100-A1-like (LOC101065219), mRNA
MPF_LOC101075367.1.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]
MPF_LOC101159291.2.2	XM_004078003.1 PREDICTED: Oryzias latipes sodium/potassium-transporting ATPase subunit alpha-3-like (LOC101159291), mRNA
MPF_contig_008714	
MPF_LOC101173086.4.5	XP_004077318.1 PREDICTED: G-protein coupled receptor 4-like [Oryzias latipes]
MPF_contig_023224	
MPF_contig_045616	
MPF_contig_028716	
MPF_contig_043137	
MPF_LOC100698082.2.2	XR_134880.1 PREDICTED: Oreochromis niloticus keratin, type I cytoskeletal 13-like (LOC100698082), miscRNA
MPF_LOC101155699.2.2	XM_004073699.1 PREDICTED: Oryzias latipes protein S100-A10-like (LOC101155699), mRNA
MPF_LOC101077514.3.5	XP_003974477.1 PREDICTED: complement factor H-like [Takifugu rubripes]
MPF_LOC100693648.1.1	XM_003456513.1 PREDICTED: Oreochromis niloticus probable methyltransferase C20orf7 homolog, mitochondrial-like (LOC100693648), mRNA
MPF_LOC100699721.2.2	XP_003460016.1 PREDICTED: bifunctional protein NCOAT-like, partial [Oreochromis niloticus]
MPF_LOC100700605.10.27	XM_003458555.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100700605), mRNA
MPF_LOC100712299.1.1	XM_003451996.1 PREDICTED: Oreochromis niloticus myoferlin-like (LOC100712299), mRNA
MPF_LOC101478586.2.2	XM_004550792.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 6-like (LOC101478586), transcript variant X2, mRNA
MPF_AHNAK.4.4	XP_687696.3 PREDICTED: neuroblast differentiation-associated protein AHNAK [Danio rerio]
MPF_LOC100707140.3.4	XP_003458392.1 PREDICTED: hypothetical protein LOC100707140 [Oreochromis niloticus]
MPF_LOC101465129.15.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA
MPF_contig_027340	
MPF_LOC101487021.1.1	XM_004540761.1 PREDICTED: Maylandia zebra thrombospondin-1-like (LOC101487021), transcript variant X2, mRNA
MPF_AHNK.16.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_LOC101485716.5.12	XM_004572825.1 PREDICTED: Maylandia zebra multivesicular body subunit 12B-like (LOC101485716), mRNA
MPF_RS13.9.9	RS13_GILMI (sp|Q9DFR6) 40S ribosomal protein S13 OS=Gillichthys mirabilis GN=rps13 PE=2 SV=3
MPF_LOC101477831.3.3	XM_004548827.1 PREDICTED: Maylandia zebra complement C1q subcomponent subunit B-like (LOC101477831), mRNA
MPF_ZKSC3.1.1	ZKSC3_HUMAN (sp|Q9BRR0) Zinc finger protein with KRAB and SCAN domains 3 OS=Homo sapiens GN=ZKSCAN3 PE=1 SV=2
MPF_LY9.3.3	LY9_HUMAN (sp|Q9HBG7) T-lymphocyte surface antigen Ly-9 OS=Homo sapiens GN=LY9 PE=1 SV=3
MPF_SI_CH211-125E6.5.1.1	XP_001337601.1 PREDICTED: type-2 ice-structuring protein-like [Danio rerio]
MPF_LOC100707411.2.2	XM_003458503.1 PREDICTED: Oreochromis niloticus E3 ubiquitin-protein ligase ZNRF2-like (LOC100707411), mRNA
MPF_LOC101469126.1.1	XM_004562729.1 PREDICTED: Maylandia zebra monocarboxylate transporter 13-like (LOC101469126), transcript variant X5, mRNA
MPF_contig_009677	
MPF_LOC101484994.1.2	XM_004555447.1 PREDICTED: Maylandia zebra UPF0524 protein C3orf70 homolog A-like (LOC101484994), mRNA
MPF_LOC101156898.3.4	XP_004071781.1 PREDICTED: uncharacterized protein LOC101156898 [Oryzias latipes]

MPF_LOC100695691.2.2	XM_003455952.1 PREDICTED: Oreochromis niloticus actin-related protein 2/3 complex subunit 1B-like (LOC100695691), mRNA
MPF_contig_024249	
MPF_LOC101475950.3.3	XM_004553845.1 PREDICTED: Maylandia zebra cAMP-specific 3',5'-cyclic phosphodiesterase 4B-like (LOC101475950), transcript variant X3, mRNA
MPF_C1QA.2.2	[BBH] C1QA_PIG (sp|Q69DL0) Complement C1q subcomponent subunit A OS=Sus scrofa GN=C1QA PE=2 SV=1
MPF_contig_032442	
MPF_LOC100691043.5.5	XM_003457742.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 12-like (LOC100691043), mRNA
MPF_LOC100710259.1.2	XM_003450909.1 PREDICTED: Oreochromis niloticus NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3-like (LOC100710259), mRNA
MPF_RL37A.1.1	RL37A_XENLA (sp|Q7SZB4) 60S ribosomal protein L37a OS=Xenopus laevis GN=rpl37a PE=3 SV=3
MPF_LOC100708534.1.1	XM_003447507.1 PREDICTED: Oreochromis niloticus myeloid-associated differentiation marker homolog (LOC100708534), mRNA
MPF_MAG.1.4	MAG_RAT (sp|P07722) Myelin-associated glycoprotein OS=Rattus norvegicus GN=Mag PE=1 SV=1
MPF_contig_020726	
MPF_contig_026335	

MPF_LOC101486559.2.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA
MPF_LOC101469336.3.3	XM_004566007.1 PREDICTED: Maylandia zebra ras-related protein M-Ras-like (LOC101469336), mRNA
MPF_LOC101475205.1.2	XM_004543789.1 PREDICTED: Maylandia zebra lissencephaly-1 homolog (LOC101475205), transcript variant X4, mRNA
MPF_contig_020945	XM_004542601.1 PREDICTED: Maylandia zebra muscleblind-like protein 1-like (LOC101483053), transcript variant X16, mRNA
MPF_LOC101477243.1.1	XM_004544896.1 PREDICTED: Maylandia zebra rho guanine nucleotide exchange factor 25-like (LOC101477243), transcript variant X3, mRNA
MPF_LOC100696784.1.1	XP_003441680.1 PREDICTED: HHIP-like protein 1-like [Oreochromis niloticus]
MPF_LOC101170487.4.4	XM_004085086.1 PREDICTED: Oryzias latipes low-density lipoprotein receptor 2-like (LOC101170487), mRNA
MPF_contig_032239	
MPF_contig_017097	
MPF_LOC101479522.1.2	XM_004547622.1 PREDICTED: Maylandia zebra acid-sensing ion channel 1-like (LOC101479522), transcript variant X5, mRNA
MPF_LOC100690793.2.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]
MPF_LOC101480396.1.1	XM_004552665.1 PREDICTED: Maylandia zebra 5'-AMP-activated protein kinase subunit gamma-2-like (LOC101480396), transcript variant X2, mRNA
MPF_LOC101468488.3.7	XM_004552241.1 PREDICTED: Maylandia zebra 40S ribosomal protein S11-like (LOC101468488), mRNA
MPF_contig_006069	
MPF_contig_015875	
MPF_contig_007959	
MPF_contig_033424	
MPF_contig_035511	XM_004558926.1 PREDICTED: Maylandia zebra ketohexokinase-like (LOC101480218), transcript variant X3, mRNA
MPF_LOC100697541.1.1	XP_003452659.1 PREDICTED: ADP-ribosylation factor GTPase-activating protein 2-like [Oreochromis niloticus]
MPF_CD63.1.2	NM_001124496.1 Oncorhynchus mykiss Cd63 antigen (cd63), mRNA gb|AY593998.1| Oncorhynchus mykiss CD63 (CD63) mRNA, complete cds

MPF_contig_035918	
MPF_LOC101481611.1.2	XM_004544911.1 PREDICTED: Maylandia zebra elongation factor Ts, mitochondrial-like (LOC101481611), mRNA
MPF_LOC100709074.1.1	XM_003448084.1 PREDICTED: Oreochromis niloticus T-complex protein 1 subunit beta-like (LOC100709074), mRNA
MPF_ANXA1.1.2	NP_001098295.1 annexin max3 [Oryzias latipes]
MPF_LOC101477695.1.9	XM_004564867.1 PREDICTED: Maylandia zebra 60S ribosomal protein L18a-like (LOC101477695), transcript variant X2, mRNA
MPF_LOC101169293.6.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA
MPF_ENPP1.1.2	XM_003446358.1 PREDICTED: Oreochromis niloticus ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA
MPF_LOC101468606.1.3	XM_004561834.1 PREDICTED: Maylandia zebra protein PBDC1-like (LOC101468606), transcript variant X2, mRNA
MPF_contig_030749	
MPF_UBC.1.5	UBC_RAT (sp|Q63429) Polyubiquitin-C OS=Rattus norvegicus GN=Ubc PE=1 SV=1
MPF_LOC101465148.1.1	XM_004569455.1 PREDICTED: Maylandia zebra brain acid soluble protein 1-like (LOC101465148), transcript variant X1, mRNA
MPF_LOC100692629.1.1	XM_003448362.1 PREDICTED: Oreochromis niloticus complement C1q subcomponent subunit C-like, transcript variant 2 (LOC100692629), mRNA
MPF_UBR4.2.2	XM_003444861.1 PREDICTED: Oreochromis niloticus ubiquitin protein ligase E3 component n-recognin 4 (UBR4), mRNA
MPF_LOC101465079.2.2	XM_004551108.1 PREDICTED: Maylandia zebra basal cell adhesion molecule-like (LOC101465079), mRNA
MPF_LOC101477400.4.4	XM_004538536.1 PREDICTED: Maylandia zebra cyclin-G2-like (LOC101477400), mRNA
MPF_CD276.3.9	CD276_XENLA (sp|Q68EV1) CD276 antigen homolog OS=Xenopus laevis GN=cd276 PE=2 SV=1
MPF_LOC100697750.1.3	XM_003459604.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 14-like (LOC100697750), mRNA
MPF_LOC101471553.1.1	XM_004572678.1 PREDICTED: Maylandia zebra protein capicua homolog (LOC101471553), transcript variant X4, mRNA
MPF_LOC100691105.1.2	XP_003449231.1 PREDICTED: cytochrome c oxidase subunit 8B, mitochondrial-like [Oreochromis niloticus]
MPF_CFAH.8.15	CFAH_BOVIN (sp|Q28085) Complement factor H OS=Bos taurus GN=CFH PE=1 SV=3
MPF_contig_025452	
MPF_LOC101472043.8.14	XM_004573789.1 PREDICTED: Maylandia zebra tight junction-associated protein 1-like (LOC101472043), transcript variant X4, mRNA
MPF_contig_037474	
MPF_MXAN_5876.1.1	YP_634013.1 hypothetical protein MXAN_5876 [Myxococcus xanthus DK 1622]
MPF_contig_011640	
MPF_LOC101473892.1.1	XM_004569569.1 PREDICTED: Maylandia zebra transforming growth factor beta-1-like (LOC101473892), transcript variant X2, mRNA
MPF_LOC101062526.1.1	XP_003962815.1 PREDICTED: d-2-hydroxyglutarate dehydrogenase, mitochondrial-like [Takifugu rubripes]
MPF_LOC100706528.2.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA
MPF_LOC100696360.1.3	XP_003446837.1 PREDICTED: signal-induced proliferation-associated 1-like protein 2-like [Oreochromis niloticus]
MPF_contig_027915	XM_004568424.1 PREDICTED: Maylandia zebra cytochrome P450 2K3-like (LOC101476301), transcript variant X1, mRNA
MPF_LOC101167345.32.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA
MPF_contig_019843	
MPF_LOC101478535.2.2	XM_004540728.1 PREDICTED: Maylandia zebra latent-transforming growth factor beta-binding protein 2-like (LOC101478535), mRNA

MPF_LOC101464586.2.2	XM_004571741.1 PREDICTED: Maylandia zebra tensin-3-like (LOC101464586), transcript variant X3, mRNA
MPF_LOC101476475.1.1	XM_004562669.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 3-like (LOC101476475), mRNA
MPF_LECG.5.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1

MPF_LOC101472370.1.1	XM_004538428.1 PREDICTED: Maylandia zebra gelsolin-like (LOC101472370), transcript variant X2, mRNA
MPF_contig_028429	
MPF_LOC101158287.1.1	XP_004073601.1 PREDICTED: iduronate 2-sulfatase-like [Oryzias latipes]
MPF_HSD17B8.1.1	XM_003457993.1 PREDICTED: Oreochromis niloticus 17-beta hydroxysteroid dehydrogenase type 8 (HSD17B8), mRNA
MPF_contig_002650	XM_004079020.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 1 (LOC101161674), mRNA
MPF_contig_022248	
MPF_LOC100696287.1.2	XP_003450735.1 PREDICTED: C-type lectin domain family 9 member A-like isoform 1 [Oreochromis niloticus]
MPF_LOC101169293.1.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA
MPF_LOC101482059.1.3	XM_004563140.1 PREDICTED: Maylandia zebra mitogen-activated protein kinase kinase kinase kinase 4-like (LOC101482059), transcript variant X2, mRNA
MPF_LOC100705069.1.1	XP_003447626.1 PREDICTED: shootin-1-like [Oreochromis niloticus]
MPF_contig_034792	
MPF_LOC101483357.1.1	XM_004573344.1 PREDICTED: Maylandia zebra transgelin-like (LOC101483357), mRNA
MPF_LOC100700712.2.3	XP_003440431.1 PREDICTED: hypothetical protein LOC100700712 [Oreochromis niloticus]
MPF_LOC100706528.1.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA
MPF_LOC100702519.1.1	XM_003441393.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702519), mRNA
MPF_LOC100555635.1.1	XP_003229374.1 PREDICTED: uncharacterized protein C14orf93-like [Anolis carolinensis]
MPF_LOC101473755.3.3	XM_004564853.1 PREDICTED: Maylandia zebra CCR4-NOT transcription complex subunit 2-like (LOC101473755), transcript variant X2, mRNA
MPF_LOC100702817.1.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA
MPF_LOC100693237.1.1	XM_003442623.1 PREDICTED: Oreochromis niloticus catechol O-methyltransferase-like (LOC100693237), mRNA
MPF_LOC101473182.1.3	XM_004566836.1 PREDICTED: Maylandia zebra sialoadhesin-like (LOC101473182), transcript variant X2, mRNA
MPF_LOC101479305.2.6	XM_004546110.1 PREDICTED: Maylandia zebra cytosolic sulfotransferase 3-like (LOC101479305), transcript variant X2, mRNA
MPF_contig_020368	XM_004550291.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101467183), transcript variant X2, mRNA
MPF_LOC101486209.1.4	XM_004551098.1 PREDICTED: Maylandia zebra uncharacterized LOC101486209 (LOC101486209), mRNA
MPF_LOC101464936.1.1	XM_004541956.1 PREDICTED: Maylandia zebra sex comb on midleg-like protein 4-like (LOC101464936), transcript variant X3, mRNA
MPF_LOC101468855.3.3	XM_004569017.1 PREDICTED: Maylandia zebra protein tweety homolog 3-like (LOC101468855), transcript variant X1, mRNA
MPF_LOC101080012.1.1	XM_003977798.1 PREDICTED: Takifugu rubripes CDP-diacylglycerol--serine O-phosphatidyltransferase-like (LOC101080012), mRNA
MPF_TNR1B.1.1	[BBH] TNR1B_MOUSE (sp|P25119) Tumor necrosis factor receptor superfamily member 1B OS=Mus musculus GN=Tnfrsf1b PE=2 SV=1
MPF_LOC101487243.1.3	XM_004570967.1 PREDICTED: Maylandia zebra pleckstrin homology domain-containing family M member 2-like (LOC101487243), transcript variant X2, mRNA
MPF_contig_036091	
MPF_LOC101070379.1.1	XP_003974368.1 PREDICTED: uncharacterized protein LOC101070379 [Takifugu rubripes]

MPF_contig_045322	
MPF_LOC100698399.1.1	XM_003444297.1 PREDICTED: Oreochromis niloticus non-specific lipid-transfer protein-like (LOC100698399), mRNA
MPF_LOC101474179.2.3	XM_004568681.1 PREDICTED: Maylandia zebra nucleolin 2-like (LOC101474179), mRNA
MPF_LOC101156352.1.1	XP_004077953.1 PREDICTED: ictacalcin-like [Oryzias latipes]
MPF_FZD6.6.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440 IMAGE:6971142), complete cds
MPF_LOC101480831.3.3	XM_004565417.1 PREDICTED: Maylandia zebra putative 60S ribosomal protein L37a-like (LOC101480831), mRNA
MPF_LOC101078462.1.1	XP_003965271.1 PREDICTED: lysosome membrane protein 2-like [Takifugu rubripes]
MPF_LOC101074275.1.1	XP_003968653.1 PREDICTED: transforming growth factor beta-1-like [Takifugu rubripes]
MPF_LOC100711510.1.8	XM_003455849.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100711510), mRNA
MPF_LOC101486559.1.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA
MPF_LOC101464886.1.1	XM_004575104.1 PREDICTED: Maylandia zebra anoctamin-5-like (LOC101464886), transcript variant X2, mRNA
MPF_LOC101466654.1.2	XM_004538580.1 PREDICTED: Maylandia zebra sodium-dependent phosphate transporter 1-B-like (LOC101466654), partial mRNA
MPF_LOC100706330.1.1	XP_003457684.1 PREDICTED: hypothetical protein LOC100706330 [Oreochromis niloticus]
MPF_LOC101464934.1.3	XM_004565357.1 PREDICTED: Maylandia zebra matrix metalloproteinase-14-like (LOC101464934), mRNA
MPF_LOC101466346.1.1	XM_004553806.1 PREDICTED: Maylandia zebra tyrosine-protein kinase ZAP-70-like (LOC101466346), transcript variant X4, mRNA
MPF_LOC101485244.1.1	XM_004568719.1 PREDICTED: Maylandia zebra zinc transporter 1-like (LOC101485244), mRNA
MPF_LOC100692921.1.1	XM_003454794.1 PREDICTED: Oreochromis niloticus P2Y purinoceptor 12-like (LOC100692921), mRNA
MPF_contig_028808	
MPF_contig_031758	XM_004550291.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101467183), transcript variant X2, mRNA
MPF_LOC101469549.1.2	XM_004573028.1 PREDICTED: Maylandia zebra interleukin-1 receptor-like 1-like (LOC101469549), mRNA
MPF_contig_008230	
MPF_LOC101477091.1.3	XM_004574318.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101477091), transcript variant X5, mRNA
MPF_LOC100690401.1.3	XP_003454006.1 PREDICTED: hypothetical protein LOC100690401 [Oreochromis niloticus]
MPF_LOC100703589.1.1	XM_003460117.1 PREDICTED: Oreochromis niloticus plasminogen activator inhibitor 1-like (LOC100703589), mRNA
MPF_LOC101168933.2.2	XP_004086950.1 PREDICTED: macrophage receptor MARCO-like [Oryzias latipes]
MPF_AHNK.21.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_contig_023757	
MPF_LOC101475584.3.5	XM_004561039.1 PREDICTED: Maylandia zebra thrombospondin type-1 domain-containing protein 7A-like (LOC101475584), mRNA
MPF_LOC101075004.1.1	XM_003964966.1 PREDICTED: Takifugu rubripes uncharacterized LOC101075004 (LOC101075004), mRNA
MPF_LOC100710693.1.3	XP_003453586.1 PREDICTED: complement factor H-like [Oreochromis niloticus]
MPF_contig_048789	
MPF_LOC100180429.3.7	XM_002120912.1 PREDICTED: Ciona intestinalis uncharacterized LOC100180429 (LOC100180429), mRNA
MPF_LOC101485262.1.1	XM_004572362.1 PREDICTED: Maylandia zebra membrane-spanning 4-domains subfamily A member 12-like (LOC101485262), mRNA
MPF_LOC100696821.2.2	XM_003452445.1 PREDICTED: Oreochromis niloticus ictacalcin-like (LOC100696821), mRNA

MPF_contig_047891	
MPF_LOC100712302.1.1	XP_003452302.1 PREDICTED: aminoacyl tRNA synthase complex-interacting multifunctional protein 1-like [Oreochromis niloticus]
MPF_LOC100706878.5.6	XP_003458391.1 PREDICTED: hypothetical protein LOC100706878 [Oreochromis niloticus]
MPF_contig_028541	
MPF_HEPHL1.1.1	XM_003446729.1 PREDICTED: Oreochromis niloticus hephaestin-like 1 (HEPHL1), mRNA
MPF_contig_014987	
MPF_LOC100689711.4.6	XP_003459483.1 PREDICTED: h-2 class I histocompatibility antigen, L-D alpha chain-like [Oreochromis niloticus]
MPF_LOC100692258.2.2	XM_003445695.1 PREDICTED: Oreochromis niloticus ferritin, heavy subunit-like (LOC100692258), mRNA
MPF_contig_020580	
MPF_CRE_07824.1.1	XP_003093184.1 hypothetical protein CRE_07824 [Caenorhabditis remanei]
MPF_LOC101471521.1.3	XM_004543486.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF128-like (LOC101471521), mRNA
MPF_LOC101480440.1.1	XM_004541919.1 PREDICTED: Maylandia zebra deleted in malignant brain tumors 1 protein-like (LOC101480440), mRNA
MPF_CRE_23222.1.2	XP_003089877.1 hypothetical protein CRE_23222 [Caenorhabditis remanei]
MPF_LOC101465872.1.1	XM_004558783.1 PREDICTED: Maylandia zebra extended synaptotagmin-1-like (LOC101465872), mRNA
MPF_LOC101478190.2.2	XM_004571703.1 PREDICTED: Maylandia zebra platelet basic protein-like (LOC101478190), mRNA
MPF_LOC101471935.1.1	XM_004545975.1 PREDICTED: Maylandia zebra transcription factor MafB-like (LOC101471935), mRNA
MPF_LOC100559296.1.1	XP_003228542.1 PREDICTED: zinc finger protein 229-like [Anolis carolinensis]
MPF_LOC100700016.1.1	XM_003447883.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100700016 (LOC100700016), mRNA
MPF_LOC100708084.3.4	XM_003447339.1 PREDICTED: Oreochromis niloticus uridine phosphorylase 2-like (LOC100708084), mRNA
MPF_LOC101467232.1.1	XM_004541226.1 PREDICTED: Maylandia zebra ceramide synthase 2-like (LOC101467232), mRNA
MPF_LOC101484703.2.2	XM_004555446.1 PREDICTED: Maylandia zebra transmembrane protein 41A-A-like (LOC101484703), mRNA
MPF_LOC100690793.1.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]
MPF_contig_037007	
MPF_LOC101473612.4.5	XM_004550873.1 PREDICTED: Maylandia zebra sodium/potassium-transporting ATPase subunit alpha-3-like (LOC101473612), transcript variant X2, mRNA
MPF_LOC101464956.1.1	XM_004545486.1 PREDICTED: Maylandia zebra large neutral amino acids transporter small subunit 3-like (LOC101464956), mRNA
MPF_LOC101464117.1.1	XM_004572292.1 PREDICTED: Maylandia zebra solute carrier family 12 member 7-like (LOC101464117), transcript variant X3, mRNA
MPF_contig_005656	
MPF_LOC100697415.3.3	XP_003444759.1 PREDICTED: neuroblast differentiation-associated protein AHNAK-like [Oreochromis niloticus]
MPF_contig_011672	XM_004550791.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 6-like (LOC101478586), transcript variant X1, mRNA
MPF_LOC100706922.1.1	XP_003446211.1 PREDICTED: transcription initiation factor TFIID subunit 2-like [Oreochromis niloticus]
MPF_K1C18.1.2	K1C18_DANRE (sp|Q7ZTS4) Keratin, type I cytoskeletal 18 OS=Danio rerio GN=krt18 PE=1 SV=2
MPF_LOC101483054.1.2	XM_004542678.1 PREDICTED: Maylandia zebra serotransferrin-like (LOC101483054), mRNA
MPF_LOC100694868.1.2	XM_003446700.1 PREDICTED: Oreochromis niloticus c-C chemokine receptor type 6-like (LOC100694868), mRNA
MPF_LOC101471731.1.2	XM_004544422.1 PREDICTED: Maylandia zebra myocyte-specific enhancer factor 2C-like (LOC101471731), transcript variant X6, mRNA
MPF_GP91PHOX.2.2	NM_001032732.1 Takifugu rubripes gp91phox protein (gp91phox), mRNA

MPF_contig_023804	
MPF_contig_036789	
MPF_LOC101486284.2.3	XM_004546431.1 PREDICTED: Maylandia zebra transmembrane protein 189-like (LOC101486284), mRNA
MPF_LOC101482854.4.4	XM_004540267.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(q) subunit alpha-like (LOC101482854), transcript variant X3, mRNA
MPF_LOC100710548.3.4	XP_003459320.1 PREDICTED: major histocompatibility complex class I-related gene protein-like [Oreochromis niloticus]
MPF_LOC101072249.3.3	XP_003966663.1 PREDICTED: target of Nesh-SH3-like [Takifugu rubripes]
MPF_LOC101169293.5.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA
MPF_LOC100706800.1.1	XM_003439818.1 PREDICTED: Oreochromis niloticus retinoic acid receptor RXR-gamma-B-like, transcript variant 1 (LOC100706800), mRNA
MPF_CFAH.14.15	CFAH_MOUSE (sp|P06909) Complement factor H OS=Mus musculus GN=Cfh PE=1 SV=2
MPF_LOC101067754.3.3	XM_003961265.1 PREDICTED: Takifugu rubripes NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4-like (LOC101067754), mRNA
MPF_LOC100704396.2.3	XP_003459961.1 PREDICTED: neoverrucotoxin subunit alpha-like [Oreochromis niloticus]
MPF_contig_044005	
MPF_LOC101481869.4.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA
MPF_LOC100711796.1.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA
MPF_contig_004128	
MPF_contig_004261	
MPF_PFL1445W.1.1	XP_001350695.2 conserved Plasmodium protein [Plasmodium falciparum 3D7]
MPF_CD28.1.1	[BBH] CD28_HUMAN (sp|P10747) T-cell-specific surface glycoprotein CD28 OS=Homo sapiens GN=CD28 PE=1 SV=1

MPF_LOC101479192.1.1	XM_004541915.1 PREDICTED: Maylandia zebra lebercilin-like (LOC101479192), transcript variant X1, mRNA
MPF_AHNK.22.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_TNF6B.1.1	TNF6B_HUMAN (sp|O95407) Tumor necrosis factor receptor superfamily member 6B OS=Homo sapiens GN=TNFRSF6B PE=1 SV=1
MPF_LOC100705618.1.1	XP_003453815.1 PREDICTED: protogenin-like [Oreochromis niloticus]
MPF_contig_044606	
MPF_contig_033640	XM_004548336.1 PREDICTED: Maylandia zebra protein kinase C and casein kinase substrate in neurons protein 2-like (LOC101473402), transcript variant X1, mRNA
MPF_LOC101486434.1.2	XM_004560149.1 PREDICTED: Maylandia zebra cathepsin K-like (LOC101486434), mRNA
MPF_LOC101061752.1.1	XM_003975168.1 PREDICTED: Takifugu rubripes SEC14-like protein 2-like (LOC101061752), mRNA
MPF_LOC100702817.3.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA
MPF_LOC101076756.1.1	XM_003972767.1 PREDICTED: Takifugu rubripes histone-lysine N-methyltransferase MLL5-like (LOC101076756), mRNA
MPF_LOC100712517.2.2	XM_003459650.1 PREDICTED: Oreochromis niloticus RNA (guanine-9-)-methyltransferase domain-containing protein 2-like (LOC100712517), mRNA
MPF_contig_004326	
MPF_LOC101480609.1.2	XM_004539422.1 PREDICTED: Maylandia zebra homeodomain-interacting protein kinase 3-like (LOC101480609), transcript variant X2, mRNA
MPF_LOC101465129.6.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA

MPF_contig_029673	
MPF_LOC101487373.23.24	XM_004576282.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101487373), mRNA
MPF_LOC100704053.3.12	XM_003440652.1 PREDICTED: Oreochromis niloticus ubiquitin-like protein FUBI-like (LOC100704053), mRNA
MPF_contig_043890	
MPF_LOC100699618.1.3	XM_003458706.1 PREDICTED: Oreochromis niloticus macrophage-capping protein-like (LOC100699618), mRNA
MPF_contig_025370	XM_004558558.1 PREDICTED: Maylandia zebra autism susceptibility gene 2 protein-like (LOC101480020), transcript variant X7, mRNA
MPF_LOC101077329.1.1	XP_003965511.1 PREDICTED: glycerol-3-phosphate acyltransferase 3-like [Takifugu rubripes]
MPF_LOC101479518.3.5	XM_004570668.1 PREDICTED: Maylandia zebra alpha-actinin-3-like (LOC101479518), mRNA
MPF_LOC100705343.3.3	XM_003450141.1 PREDICTED: Oreochromis niloticus claudin-8-like (LOC100705343), mRNA
MPF_LOC101167345.13.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA
MPF_contig_017955	
MPF_LOC101475629.1.1	XM_004570493.1 PREDICTED: Maylandia zebra lactosylceramide 1,3-N-acetyl-beta-D-glucosaminyltransferase Alike (LOC101475629), transcript variant X2, mRNA
MPF_LOC101487936.1.3	XM_004552317.1 PREDICTED: Maylandia zebra F-box/LRR-repeat protein 20-like (LOC101487936), transcript variant X2, mRNA
MPF_LOC101466772.1.2	XM_004542617.1 PREDICTED: Maylandia zebra glypican-5-like (LOC101466772), transcript variant X2, mRNA
MPF_contig_026589	
MPF_LOC101480505.1.1	XM_004557175.1 PREDICTED: Maylandia zebra ankyrin repeat domain-containing protein 29-like (LOC101480505), transcript variant X3, mRNA
MPF_LOC101161574.12.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA
MPF_contig_013979	XM_004551640.1 PREDICTED: Maylandia zebra 40S ribosomal protein S24-like (LOC101482129), transcript variant X1, mRNA
MPF_LOC100692490.2.4	XM_003457423.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L37a-like (LOC100692490), mRNA
MPF_LOC100706186.1.2	XM_003460059.1 PREDICTED: Oreochromis niloticus calpain-2 catalytic subunit-like (LOC100706186), mRNA
MPF_LOC101466612.1.2	XM_004549597.1 PREDICTED: Maylandia zebra zinc finger protein 462-like (LOC101466612), transcript variant X1, mRNA
MPF_LOC101473441.1.1	XM_004558810.1 PREDICTED: Maylandia zebra transcription factor NF-E2 45 kDa subunit-like (LOC101473441), transcript variant X2, mRNA
MPF_NEMVEDRAFT_V1G118504.1.1	XP_001628905.1 predicted protein [Nematostella vectensis]
MPF_contig_024386	
MPF_HACE1.1.3	HACE1_DANRE (sp|F8W2M1) E3 ubiquitin-protein ligase HACE1 OS=Danio rerio GN=hace1 PE=3 SV=2
MPF_OSTC.2.3	OSTC_DANRE (sp|Q7ZWJ3) Oligosaccharyltransferase complex subunit ostc OS=Danio rerio GN=ostc PE=2 SV=1
MPF_contig_032849	
MPF_LOC101162897.2.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]
MPF_LOC100700407.1.1	XM_003454414.1 PREDICTED: Oreochromis niloticus IGF-like family receptor 1-like (LOC100700407), mRNA
MPF_LOC101168228.1.1	XP_004076087.1 PREDICTED: T-cell immunoglobulin and mucin domain-containing protein 4-like [Oryzias latipes]
MPF_ZC2HC1C.1.1	XP_003924603.1 PREDICTED: zinc finger C2HC domain-containing protein 1C homolog isoform 1 [Saimiri boliviensis boliviensis]
MPF_contig_009740	
MPF_LOC101161574.4.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA
MPF_contig_032895	

MPF_contig_015435	
MPF_LOC101488070.1.1	XM_004543546.1 PREDICTED: Maylandia zebra neprilysin-like (LOC101488070), transcript variant X1, mRNA
MPF_LOC101166970.1.1	XP_004073985.1 PREDICTED: uncharacterized protein LOC101166970 [Oryzias latipes]
MPF_C1QC.1.1	NP_001135251.1 complement C1q subcomponent subunit C precursor [Salmo salar]
MPF_contig_003837	
MPF_LOC101472300.1.1	XM_004568586.1 PREDICTED: Maylandia zebra uncharacterized LOC101472300 (LOC101472300), mRNA
MPF_LOC100709648.6.13	XM_003457730.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S4-like (LOC100709648), mRNA
MPF_contig_037247	
MPF_contig_015500	
MPF_LOC100488659.3.10	XP_002933173.1 PREDICTED: hypothetical protein LOC100488659 [Xenopus (Silurana) tropicalis]
MPF_LOC101477280.6.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA
MPF_contig_028860	
MPF_LOC101076460.1.1	XP_003978301.1 PREDICTED: homeobox protein CDX-1-like [Takifugu rubripes]

MPF_RTBS.12.36	RTBS_DROME (sp|Q95SX7) Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
MPF_LOC100695830.1.2	XM_003445456.1 PREDICTED: Oreochromis niloticus serine/arginine-rich splicing factor 4-like, transcript variant 1 (LOC100695830), mRNA
MPF_LOC101486993.1.1	XM_004554270.1 PREDICTED: Maylandia zebra sodium-dependent neutral amino acid transporter SLC6A17-like (LOC101486993), mRNA
MPF_contig_028605	
MPF_contig_015464	
MPF_LOC101076840.1.1	XM_003974902.1 PREDICTED: Takifugu rubripes chemokine-like receptor 1-like (LOC101076840), mRNA
MPF_contig_022962	
MPF_LOC101488089.1.1	XM_004570084.1 PREDICTED: Maylandia zebra uncharacterized LOC101488089 (LOC101488089), transcript variant X3, mRNA
MPF_contig_027052	
MPF_LOC101063580.1.1	XP_003966085.1 PREDICTED: syndecan-2-like [Takifugu rubripes]
MPF_LOC100703560.1.2	XM_003453596.1 PREDICTED: Oreochromis niloticus BRCA1-A complex subunit Abraxas-like (LOC100703560), mRNA
MPF_LOC101468563.1.2	XM_004572588.1 PREDICTED: Maylandia zebra alkaline nuclease-like (LOC101468563), transcript variant X6, mRNA
MPF_contig_014816	
MPF_LOC101068301.2.3	XM_003966217.1 PREDICTED: Takifugu rubripes protein S100-A11-like (LOC101068301), mRNA
MPF_contig_037637	
MPF_LOC100005864.2.2	XP_001921726.1 PREDICTED: GTPase IMAP family member 8-like [Danio rerio]
MPF_LOC101487734.1.2	XM_004571292.1 PREDICTED: Maylandia zebra cytohesin-4-like (LOC101487734), mRNA
MPF_LOC101473855.10.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA
MPF_contig_019388	
MPF_LOC101471890.1.1	XM_004559351.1 PREDICTED: Maylandia zebra nuclear GTPase SLIP-GC-like (LOC101471890), mRNA

MPF_RTXE.3.6	RTXE_DROME (sp|Q9NBX4) Probable RNA-directed DNA polymerase from transposon X-element OS=Drosophila melanogaster GN=X-elementORF2 PE=3 SV=1
MPF_LOC101156534.1.3	XR_177556.1 PREDICTED: Oryzias latipes synaptotagmin-1-like (LOC101156534), misc_RNA
MPF_LOC100699007.2.2	XM_003442225.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100699007, transcript variant 2 (LOC100699007), mRNA
MPF_contig_025924	XM_004574349.1 PREDICTED: Maylandia zebra protein FAM49A-like (LOC101486310), transcript variant X2, mRNA
MPF_BLCAP.2.2	[BBH] BLCAP_DANRE (sp|Q9IB61) Bladder cancer-associated protein OS=Danio rerio GN=blcap PE=3 SV=1
MPF_contig_026907	
MPF_contig_032259	
MPF_contig_023989	
MPF_contig_031639	
MPF_contig_021432	
MPF_LOC101160141.1.1	XR_177319.1 PREDICTED: Oryzias latipes keratin, type I cytoskeletal 13-like (LOC101160141), misc_RNA
MPF_LOC101467183.1.2	XM_004550296.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101467183), transcript variant X7, mRNA
MPF_LOC101468196.2.2	XM_004575285.1 PREDICTED: Maylandia zebra caspase-12-like (LOC101468196), mRNA
MPF_contig_012573	
MPF_contig_021708	
MPF_LOC101481376.3.4	XM_004557456.1 PREDICTED: Maylandia zebra heat shock protein beta-1-like (LOC101481376), mRNA
MPF_LOC101476137.1.1	XM_004574406.1 PREDICTED: Maylandia zebra baculoviral IAP repeat-containing protein 6-like (LOC101476137), transcript variant X5, mRNA
MPF_LOC101477938.4.9	XM_004574058.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101477938), mRNA
MPF_LOC101477850.6.10	XM_004575562.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12-like (LOC101477850), mRNA
MPF_LOC100695137.3.3	XP_003447509.1 PREDICTED: high affinity immunoglobulin epsilon receptor subunit gamma-like [Oreochromis niloticus]
MPF_LOC101476292.1.1	XM_004567039.1 PREDICTED: Maylandia zebra transgelin-like (LOC101476292), transcript variant X2, mRNA
MPF_LOC100708025.2.2	XM_003456564.1 PREDICTED: Oreochromis niloticus cytohesin-4-like (LOC100708025), mRNA
MPF_AHNK.20.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_LOC100702843.2.2	XP_003455945.1 PREDICTED: protein-tyrosine kinase 2-beta-like [Oreochromis niloticus]
MPF_LOC101474461.1.1	XM_004546190.1 PREDICTED: Maylandia zebra ataxin-1-like (LOC101474461), transcript variant X2, mRNA
MPF_CD276.6.9	CD276_XENLA (sp|Q68EV1) CD276 antigen homolog OS=Xenopus laevis GN=cd276 PE=2 SV=1
MPF_LOC100697337.2.4	XP_003446015.1 PREDICTED: hypothetical protein LOC100697337 [Oreochromis niloticus]
MPF_CD4.1.1	NP_001072091.1 T-cell surface glycoprotein CD4 [Takifugu rubripes]
MPF_contig_006498	
MPF_contig_031891	
MPF_LOC101487485.1.1	XM_004560899.1 PREDICTED: Maylandia zebra fibroleukin-like (LOC101487485), mRNA
MPF_CD48.2.4	CD48_MOUSE (sp|P18181) CD48 antigen OS=Mus musculus GN=Cd48 PE=1 SV=1
MPF_contig_042687	
MPF_LOC100697522.1.1	XM_003447958.1 PREDICTED: Oreochromis niloticus N-acetylmuramoyl-L-alanine amidase-like (LOC100697522), mRNA

MPF_contig_035115	
MPF_contig_023056	
MPF_LOC101168710.1.1	XP_004070984.1 PREDICTED: CD27 antigen-like [Oryzias latipes]
MPF_LOC101473901.1.2	XM_004572233.1 PREDICTED: Maylandia zebra CDC42 small effector protein 1-like (LOC101473901), transcript variant X2, mRNA
MPF_LOC101478250.3.3	XM_004538353.1 PREDICTED: Maylandia zebra flocculation protein FLO11-like (LOC101478250), transcript variant X3, mRNA
MPF_LOC100696796.2.2	XM_003445884.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100696796 (LOC100696796), mRNA
MPF_LOC100698701.1.2	XM_003455230.1 PREDICTED: Oreochromis niloticus protein S100-A13-like (LOC100698701), mRNA
MPF_LOC101467030.1.1	XM_004563996.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 31-like (LOC101467030), mRNA
MPF_LOC445921.1.1	XP_003979513.1 PREDICTED: Ig mu chain C region membrane-bound form [Takifugu rubripes]
MPF_LOC101477280.1.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA

MPF_LOC101160373.1.1	XP_004083232.1 PREDICTED: DNA damage-regulated autophagy modulator protein 1-like [Oryzias latipes]
MPF_LOC101474504.4.5	XM_004557613.1 PREDICTED: Maylandia zebra anthrax toxin receptor 1-like (LOC101474504), mRNA
MPF_contig_026208	
MPF_contig_009643	
MPF_LOC101475513.1.1	XM_004545621.1 PREDICTED: Maylandia zebra EGF-containing fibulin-like extracellular matrix protein 2-like (LOC101475513), mRNA
MPF_contig_026183	XM_004548669.1 PREDICTED: Maylandia zebra uncharacterized LOC101485992 (LOC101485992), transcript variant X3, mRNA
MPF_contig_027568	
MPF_LOC101064915.1.1	XM_003967542.1 PREDICTED: Takifugu rubripes thromboxane-A synthase-like (LOC101064915), mRNA
MPF_LOC100691990.2.2	XM_003445526.1 PREDICTED: Oreochromis niloticus annexin A1-like (LOC100691990), mRNA
MPF_LOC101464899.2.4	XM_004553991.1 PREDICTED: Maylandia zebra protein bassoon-like (LOC101464899), transcript variant X2, mRNA
MPF_LOC101479507.2.2	XM_004568789.1 PREDICTED: Maylandia zebra T-complex protein 1 subunit alpha-like (LOC101479507), mRNA
MPF_LOC101065219.1.3	XM_003969289.1 PREDICTED: Takifugu rubripes protein S100-A1-like (LOC101065219), mRNA
MPF_LOC100711484.7.8	XM_003448843.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100711484), mRNA
MPF_LOC101155558.1.1	XM_004082371.1 PREDICTED: Oryzias latipes interferon alpha-inducible protein 27-like protein 2-like (LOC101155558), mRNA
MPF_LOC101476071.1.1	XM_004541164.1 PREDICTED: Maylandia zebra uncharacterized LOC101476071 (LOC101476071), mRNA
MPF_LOC101486169.4.4	XM_004566076.1 PREDICTED: Maylandia zebra cyclin-T2-like (LOC101486169), mRNA
MPF_contig_014120	
MPF_contig_031514	
MPF_LOC101469505.1.1	XM_004563094.1 PREDICTED: Maylandia zebra ephrin-B2a-like (LOC101469505), transcript variant X2, mRNA
MPF_contig_043487	
MPF_contig_016882	
MPF_LOC100710612.1.1	XM_003454616.1 PREDICTED: Oreochromis niloticus macrophage mannose receptor 1-like (LOC100710612), mRNA
MPF_ACBD5.1.1	ACBD5_PONAB (sp|Q5R7V3) Acyl-CoA-binding domain-containing protein 5 OS=Pongo abelii GN=ACBD5 PE=2 SV=1

MPF_contig_020194	
MPF_LOC101465099.1.1	XM_004557394.1 PREDICTED: Maylandia zebra moesin-like (LOC101465099), mRNA
MPF_LOC101487032.1.1	XM_004543159.1 PREDICTED: Maylandia zebra ADM-like (LOC101487032), transcript variant X1, mRNA
MPF_LOC101476871.1.3	XM_004569314.1 PREDICTED: Maylandia zebra nuclear factor 1 C-type-like (LOC101476871), transcript variant X2, mRNA
MPF_AHNK.11.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
MPF_contig_021336	
MPF_LOC101467829.1.2	XM_004565458.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase pim-1-like (LOC101467829), mRNA
MPF_LOC101487208.1.1	XM_004564346.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase ZFP91-like (LOC101487208), transcript variant X3, mRNA
MPF_LOC101475700.1.3	XM_004564763.1 PREDICTED: Maylandia zebra phosphate carrier protein, mitochondrial-like (LOC101475700), transcript variant X2, mRNA
MPF_LOC101065219.2.3	XM_003969289.1 PREDICTED: Takifugu rubripes protein S100-A1-like (LOC101065219), mRNA
MPF_LOC101479628.3.3	XM_004554593.1 PREDICTED: Maylandia zebra proto-oncogene c-Rel-like (LOC101479628), mRNA
MPF_contig_011981	
MPF_LOC101156484.2.2	XM_004067491.1 PREDICTED: Oryzias latipes CD81 antigen-like (LOC101156484), mRNA
MPF_LOC101478816.1.1	XM_004541641.1 PREDICTED: Maylandia zebra ubiquitin carboxyl-terminal hydrolase 45-like (LOC101478816), transcript variant X1, mRNA
MPF_CFAH.6.15	CFAH_HUMAN (sp|P08603) Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4
MPF_LOC101473855.2.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA
MPF_LOC101469207.1.1	XM_004560645.1 PREDICTED: Maylandia zebra c-Jun-amino-terminal kinase-interacting protein 3-like (LOC101469207), transcript variant X10, mRNA
MPF_LOC101482347.1.1	XR_191458.1 PREDICTED: Maylandia zebra TBC1 domain family member 13-like (LOC101482347), transcript variant X2, misc_RNA
MPF_LOC100712330.1.2	XM_003438072.1 PREDICTED: Oreochromis niloticus ATP synthase subunit g, mitochondrial-like (LOC100712330), mRNA
MPF_LOC101168049.1.1	XM_004072873.1 PREDICTED: Oryzias latipes sushi domain-containing protein 1-like (LOC101168049), mRNA
MPF_LOC101486284.3.3	XM_004546431.1 PREDICTED: Maylandia zebra transmembrane protein 189-like (LOC101486284), mRNA
MPF_LOC101159641.5.35	XM_004085298.1 PREDICTED: Oryzias latipes tenascin-like (LOC101159641), mRNA
MPF_LOC101479481.1.1	XM_004563952.1 PREDICTED: Maylandia zebra latent-transforming growth factor beta-binding protein 3-like (LOC101479481), transcript variant X2, mRNA
MPF_LOC100707166.2.2	XM_003442172.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100707166 (LOC100707166), mRNA
MPF_LOC101077496.1.1	XM_003968940.1 PREDICTED: Takifugu rubripes gamma-glutamylcyclotransferase-like (LOC101077496), mRNA
MPF_LOC101063002.1.1	XP_003971894.1 PREDICTED: LOW QUALITY PROTEIN: T-cell activation Rho GTPase-activating protein-like [Takifugu rubripes]
MPF_LOC101474649.1.2	XM_004569663.1 PREDICTED: Maylandia zebra zinc finger protein 729-like (LOC101474649), mRNA
MPF_LOC101469758.1.3	XM_004558073.1 PREDICTED: Maylandia zebra estradiol 17-beta-dehydrogenase 12-B-like (LOC101469758), mRNA
MPF_contig_017190	
MPF_RS7.10.10	RS7_TAKRU (sp|P50894) 40S ribosomal protein S7 OS=Takifugu rubripes GN=rps7 PE=3 SV=1
MPF_IKBKB.2.2	XM_003451030.1 PREDICTED: Oreochromis niloticus inhibitor of kappa light polypeptide gene enhancer in Bcells, kinase beta (IKBKB), mRNA
MPF_LOC101161674.2.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA
MPF_LOC101483532.1.2	XM_004543245.1 PREDICTED: Maylandia zebra transcription factor PU.1-like (LOC101483532), transcript variant

MPF_LOC101487772.1.2	XM_004559324.1 PREDICTED: Maylandia zebra alcohol dehydrogenase 1-like (LOC101487772), mRNA

	X2, mRNA
MPF_RS6.6.11	RS6_PROMA (sp|Q7V9F9) 30S ribosomal protein S6 OS=Prochlorococcus marinus (strain SARG / CCMP1375 / SS120) GN=rpsF PE=3 SV=1
MPF_LOC101071928.1.1	XP_003978669.1 PREDICTED: uncharacterized protein LOC101071928 [Takifugu rubripes]

3. Supplementary table 4

Phylofish Gene ID	Gene Description	FRD (pvalue)	Log FC ([I vs [II])	Regulation ([I] vs [II])	Log FC ([I vs [III])	Regulation ([I] vs [III])	Log FC ([I vs [IV])	Regulation ([I] vs [IV])	Log FC ([II vs [III])	Regulation ([II] vs [III])	Log FC ([II vs [IV])	Regulation ([II] vs [IV])	Log FC ([III vs [IV])	Regulation ([III] vs [IV])
MPF_contig_015464		0.0039	-0.4093	down	-1.4861	down	-4.4432	down	-1.0768	down	-4.0339	down	-2.9571	down
MPF_LOC100708533.1.1	XM_003447172.1 PREDICTED: Oreochromis niloticus annexin A2-like (LOC100708533), mRNA	0.0041	-1.0467	down	-0.5793	down	-3.2945	down	0.4674	up	-2.2478	down	-2.7152	down
MPF_LOC101474478.3.3	XM_004572875.1 PREDICTED: Maylandia zebra neuritin-like (LOC101474478), mRNA	0.0041	0.3427	up	-0.5309	down	-2.6131	down	-0.8735	down	-2.9558	down	-2.0822	down
MPF_contig_006069		0.0041	-0.3981	down	-0.7359	down	-3.0060	down	-0.3379	down	-2.6079	down	-2.2700	down
MPF_NCKAP1L.2.2	XM_003451841.1 PREDICTED: Oreochromis niloticus NCK-associated protein 1-like (NCKAP1L), mRNA	0.0041	-0.1894	down	-1.3651	down	-3.5983	down	-1.1757	down	-3.4089	down	-2.2332	down
MPF_contig_034792		0.0041	-0.5054	down	-0.9008	down	-2.6359	down	-0.3955	down	-2.1305	down	-1.7351	down
MPF_LOC100690727.1.1	XM_003443255.1 PREDICTED: Oreochromis niloticus ribosomal RNA processing protein 1 homolog B-like (LOC100690727), mRNA	0.0041	-0.2749	down	-0.2245	down	-1.9120	down	0.0504	up	-1.6372	down	-1.6876	down
MPF_LOC101487307.4.5	XM_004564717.1 PREDICTED: Maylandia zebra ankyrin repeat domaincontaining protein 6-like (LOC101487307), transcript variant X4, mRNA	0.0041	-0.7010	down	-1.2594	down	-3.7440	down	-0.5584	down	-3.0430	down	-2.4846	down

MPF_AHNK.22.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiationassociated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.0041	-0.3591	down	-1.1026	down	-3.2511	down	-0.7435	down	-2.8920	down	-2.1485	down
MPF_contig_023516		0.0041	-0.3860	down	-1.0092	down	-2.6618	down	-0.6232	down	-2.2757	down	-1.6526	down
MPF_MIR24-5.1.1	NR_048933.1 Danio rerio microRNA mir-24-5 (mir24-5), microRNA	0.0041	-0.3379	down	-0.5418	down	-2.7950	down	-0.2038	down	-2.4571	down	-2.2532	down
MPF_contig_033415		0.0046	-0.5801	down	-0.7174	down	-2.8092	down	-0.1374	down	-2.2291	down	-2.0918	down
MPF_contig_020534		0.0047	0.0717	up	-1.0804	down	-3.7069	down	-1.1520	down	-3.7785	down	-2.6265	down
MPF_contig_014892		0.0047	-0.1685	down	-0.1344	down	-2.3788	down	0.0340	up	-2.2103	down	-2.2444	down
MPF_TNR1B.1.1	[BBH] TNR1B_MOUSE (sp|P25119) Tumor necrosis factor receptor superfamily member 1B OS=Mus musculus GN=Tnfrsf1b PE=2 SV=1	0.0047	-0.0406	down	-1.5220	down	-4.7114	down	-1.4814	down	-4.6708	down	-3.1894	down
MPF_contig_020580		0.0047	-0.4307	down	-1.2588	down	-3.3446	down	-0.8280	down	-2.9139	down	-2.0858	down
MPF_CRE_07824.1.1	XP_003093184.1 hypothetical protein CRE_07824 [Caenorhabditis remanei]	0.0047	-0.4824	down	-0.8049	down	-3.5176	down	-0.3225	down	-3.0352	down	-2.7127	down
MPF_LOC101476819.7.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0.0047	-0.7017	down	-1.1007	down	-3.2675	down	-0.3989	down	-2.5658	down	-2.1669	down

MPF_LOC101474190.1.1	XM_004547121.1 PREDICTED: Maylandia zebra RING finger protein 122-like (LOC101474190), transcript variant X1, mRNA	0.0047	-0.0139	down	0.0358	up	0.9154	up	0.0497	up	0.9292	up	0.8796	up
MPF_LOC101480436.4.4	XM_004564408.1 PREDICTED: Maylandia zebra cbp/p300-interacting transactivator 3-like (LOC101480436), mRNA	0.0047	-0.1277	down	-0.6828	down	-3.5281	down	-0.5551	down	-3.4004	down	-2.8453	down
MPF_RS6.6.11	RS6_PROMA (sp|Q7V9F9) 30S ribosomal protein S6 OS=Prochlorococcus marinus (strain SARG / CCMP1375 / SS120) GN=rpsF PE=3 SV=1	0.0047	-0.3189	down	-1.5986	down	-4.6184	down	-1.2797	down	-4.2995	down	-3.0198	down
MPF_POPTRDRAFT_794775.3.5	XP_002338344.1 predicted protein [Populus trichocarpa]	0.0047	0.0524	up	-0.4347	down	-1.6806	down	-0.4870	down	-1.7329	down	-1.2459	down
MPF_contig_046286		0.0047	0.1741	up	0.1394	up	0.8504	up	-0.0347	down	0.6763	up	0.7110	up
MPF_contig_015023		0.0051	-0.0010	down	-0.6696	down	-2.1228	down	-0.6686	down	-2.1218	down	-1.4532	down
MPF_LOC100135188.1.5	NP_001107363.1 uncharacterized protein LOC100135188 [Xenopus (Silurana) tropicalis]	0.0054	-0.8082	down	-1.2280	down	-3.6072	down	-0.4199	down	-2.7990	down	-2.3792	down
MPF_contig_044869	XM_004575909.1 PREDICTED: Maylandia zebra neurabin-2-like (LOC101486611), transcript variant X1, mRNA	0.0054	-0.1413	down	-0.8445	down	-3.2242	down	-0.7032	down	-3.0830	down	-2.3798	down
MPF_contig_034756	XM_004561310.1 PREDICTED: Maylandia zebra transcription factor 7like 2-like (LOC101473558), transcript variant X5, mRNA	0.0054	-0.1426	down	0.1148	up	1.1066	up	0.2574	up	1.2492	up	0.9919	up

MPF_contig_004075		0.0054	-0.9274	down	-0.5563	down	-2.2489	down	0.3711	up	-1.3215	down	-1.6926	down
MPF_LOC100695240.1.2	XP_003452569.1 PREDICTED: calcium/calmodulindependent protein kinase type IV-like [Oreochromis niloticus]	0.0054	-0.5066	down	-0.6376	down	-2.7749	down	-0.1310	down	-2.2683	down	-2.1373	down
MPF_LOC100694934.2.2	XP_003442506.1 PREDICTED: putative Nacetylglucosamine-6phosphate deacetylase-like [Oreochromis niloticus]	0.0054	-0.1760	down	-0.1117	down	0.8290	up	0.0643	up	1.0050	up	0.9407	up
MPF_DMBT1.5.9	DMBT1_RABIT (sp|Q95218) Deleted in malignant brain tumors 1 protein OS=Oryctolagus cuniculus GN=Dmbt1 PE=1 SV=2	0.0054	-0.3868	down	-1.6391	down	-2.9970	down	-1.2523	down	-2.6102	down	-1.3580	down
MPF_contig_028818		0.0054	-0.5969	down	-1.0337	down	-3.4257	down	-0.4367	down	-2.8288	down	-2.3920	down
MPF_LOC100700602.2.2	XP_003457975.1 PREDICTED: hypothetical protein LOC100700602 [Oreochromis niloticus]	0.0055	0.2445	up	-1.1112	down	-3.8128	down	-1.3557	down	-4.0573	down	-2.7016	down
MPF_LOC101169293.6.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.0055	-0.3868	down	-0.7641	down	-1.8880	down	-0.3773	down	-1.5012	down	-1.1238	down
MPF_MAG.1.4	MAG_RAT (sp|P07722) Myelin-associated glycoprotein OS=Rattus norvegicus GN=Mag PE=1 SV=1	0.0055	-0.7882	down	-1.5153	down	-3.5558	down	-0.7271	down	-2.7676	down	-2.0405	down
MPF_contig_037105		0.0056	0.1369	up	-0.0500	down	-0.9139	down	-0.1869	down	-1.0508	down	-0.8639	down

MPF_LOC101168682.3.3	XM_004066371.1 PREDICTED: Oryzias latipes protein S100-B-like, transcript variant 2 (LOC101168682), mRNA	0.0060	-0.3423	down	-1.2321	down	-4.0873	down	-0.8897	down	-3.7449	down	-2.8552	down
MPF_LOC101159641.10.35	XM_004085298.1 PREDICTED: Oryzias latipes tenascin-like (LOC101159641), mRNA	0.0060	-0.4339	down	-0.5425	down	-2.4596	down	-0.1087	down	-2.0258	down	-1.9171	down
MPF_LOC101169532.9.45	XP_004070110.1 PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Oryzias latipes]	0.0060	-0.0053	down	-0.3659	down	-1.1213	down	-0.3606	down	-1.1160	down	-0.7554	down
MPF_contig_018575		0.0060	-0.3144	down	-1.2755	down	-3.2446	down	-0.9611	down	-2.9302	down	-1.9691	down
MPF_LOC100706878.5.6	XP_003458391.1 PREDICTED: hypothetical protein LOC100706878 [Oreochromis niloticus]	0.0060	-0.3418	down	-1.8671	down	-3.5933	down	-1.5254	down	-3.2515	down	-1.7261	down
MPF_LOC101466470.1.1	XM_004561464.1 PREDICTED: Maylandia zebra protein FAM43A-like (LOC101466470), mRNA	0.0060	-0.6164	down	-0.8498	down	-3.2866	down	-0.2334	down	-2.6702	down	-2.4368	down
MPF_LOC100695830.1.2	XM_003445456.1 PREDICTED: Oreochromis niloticus serine/arginine-rich splicing factor 4-like, transcript variant 1 (LOC100695830), mRNA	0.0060	0.0737	up	-1.4650	down	-3.9327	down	-1.5387	down	-4.0064	down	-2.4677	down
MPF_contig_042931		0.0060	-0.0081	down	-0.8633	down	-2.6883	down	-0.8553	down	-2.6802	down	-1.8249	down

MPF_KRA43.1.2	KRA43_HUMAN (sp|Q9BYR4) Keratinassociated protein 4-3 OS=Homo sapiens GN=KRTAP4-3 PE=2 SV=2	0.0060	-0.5036	down	-1.1506	down	-3.4051	down	-0.6470	down	-2.9015	down	-2.2545	down
MPF_LOC101487377.1.3	XM_004555180.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 30-like (LOC101487377), transcript variant X2, mRNA	0.0060	-0.0746	down	-1.6032	down	-3.3686	down	-1.5286	down	-3.2940	down	-1.7654	down
MPF_ABLIM1A.5.5	NM_001114316.1 Danio rerio actin binding LIM protein 1a (ablim1a), mRNA gb|BC155652.1| Danio rerio zgc:172321, mRNA (cDNA clone MGC:172321 IMAGE:7043511), complete cds	0.0060	-0.2926	down	0.1725	up	1.0973	up	0.4651	up	1.3899	up	0.9248	up
MPF_LOC101481918.2.3	XM_004548550.1 PREDICTED: Maylandia zebra dual specificity protein phosphatase 7-like (LOC101481918), mRNA	0.0060	-0.4251	down	-1.0307	down	-2.4842	down	-0.6056	down	-2.0590	down	-1.4534	down
MPF_contig_021996		0.0064	0.1478	up	0.3053	up	0.7365	up	0.1575	up	0.5888	up	0.4312	up
MPF_LOC100705728.7.17	XM_003459563.1 PREDICTED: Oreochromis niloticus zinc finger protein RFP-like (LOC100705728), mRNA	0.0064	-0.2904	down	0.1348	up	1.0932	up	0.4252	up	1.3836	up	0.9584	up
MPF_LOC101468583.1.7	XM_004576296.1 PREDICTED: Maylandia zebra uncharacterized LOC101468583 (LOC101468583), mRNA	0.0065	-0.7255	down	-0.8043	down	-2.4393	down	-0.0789	down	-1.7138	down	-1.6349	down

MPF_contig_045616		0.0065	-1.1250	down	-1.6863	down	-4.1349	down	-0.5613	down	-3.0099	down	-2.4486	down
MPF_LOC101485716.5.12	XM_004572825.1 PREDICTED: Maylandia zebra multivesicular body subunit 12B-like (LOC101485716), mRNA	0.0065	-0.1870	down	-1.0260	down	-3.3573	down	-0.8390	down	-3.1702	down	-2.3313	down
MPF_PDE4DIP.2.2	XP_003438008.1 PREDICTED: myomegalin [Oreochromis niloticus]	0.0065	0.0179	up	0.0681	up	1.0417	up	0.0502	up	1.0238	up	0.9736	up
MPF_LOC101161574.12.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.0065	-0.4685	down	-1.6585	down	-3.6769	down	-1.1901	down	-3.2084	down	-2.0183	down
MPF_LOC101470306.1.1	XM_004574119.1 PREDICTED: Maylandia zebra uncharacterized LOC101470306 (LOC101470306), mRNA	0.0065	-0.5669	down	-1.2075	down	-3.5912	down	-0.6406	down	-3.0243	down	-2.3837	down
MPF_LOC101479795.2.2	XM_004547426.1 PREDICTED: Maylandia zebra uncharacterized LOC101479795 (LOC101479795), mRNA	0.0065	-0.2176	down	0.0930	up	0.9162	up	0.3107	up	1.1338	up	0.8231	up
MPF_LOC101478816.1.1	XM_004541641.1 PREDICTED: Maylandia zebra ubiquitin carboxylterminal hydrolase 45-like (LOC101478816), transcript variant X1, mRNA	0.0065	-0.9635	down	-1.4713	down	-3.5103	down	-0.5078	down	-2.5467	down	-2.0389	down
MPF_LOC101469119.3.3	XM_004561571.1	0.0065	-0.1209	down	0.2023	up	1.1083	up	0.3232	up	1.2292	up	0.9060	up

	PREDICTED: Maylandia zebra cadherin-2-like (LOC101469119), mRNA													
MPF_LOC101474346.2.2	XM_004540807.1 PREDICTED: Maylandia zebra protein phosphatase 1 regulatory subunit 14B-like (LOC101474346), mRNA	0.0066	-0.0814	down	0.2168	up	0.9725	up	0.2982	up	1.0539	up	0.7557	up
MPF_LOC100712339.1.2	XP_003460124.1 PREDICTED: protein JTBlike [Oreochromis niloticus]	0.0066	0.0951	up	0.2395	up	0.7198	up	0.1444	up	0.6247	up	0.4803	up
MPF_LOC101464596.2.2	XM_004551025.1 PREDICTED: Maylandia zebra sodium/hydrogen exchanger 1-like (LOC101464596), transcript variant X2, mRNA	0.0066	-0.4558	down	-1.1698	down	-3.5130	down	-0.7140	down	-3.0572	down	-2.3432	down
MPF_LOC100711510.1.8	XM_003455849.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100711510), mRNA	0.0066	-0.2609	down	-1.5734	down	-3.8077	down	-1.3125	down	-3.5468	down	-2.2343	down
MPF_contig_015520		0.0066	-0.0600	down	0.1950	up	0.7910	up	0.2549	up	0.8509	up	0.5960	up
MPF_LOC100701834.2.2	XM_003448970.1 PREDICTED: Oreochromis niloticus probable G-protein coupled receptor 171-like (LOC100701834), mRNA	0.0066	0.1791	up	-0.9225	down	-2.7268	down	-1.1016	down	-2.9059	down	-1.8043	down
MPF_LOC100689749.1.1	XP_003445652.1 PREDICTED: G proteincoupled receptor kinase 5like [Oreochromis niloticus]	0.0066	-0.2470	down	0.1676	up	1.0214	up	0.4147	up	1.2685	up	0.8538	up
MPF_contig_022848		0.0068	-0.2053	down	0.1563	up	1.1107	up	0.3616	up	1.3161	up	0.9544	up

MPF_LOC101466654.1.2	XM_004538580.1 PREDICTED: Maylandia zebra sodium-dependent phosphate transporter 1-Blike (LOC101466654), partial mRNA	0.0068	-0.6581	down	-1.7603	down	-3.4918	down	-1.1022	down	-2.8337	down	-1.7316	down
MPF_LOC100690883.1.2	XP_003458178.1 PREDICTED: zinc finger protein 84-like [Oreochromis niloticus]	0.0068	0.0675	up	0.1234	up	0.9903	up	0.0559	up	0.9228	up	0.8669	up
MPF_contig_006781	XM_004572062.1 PREDICTED: Maylandia zebra polypyrimidine tractbinding protein 2-like (LOC101478106), transcript variant X2, mRNA	0.0069	-0.0184	down	0.1645	up	1.0071	up	0.1830	up	1.0256	up	0.8426	up
MPF_LOC100706983.6.11	XM_003460062.1 PREDICTED: Oreochromis niloticus 28S ribosomal protein S28, mitochondriallike (LOC100706983), mRNA	0.0073	-1.2623	down	-1.0833	down	-2.9313	down	0.1789	up	-1.6690	down	-1.8479	down
MPF_contig_019576		0.0077	-0.2273	down	0.0730	up	1.1134	up	0.3003	up	1.3408	up	1.0405	up
MPF_contig_047566		0.0078	-0.0854	down	-0.5344	down	-2.1725	down	-0.4490	down	-2.0871	down	-1.6381	down
MPF_contig_014802		0.0078	-0.0574	down	-0.6690	down	-2.2738	down	-0.6116	down	-2.2163	down	-1.6047	down
MPF_LOC101161574.6.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.0078	-0.2846	down	-1.4998	down	-3.7178	down	-1.2152	down	-3.4332	down	-2.2180	down
MPF_contig_004922		0.0080	-0.4303	down	-1.2572	down	-3.2666	down	-0.8270	down	-2.8363	down	-2.0093	down

MPF_LOC101468451.1.1	XM_004567195.1 PREDICTED: Maylandia zebra WW domain-containing adapter protein with coiled-coil-like (LOC101468451), transcript variant X2, mRNA	0.0080	0.4915	up	0.2691	up	1.2348	up	-0.2224	down	0.7433	up	0.9657	up
MPF_contig_033812		0.0080	-0.1210	down	0.1267	up	0.8111	up	0.2477	up	0.9321	up	0.6844	up
MPF_PHUM_PHUM529360.2.2	XP_002431439.1 ngd5/osm-6/ift52, putative [Pediculus humanus corporis]	0.0080	-0.3932	down	-0.4713	down	-3.4035	down	-0.0781	down	-3.0103	down	-2.9322	down
MPF_LOC101487291.5.6	XM_004560239.1 PREDICTED: Maylandia zebra constitutive coactivator of PPAR-gamma-like protein 2-like (LOC101487291), mRNA	0.0080	-0.0750	down	0.1107	up	0.7813	up	0.1857	up	0.8563	up	0.6705	up
MPF_LOC101469089.8.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA	0.0080	-0.1522	down	0.1838	up	0.8582	up	0.3360	up	1.0104	up	0.6744	up
MPF_LOC100488659.3.10	XP_002933173.1 PREDICTED: hypothetical protein LOC100488659 [Xenopus (Silurana) tropicalis]	0.0080	-0.0078	down	-1.0829	down	-3.3650	down	-1.0752	down	-3.3572	down	-2.2820	down
MPF_contig_028860		0.0080	-0.9902	down	-1.7266	down	-4.8265	down	-0.7365	down	-3.8363	down	-3.0999	down

MPF_RTBS.12.36	RTBS_DROME (sp|Q95SX7) Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1	0.0080	-0.7849	down	-1.5450	down	-4.3867	down	-0.7601	down	-3.6018	down	-2.8417	down
MPF_LOC101473149.5.5	XM_004560655.1 PREDICTED: Maylandia zebra V-type proton ATPase 16 kDa proteolipid subunitlike (LOC101473149), mRNA	0.0080	-0.1366	down	0.0763	up	1.0267	up	0.2129	up	1.1632	up	0.9504	up
MPF_contig_024224		0.0081	0.1625	up	-2.2997	down	-4.7087	down	-2.4623	down	-4.8713	down	-2.4090	down
MPF_LOC100706983.1.1 1	XP_003460110.1 PREDICTED: 28S ribosomal protein S28, mitochondriallike [Oreochromis niloticus]	0.0082	-0.4197	down	-0.4902	down	-2.7824	down	-0.0705	down	-2.3627	down	-2.2921	down
MPF_LOC100709406.1.1	XP_003440884.1 PREDICTED: interleukin-17Flike [Oreochromis niloticus]	0.0084	0.0798	up	0.2227	up	1.0040	up	0.1429	up	0.9242	up	0.7813	up
MPF_LOC100696224.1.1	XP_003457485.1 PREDICTED: chromodomainhelicase-DNA-binding protein 8-like [Oreochromis niloticus]	0.0084	0.3152	up	0.2401	up	1.2517	up	-0.0751	down	0.9365	up	1.0116	up
MPF_LOC101481643.1.2	XM_004574978.1 PREDICTED: Maylandia zebra sesquipedalian-1-like (LOC101481643), transcript variant X2, mRNA	0.0084	-0.1506	down	0.2683	up	1.0723	up	0.4189	up	1.2228	up	0.8039	up
MPF_LOC101469930.1.1	XM_004551309.1 PREDICTED: Maylandia zebra inosine-uridine preferring nucleoside hydrolase-like (LOC101469930), transcript variant X2, mRNA	0.0084	0.0958	up	0.2283	up	1.2571	up	0.1325	up	1.1613	up	1.0288	up

MPF_LOC101482596.1.5	XM_004548845.1 PREDICTED: Maylandia zebra transmembrane prostate androgen-induced protein-like (LOC101482596), transcript variant X2, mRNA	0.0084	-0.3370	down	0.1822	up	1.0523	up	0.5191	up	1.3892	up	0.8701	up
MPF_contig_036057		0.0088	-0.2157	down	0.1358	up	1.1336	up	0.3515	up	1.3493	up	0.9979	up
MPF_LOC101486310.2.2	XM_004574350.1 PREDICTED: Maylandia zebra protein FAM49A-like (LOC101486310), transcript variant X3, mRNA	0.0088	0.1495	up	0.3774	up	0.9502	up	0.2279	up	0.8007	up	0.5728	up
MPF_LOC100695788.1.1	XP_003437652.1 PREDICTED: ribonuclease P protein subunit p29-like [Oreochromis niloticus]	0.0088	0.2303	up	0.3129	up	1.2124	up	0.0826	up	0.9821	up	0.8995	up
MPF_LOC101482059.1.3	XM_004563140.1 PREDICTED: Maylandia zebra mitogen-activated protein kinase kinase kinase kinase 4-like (LOC101482059), transcript variant X2, mRNA	0.0088	-0.0310	down	-1.4738	down	-2.8861	down	-1.4429	down	-2.8551	down	-1.4122	down
MPF_contig_019388		0.0088	-0.2756	down	-1.0878	down	-2.9047	down	-0.8123	down	-2.6291	down	-1.8168	down
MPF_contig_032259		0.0088	0.0264	up	-1.2495	down	-3.7410	down	-1.2758	down	-3.7674	down	-2.4915	down
MPF_LOC100702463.1.1	XM_003449473.1 PREDICTED: Oreochromis niloticus nucleolar complex protein 3 homolog (LOC100702463), mRNA	0.0089	-0.0952	down	0.3407	up	1.2972	up	0.4359	up	1.3924	up	0.9565	up
MPF_LOC100703239.1.1	XP_003440200.1 PREDICTED: hypothetical protein LOC100703239 [Oreochromis niloticus]	0.0089	-0.8164	down	-1.2662	down	-4.2274	down	-0.4498	down	-3.4110	down	-2.9612	down

MPF_LOC101480805.1.1	XM_004560594.1 PREDICTED: Maylandia zebra spartin-like (LOC101480805), transcript variant X2, mRNA	0.0089	0.0348	up	0.1848	up	0.7041	up	0.1500	up	0.6693	up	0.5193	up
MPF_contig_003522	XM_004551014.1 PREDICTED: Maylandia zebra akirin-1-like (LOC101486208), transcript variant X1, mRNA	0.0091	-0.7196	down	-1.6904	down	-3.2837	down	-0.9708	down	-2.5641	down	-1.5933	down
MPF_contig_014890		0.0091	-0.5647	down	-0.3144	down	-2.1882	down	0.2502	up	-1.6235	down	-1.8738	down
MPF_LOC100638560.2.2	XP_003388433.1 PREDICTED: hypothetical protein LOC100638560 [Amphimedon queenslandica]	0.0091	-0.2714	down	-0.1228	down	0.7883	up	0.1486	up	1.0597	up	0.9111	up
MPF_LOC100706983.10.11	XM_003460062.1 PREDICTED: Oreochromis niloticus 28S ribosomal protein S28, mitochondriallike (LOC100706983), mRNA	0.0091	-0.9199	down	-0.8032	down	-2.6446	down	0.1167	up	-1.7246	down	-1.8413	down
MPF_HMGA1B.5.6	NM_001077276.1 Danio rerio high mobility group AT-hook 1b (hmga1b), mRNA	0.0091	0.1645	up	0.3201	up	0.8390	up	0.1556	up	0.6745	up	0.5189	up
MPF_ACBD5.1.1	ACBD5_PONAB (sp|Q5R7V3) Acyl-CoAbinding domain-containing protein 5 OS=Pongo abelii GN=ACBD5 PE=2 SV=1	0.0091	-0.6526	down	-1.3087	down	-2.7051	down	-0.6560	down	-2.0524	down	-1.3964	down
MPF_LOC101469933.1.1	XM_004575028.1 PREDICTED: Maylandia zebra zinc finger protein 578like (LOC101469933), transcript variant X2, mRNA	0.0094	0.0072	up	-0.0096	down	0.5780	up	-0.0168	down	0.5709	up	0.5876	up

MPF_LOC100707133.10.12	XP_003457606.1 PREDICTED: hypothetical protein LOC100707133 [Oreochromis niloticus]	0.0094	0.3695	up	0.0585	up	-1.9521	down	-0.3110	down	-2.3216	down	-2.0106	down
MPF_contig_006466		0.0094	-0.0643	down	0.2201	up	0.9958	up	0.2845	up	1.0602	up	0.7757	up
MPF_LOC101474249.2.3	XM_004540423.1 PREDICTED: Maylandia zebra DNA-binding protein inhibitor ID-3-A-like (LOC101474249), mRNA	0.0094	0.2643	up	0.3416	up	1.2629	up	0.0773	up	0.9986	up	0.9213	up
MPF_LOC101475324.3.5	XM_004570832.1 PREDICTED: Maylandia zebra MOB kinase activator 2like (LOC101475324), transcript variant X4, mRNA	0.0095	-0.4038	down	-0.5206	down	-1.9813	down	-0.1168	down	-1.5774	down	-1.4607	down
MPF_LOC101473558.2.2	XM_004561318.1 PREDICTED: Maylandia zebra transcription factor 7like 2-like (LOC101473558), transcript variant X13, mRNA	0.0096	-0.0314	down	0.1078	up	1.0859	up	0.1392	up	1.1173	up	0.9781	up
MPF_contig_025000	XM_003963344.1 PREDICTED: Takifugu rubripes 60S ribosomal protein L32-like, transcript variant 1 (LOC101066639), mRNA	0.0096	-0.1261	down	0.1683	up	0.7837	up	0.2944	up	0.9098	up	0.6154	up
MPF_contig_023930		0.0097	-0.5937	down	-1.5883	down	-3.8897	down	-0.9946	down	-3.2959	down	-2.3013	down
MPF_LOC101479312.2.2	XM_004548084.1 PREDICTED: Maylandia zebra tribbles homolog 1-like (LOC101479312), mRNA	0.0097	-0.6708	down	-1.5994	down	-3.9382	down	-0.9286	down	-3.2673	down	-2.3387	down

MPF_contig_040282	XM_004570345.1 PREDICTED: Maylandia zebra caskin-1-like (LOC101486956), transcript variant X2, mRNA	0.0097	-0.1179	down	-0.0268	down	0.6772	up	0.0912	up	0.7951	up	0.7040	up
MPF_contig_005369	XM_004566994.1 PREDICTED: Maylandia zebra rap1 GTPase-activating protein 2-like (LOC101464757), transcript variant X2, mRNA	0.0098	-0.1606	down	0.1647	up	1.0065	up	0.3252	up	1.1671	up	0.8419	up
MPF_contig_000796	XM_004539264.1 PREDICTED: Maylandia zebra alpha-1,6-mannosylglycoprotein 6-betaN-acetylglucosaminyltransferase B-like (LOC101479752), transcript variant X1, mRNA	0.0098	0.0255	up	0.2160	up	0.8443	up	0.1905	up	0.8189	up	0.6284	up
MPF_LOC100700805.2.2	XM_003440887.1 PREDICTED: Oreochromis niloticus claudin-10-like (LOC100700805), mRNA	0.0098	-0.1472	down	0.1172	up	0.9471	up	0.2643	up	1.0942	up	0.8299	up
MPF_LOC100698574.1.2	XP_003445184.1 PREDICTED: receptor-type tyrosine-protein phosphatase C-like [Oreochromis niloticus]	0.0098	-0.4816	down	-1.4089	down	-3.0743	down	-0.9273	down	-2.5928	down	-1.6654	down
MPF_LOC101469240.1.1	XM_004544118.1 PREDICTED: Maylandia zebra charged multivesicular body protein 7-like (LOC101469240), mRNA	0.0098	-0.0486	down	0.2608	up	0.4867	up	0.3094	up	0.5353	up	0.2259	up

MPF_LOC101474004.1.1	XM_004550968.1 PREDICTED: Maylandia zebra replication protein A 32 kDa subunit-like (LOC101474004), transcript variant X2, mRNA	0.0101	-0.0446	down	-0.1166	down	1.0555	up	-0.0720	down	1.1001	up	1.1721	up
MPF_LOC101466332.2.2	XM_004574102.1 PREDICTED: Maylandia zebra heterogeneous nuclear ribonucleoprotein L-like (LOC101466332), mRNA	0.0101	-0.1083	down	0.2491	up	0.8070	up	0.3573	up	0.9153	up	0.5580	up
MPF_contig_032910		0.0101	-0.7484	down	-0.7164	down	-3.5480	down	0.0320	up	-2.7996	down	-2.8316	down
MPF_contig_027303		0.0103	-0.0706	down	0.1366	up	1.0326	up	0.2072	up	1.1032	up	0.8960	up
MPF_LOC101156017.1.1	XP_004072239.1 PREDICTED: prostate stem cell antigen-like [Oryzias latipes]	0.0106	-0.4083	down	-0.4965	down	-1.5235	down	-0.0882	down	-1.1152	down	-1.0270	down
MPF_LOC101167302.2.2	XP_004073563.1 PREDICTED: PDZ and LIM domain protein 7-like [Oryzias latipes]	0.0107	-0.0624	down	0.1829	up	0.9447	up	0.2453	up	1.0072	up	0.7619	up
MPF_contig_032831		0.0107	-0.8450	down	-1.2036	down	-3.4027	down	-0.3586	down	-2.5577	down	-2.1991	down
MPF_contig_037429		0.0107	0.0983	up	0.0009	up	-0.4716	down	-0.0974	down	-0.5700	down	-0.4725	down
MPF_LOC100701712.1.1	XM_003441390.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100701712 (LOC100701712), mRNA	0.0107	-0.3304	down	-0.8802	down	-3.0226	down	-0.5498	down	-2.6922	down	-2.1423	down
MPF_contig_021187		0.0107	0.1511	up	0.1543	up	0.7005	up	0.0031	up	0.5494	up	0.5463	up
MPF_contig_023176		0.0107	-0.1684	down	-1.5698	down	-2.9436	down	-1.4013	down	-2.7752	down	-1.3738	down
MPF_contig_024721		0.0107	-0.7023	down	-0.8556	down	-3.0784	down	-0.1534	down	-2.3761	down	-2.2227	down

MPF_LOC101478889.2.3	XM_004561424.1 PREDICTED: Maylandia zebra protein yippee-like 2like (LOC101478889), transcript variant X2, mRNA	0.0107	-0.0404	down	-0.0315	down	0.6400	up	0.0089	up	0.6804	up	0.6715	up
MPF_LOC101484929.2.3	XM_004542976.1 PREDICTED: Maylandia zebra CMP-N-acetylneuraminate-beta-1,4galactoside alpha-2,3sialyltransferase-like (LOC101484929), mRNA	0.0107	0.2216	up	-1.2207	down	-3.8320	down	-1.4423	down	-4.0536	down	-2.6113	down
MPF_LOC100695520.1.1	XP_003458434.1 PREDICTED: glycosyltransferase-like domain-containing protein 1like [Oreochromis niloticus]	0.0108	0.3025	up	0.3225	up	0.6422	up	0.0200	up	0.3397	up	0.3197	up
MPF_contig_016380		0.0108	-0.2116	down	0.1308	up	0.9681	up	0.3423	up	1.1797	up	0.8373	up
MPF_LOC101472438.1.4	XM_004575387.1 PREDICTED: Maylandia zebra collagen alpha-5(IV) chain-like (LOC101472438), mRNA	0.0109	-0.7559	down	-1.2078	down	-3.7400	down	-0.4520	down	-2.9841	down	-2.5321	down
MPF_CD63.1.2	NM_001124496.1 Oncorhynchus mykiss Cd63 antigen (cd63), mRNA gb|AY593998.1| Oncorhynchus mykiss CD63 (CD63) mRNA, complete cds	0.0110	-0.3282	down	-1.3393	down	-3.4353	down	-1.0111	down	-3.1071	down	-2.0960	down
MPF_LOC101479065.1.1	XM_004552479.1 PREDICTED: Maylandia zebra synaptotagmin-C-like (LOC101479065), mRNA	0.0110	-0.0563	down	0.0936	up	0.7097	up	0.1499	up	0.7660	up	0.6161	up

MPF_LOC100702591.1.2	XM_003459100.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100702591), mRNA	0.0110	0.1858	up	0.2068	up	1.0192	up	0.0210	up	0.8333	up	0.8124	up
MPF_contig_044527		0.0111	-0.3012	down	0.0203	up	1.1069	up	0.3216	up	1.4082	up	1.0866	up
MPF_contig_015699		0.0112	-0.0504	down	-0.2996	down	-1.4408	down	-0.2492	down	-1.3904	down	-1.1412	down
MPF_contig_045323		0.0112	-0.7384	down	-1.7233	down	-3.9938	down	-0.9849	down	-3.2554	down	-2.2705	down
MPF_FZD6.6.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440 IMAGE:6971142), complete cds	0.0112	-0.9202	down	-1.7748	down	-4.1382	down	-0.8547	down	-3.2180	down	-2.3633	down
MPF_LOC101477091.1.3	XM_004574318.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101477091), transcript variant X5, mRNA	0.0112	0.0858	up	-0.6071	down	-2.0006	down	-0.6929	down	-2.0863	down	-1.3934	down
MPF_LOC101477600.1.1	XM_004540339.1 PREDICTED: Maylandia zebra phospholipase B1, membrane-associated-like (LOC101477600), mRNA	0.0112	0.0820	up	0.3211	up	1.0309	up	0.2391	up	0.9489	up	0.7098	up
MPF_LOC101484019.1.1	XM_004545115.1 PREDICTED: Maylandia zebra copine-5-like (LOC101484019), mRNA	0.0112	-0.4559	down	-0.0129	down	1.0712	up	0.4430	up	1.5271	up	1.0841	up

MPF_contig_003963	XM_004541039.1 PREDICTED: Maylandia zebra clathrin light chain Blike (LOC101468249), transcript variant X1, mRNA	0.0114	0.0661	up	0.1611	up	0.6220	up	0.0950	up	0.5560	up	0.4610	up
MPF_contig_048538		0.0115	0.1910	up	0.2653	up	1.0532	up	0.0743	up	0.8623	up	0.7880	up
MPF_LOC100703120.2.3	XP_003458215.1 PREDICTED: hypothetical protein LOC100703120 [Oreochromis niloticus]	0.0119	-0.7478	down	-0.5276	down	-2.7183	down	0.2202	up	-1.9705	down	-2.1908	down
MPF_contig_031996		0.0119	0.3826	up	-0.4539	down	-1.8609	down	-0.8365	down	-2.2435	down	-1.4070	down
MPF_contig_023699		0.0120	0.7489	up	-1.7967	down	-3.7510	down	-2.5456	down	-4.4999	down	-1.9543	down
MPF_LOC101470738.5.20	XM_004560737.1 PREDICTED: Maylandia zebra actin, cytoplasmic 1like (LOC101470738), mRNA	0.0123	-0.1774	down	-0.1923	down	1.0989	up	-0.0150	down	1.2763	up	1.2913	up
MPF_contig_023972		0.0123	0.0753	up	0.1546	up	0.6592	up	0.0793	up	0.5838	up	0.5046	up
MPF_LOC101170487.4.4	XM_004085086.1 PREDICTED: Oryzias latipes low-density lipoprotein receptor 2-like (LOC101170487), mRNA	0.0123	0.0417	up	-0.8705	down	-2.7759	down	-0.9122	down	-2.8176	down	-1.9054	down
MPF_LOC101466726.1.1	XM_004552330.1 PREDICTED: Maylandia zebra telethonin-like (LOC101466726), mRNA	0.0123	-0.1386	down	0.2154	up	0.8924	up	0.3539	up	1.0310	up	0.6770	up
MPF_LOC100712339.2.2	XP_003460124.1 PREDICTED: protein JTBlike [Oreochromis niloticus]	0.0123	0.0641	up	0.2455	up	0.7151	up	0.1813	up	0.6510	up	0.4696	up
MPF_LOC100695076.5.8	XP_003455918.1 PREDICTED: hypothetical protein LOC100695076 [Oreochromis niloticus]	0.0123	-0.1114	down	0.1421	up	1.0463	up	0.2535	up	1.1577	up	0.9042	up

MPF_LOC101477442.1.1	XM_004547420.1 PREDICTED: Maylandia zebra GTP-binding protein REM 1-like (LOC101477442), transcript variant X4, mRNA	0.0123	-0.1298	down	0.2429	up	0.8375	up	0.3727	up	0.9673	up	0.5946	up

MPF_LOC100694868.1.2	XM_003446700.1 PREDICTED: Oreochromis niloticus c-C chemokine receptor type 6-like (LOC100694868), mRNA	0.0123	-0.3339	down	-1.0958	down	-2.0712	down	-0.7619	down	-1.7373	down	-0.9754	down
MPF_LOC101474085.2.2	XM_004568504.1 PREDICTED: Maylandia zebra cyclin-Y-like (LOC101474085), transcript variant X4, mRNA	0.0123	0.0930	up	0.2098	up	0.9744	up	0.1169	up	0.8814	up	0.7646	up
MPF_LOC101465129.6.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNAbinding protein A-like (LOC101465129), transcript variant X4, mRNA	0.0123	-0.6535	down	-1.0363	down	-2.4892	down	-0.3828	down	-1.8357	down	-1.4529	down
MPF_LOC101483324.1.1	XM_004541004.1 PREDICTED: Maylandia zebra regulator of cell cycle RGCC-like (LOC101483324), mRNA	0.0123	0.0585	up	0.1304	up	0.8394	up	0.0720	up	0.7809	up	0.7090	up
MPF_LOC100711484.7.8	XM_003448843.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100711484), mRNA	0.0123	0.0116	up	0.1563	up	0.6022	up	0.1447	up	0.5906	up	0.4460	up

MPF_LOC101474859.8.2 1	XM_004575478.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 4like (LOC101474859), transcript variant X2, mRNA	0.0123	-0.1178	down	0.2378	up	1.3360	up	0.3556	up	1.4538	up	1.0982	up
MPF_contig_038379		0.0124	-0.1773	down	-1.3784	down	-2.9808	down	-1.2011	down	-2.8035	down	-1.6024	down
MPF_contig_016515		0.0124	-0.1857	down	0.1688	up	1.0295	up	0.3544	up	1.2152	up	0.8608	up
MPF_LOC100707640.2.2	XP_003451524.1 PREDICTED: hypothetical protein LOC100707640 [Oreochromis niloticus]	0.0126	-0.1185	down	-0.3259	down	-1.7541	down	-0.2073	down	-1.6356	down	-1.4283	down
MPF_LOC101465052.1.1	XM_004568916.1 PREDICTED: Maylandia zebra V-set and transmembrane domaincontaining protein 2A-like (LOC101465052), mRNA	0.0126	-0.1333	down	0.3049	up	1.2393	up	0.4382	up	1.3726	up	0.9344	up
MPF_LOC100690432.1.1	XM_003439085.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100690432 (LOC100690432), mRNA	0.0126	-0.5843	down	-0.8811	down	-2.3827	down	-0.2969	down	-1.7985	down	-1.5016	down
MPF_RTBS.7.36	RTBS_DROME (sp|Q95SX7) Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1	0.0127	-0.1658	down	0.2264	up	0.9216	up	0.3922	up	1.0875	up	0.6953	up
MPF_CR2.1.1	CR2_MOUSE (sp|P19070) Complement receptor type 2 OS=Mus musculus GN=Cr2	0.0127	-0.4785	down	-1.4401	down	-3.3678	down	-0.9615	down	-2.8892	down	-1.9277	down

	PE=2 SV=1													
MPF_LOC101483357.1.1	XM_004573344.1 PREDICTED: Maylandia zebra transgelin-like (LOC101483357), mRNA	0.0127	-0.3495	down	-1.9076	down	-3.6236	down	-1.5581	down	-3.2741	down	-1.7160	down
MPF_contig_004128		0.0127	-0.5128	down	-1.1600	down	-3.2604	down	-0.6472	down	-2.7476	down	-2.1004	down
MPF_LOC100005864.2.2	XP_001921726.1 PREDICTED: GTPase IMAP family member 8-like [Danio rerio]	0.0127	-0.8608	down	-0.9377	down	-3.5151	down	-0.0769	down	-2.6543	down	-2.5774	down
MPF_contig_008885		0.0127	-0.0883	down	0.0176	up	0.8584	up	0.1059	up	0.9466	up	0.8407	up
MPF_contig_033538	XM_004562711.1 PREDICTED: Maylandia zebra uncharacterized LOC101464922 (LOC101464922), transcript variant X1, mRNA	0.0128	-0.1131	down	-0.0023	down	0.9132	up	0.1108	up	1.0264	up	0.9156	up
MPF_LOC100707640.1.2	XP_003451524.1 PREDICTED: hypothetical protein LOC100707640 [Oreochromis niloticus]	0.0128	-0.3759	down	-0.4695	down	-1.8417	down	-0.0936	down	-1.4658	down	-1.3722	down
MPF_contig_020194		0.0128	-1.0225	down	-2.0210	down	-4.5036	down	-0.9985	down	-3.4812	down	-2.4826	down
MPF_contig_015435		0.0129	-0.7685	down	-1.5403	down	-3.6865	down	-0.7717	down	-2.9180	down	-2.1463	down
MPF_contig_025924	XM_004574349.1 PREDICTED: Maylandia zebra protein FAM49A-like (LOC101486310), transcript variant X2, mRNA	0.0129	-0.4247	down	-1.6490	down	-3.4886	down	-1.2243	down	-3.0639	down	-1.8395	down

MPF_LOC100698387.1.1	XP_003440011.1 PREDICTED: leucine-rich repeat-containing protein 15like [Oreochromis niloticus]	0.0130	0.0934	up	-0.1319	down	0.9436	up	-0.2253	down	0.8502	up	1.0756	up
MPF_LOC100706528.3.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0.0130	0.2062	up	0.3714	up	0.9001	up	0.1652	up	0.6939	up	0.5287	up
MPF_contig_023224		0.0130	-0.2959	down	-2.0479	down	-4.2321	down	-1.7520	down	-3.9362	down	-2.1842	down
MPF_LOC101484255.1.1	XM_004555723.1 PREDICTED: Maylandia zebra SH2 domain-containing protein 3C-like (LOC101484255), transcript variant X1, mRNA	0.0130	-0.4908	down	-1.2261	down	-3.4391	down	-0.7353	down	-2.9483	down	-2.2130	down
MPF_LOC101468583.5.7	XM_004576296.1 PREDICTED: Maylandia zebra uncharacterized LOC101468583 (LOC101468583), mRNA	0.0130	-0.0293	down	-0.1643	down	-1.2268	down	-0.1350	down	-1.1975	down	-1.0625	down
MPF_contig_023403		0.0130	-0.4737	down	-0.6679	down	-1.6515	down	-0.1943	down	-1.1779	down	-0.9836	down
MPF_contig_035918		0.0130	-0.9384	down	-1.7333	down	-3.1126	down	-0.7949	down	-2.1741	down	-1.3792	down
MPF_LOC101169293.1.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.0130	-0.4574	down	-0.8595	down	-2.4662	down	-0.4021	down	-2.0089	down	-1.6067	down

MPF_LOC101467841.2.2	XM_004567099.1 PREDICTED: Maylandia zebra kin of IRRE-like protein 1-like (LOC101467841), transcript variant X2, mRNA	0.0130	-0.1705	down	0.1674	up	1.0589	up	0.3379	up	1.2294	up	0.8915	up
MPF_LOC100704053.3.1 2	XM_003440652.1 PREDICTED: Oreochromis niloticus ubiquitin-like protein FUBI-like (LOC100704053), mRNA	0.0130	0.0058	up	-1.2023	down	-1.9689	down	-1.2081	down	-1.9747	down	-0.7666	down
MPF_LOC101171771.2.2	XM_004077345.1 PREDICTED: Oryzias latipes uncharacterized LOC101171771 (LOC101171771), mRNA	0.0130	-0.1285	down	-0.5318	down	-3.2438	down	-0.4033	down	-3.1152	down	-2.7120	down
MPF_LOC101473761.1.1	XM_004565743.1 PREDICTED: Maylandia zebra gamma-aminobutyric acid receptor-associated protein-like 2-like (LOC101473761), mRNA	0.0130	-0.1889	down	0.1594	up	0.9531	up	0.3483	up	1.1421	up	0.7937	up
MPF_contig_048760		0.0130	-0.0446	down	0.1893	up	0.9735	up	0.2339	up	1.0180	up	0.7842	up
MPF_LOC100691946.1.4	XM_003456019.1 PREDICTED: Oreochromis niloticus serine incorporator 1like (LOC100691946), mRNA	0.0130	0.1331	up	0.1078	up	0.9264	up	-0.0252	down	0.7933	up	0.8186	up
MPF_LOC101479404.3.4	XM_004570313.1 PREDICTED: Maylandia zebra prolactin-1-like (LOC101479404), mRNA	0.0130	-0.1841	down	-0.9853	down	-3.1919	down	-0.8012	down	-3.0079	down	-2.2066	down
MPF_contig_044581		0.0130	0.0798	up	0.1836	up	0.6320	up	0.1038	up	0.5522	up	0.4484	up
MPF_contig_021826		0.0130	-0.2524	down	-0.5595	down	-2.4914	down	-0.3071	down	-2.2390	down	-1.9319	down

MPF_LOC100705526.1.1	XM_003453520.1 PREDICTED: Oreochromis niloticus glutaredoxin-2, mitochondrial-like, transcript variant 4 (LOC100705526), mRNA	0.0131	-0.0925	down	0.2717	up	0.8186	up	0.3642	up	0.9111	up	0.5469	up
MPF_LOC101467152.1.1	XM_004567377.1 PREDICTED: Maylandia zebra glutaredoxin-2, mitochondrial-like (LOC101467152), transcript variant X2, mRNA	0.0131	-0.0877	down	0.2700	up	0.8166	up	0.3577	up	0.9042	up	0.5465	up
MPF_LOC100691160.2.2	XP_003459991.1 PREDICTED: 5-hydroxytryptamine receptor 3A-like [Oreochromis niloticus]	0.0131	0.2100	up	-0.9303	down	-2.0433	down	-1.1403	down	-2.2533	down	-1.1130	down
MPF_contig_002843		0.0131	-0.1666	down	0.1225	up	0.8394	up	0.2891	up	1.0060	up	0.7169	up
MPF_LOC100691083.1.3	XM_003444020.1 PREDICTED: Oreochromis niloticus diacylglycerol Oacyltransferase 1-like (LOC100691083), mRNA	0.0131	0.1098	up	0.1093	up	0.6881	up	-0.0005	down	0.5783	up	0.5788	up
MPF_BM1_02870.1.1	XP_001892072.1 T-cell receptor beta chain ANA 11 [Brugia malayi]	0.0131	-0.2275	down	0.1020	up	0.9576	up	0.3295	up	1.1851	up	0.8557	up
MPF_contig_009872		0.0131	-0.0807	down	0.0664	up	-1.7102	down	0.1471	up	-1.6294	down	-1.7766	down
MPF_LOC100695994.11.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.0131	0.2366	up	0.4141	up	0.7459	up	0.1775	up	0.5093	up	0.3318	up
MPF_DEPDC5.2.2	XM_003459178.1 PREDICTED: Oreochromis niloticus DEP domain containing 5 (DEPDC5),	0.0131	0.0133	up	0.2464	up	1.0185	up	0.2330	up	1.0052	up	0.7722	up

	mRNA													
MPF_LOC100698619.1.1	XP_003455532.1 PREDICTED: hypothetical protein LOC100698619 [Oreochromis niloticus]	0.0134	-0.1379	down	0.0882	up	0.9944	up	0.2261	up	1.1323	up	0.9062	up
MPF_LOC101471209.1.3	XM_004561763.1 PREDICTED: Maylandia zebra protein Jade-2-like (LOC101471209), mRNA	0.0134	-0.1653	down	0.1132	up	0.9578	up	0.2784	up	1.1230	up	0.8446	up
MPF_THAP9.1.1	[BBH] THAP9_HUMAN (sp|Q9H5L6) DNA transposase THAP9 OS=Homo sapiens GN=THAP9 PE=1 SV=2	0.0134	-0.3866	down	-1.4255	down	-3.3492	down	-1.0389	down	-2.9626	down	-1.9237	down
MPF_LOC100693993.1.1	XM_003453809.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693993 (LOC100693993), mRNA	0.0134	-0.3189	down	-1.0499	down	-3.2331	down	-0.7310	down	-2.9142	down	-2.1832	down
MPF_LOC101480702.3.4	XM_004557634.1 PREDICTED: Maylandia zebra mitogen-activated protein kinase 8B-like (LOC101480702), mRNA	0.0134	-0.3486	down	-0.5725	down	-2.8193	down	-0.2239	down	-2.4707	down	-2.2468	down
MPF_LOC101158949.1.1	XR_177430.1 PREDICTED: Oryzias latipes ubinuclein-2like (LOC101158949), misc_RNA	0.0134	-0.2296	down	-0.0326	down	0.9615	up	0.1970	up	1.1911	up	0.9941	up
MPF_contig_047891		0.0134	-0.6480	down	-2.2133	down	-4.1898	down	-1.5653	down	-3.5418	down	-1.9765	down
MPF_contig_043522		0.0134	-0.2089	down	0.1925	up	0.8750	up	0.4014	up	1.0839	up	0.6825	up

MPF_LOC101475042.1.1	XM_004549634.1 PREDICTED: Maylandia zebra dymeclin-like (LOC101475042), transcript variant X1, mRNA	0.0135	0.0141	up	0.0767	up	0.7699	up	0.0626	up	0.7558	up	0.6932	up
MPF_LOC101486107.1.1	XM_004550367.1 PREDICTED: Maylandia zebra AF4/FMR2 family member 4-like (LOC101486107), transcript variant X1, mRNA	0.0136	-0.0745	down	0.0199	up	1.0345	up	0.0944	up	1.1090	up	1.0146	up
MPF_SGS4.2.10	SGS4_DROME (sp|Q00725) Salivary glue protein Sgs-4 OS=Drosophila melanogaster GN=Sgs4 PE=2 SV=1	0.0136	-0.7192	down	-0.6225	down	-1.7099	down	0.0966	up	-0.9907	down	-1.0873	down
MPF_LOC101172990.10.36	XM_004073898.1 PREDICTED: Oryzias latipes uncharacterized LOC101172990 (LOC101172990), mRNA	0.0136	-0.2052	down	0.1561	up	1.0645	up	0.3613	up	1.2697	up	0.9084	up
MPF_LOC101471890.1.1	XM_004559351.1 PREDICTED: Maylandia zebra nuclear GTPase SLIPGC-like (LOC101471890), mRNA	0.0136	-0.7111	down	-1.2292	down	-3.3953	down	-0.5181	down	-2.6842	down	-2.1660	down
MPF_LOC101464835.1.1	XM_004566087.1 PREDICTED: Maylandia zebra dickkopf-related protein 3-like (LOC101464835), mRNA	0.0136	-0.2133	down	0.2545	up	1.3754	up	0.4677	up	1.5887	up	1.1209	up
MPF_LOC101473612.4.5	XM_004550873.1 PREDICTED: Maylandia zebra sodium/potassiumtransporting ATPase subunit alpha-3-like (LOC101473612), transcript variant X2, mRNA	0.0136	-0.7301	down	-2.0552	down	-4.2585	down	-1.3251	down	-3.5284	down	-2.2033	down

MPF_contig_014940		0.0136	-0.3605	down	-0.9904	down	-3.3801	down	-0.6299	down	-3.0196	down	-2.3897	down
MPF_LOC100700407.1.1	XM_003454414.1 PREDICTED: Oreochromis niloticus IGF-like family receptor 1-like (LOC100700407), mRNA	0.0137	-0.5823	down	-1.9947	down	-4.8382	down	-1.4124	down	-4.2560	down	-2.8435	down
MPF_LOC100689805.1.1	XP_003457862.1 PREDICTED: probable signal peptidase complex subunit 2like [Oreochromis niloticus]	0.0138	-0.1480	down	0.2206	up	1.1550	up	0.3685	up	1.3030	up	0.9345	up
MPF_contig_007959		0.0139	-0.4920	down	-0.8807	down	-2.5970	down	-0.3887	down	-2.1049	down	-1.7163	down
MPF_contig_013449		0.0139	-0.1257	down	0.2338	up	0.8533	up	0.3595	up	0.9790	up	0.6194	up
MPF_LOC101483390.1.1	XM_004557184.1 PREDICTED: Maylandia zebra aquaporin-12-like (LOC101483390), mRNA	0.0139	-0.1325	down	0.1813	up	0.7515	up	0.3138	up	0.8840	up	0.5702	up
MPF_LOC101487772.1.2	XM_004559324.1 PREDICTED: Maylandia zebra alcohol dehydrogenase 1-like (LOC101487772), mRNA	0.0139	0.1926	up	0.3706	up	0.8796	up	0.1779	up	0.6870	up	0.5090	up
MPF_LOC100691587.1.1	XM_003458842.1 PREDICTED: Oreochromis niloticus mitochondrial chaperone BCS1-like (LOC100691587), mRNA	0.0139	-0.1269	down	0.2532	up	1.1164	up	0.3802	up	1.2434	up	0.8632	up
MPF_LOC101478250.3.3	XM_004538353.1 PREDICTED: Maylandia zebra flocculation protein FLO11-like (LOC101478250), transcript variant X3, mRNA	0.0139	-0.1227	down	-2.5079	down	-5.3257	down	-2.3851	down	-5.2030	down	-2.8179	down

MPF_LOC101481678.1.3	XM_004560040.1 PREDICTED: Maylandia zebra polyadenylate-binding protein 1-like (LOC101481678), transcript variant X2, mRNA	0.0142	0.1353	up	0.3042	up	0.5485	up	0.1688	up	0.4132	up	0.2443	up
MPF_LOC101481489.4.6	XM_004564502.1 PREDICTED: Maylandia zebra 40S ribosomal protein S13-like (LOC101481489), mRNA	0.0142	0.0270	up	-0.6990	down	-1.5585	down	-0.7260	down	-1.5854	down	-0.8594	down
MPF_contig_027052		0.0142	-0.2373	down	-0.6114	down	-2.6728	down	-0.3742	down	-2.4355	down	-2.0613	down
MPF_LOC100692952.1.1	XM_003439342.1 PREDICTED: Oreochromis niloticus condensin-2 complex subunit G2-like (LOC100692952), mRNA	0.0142	0.2675	up	0.5561	up	1.1209	up	0.2886	up	0.8533	up	0.5648	up
MPF_LOC101465092.2.3	XM_004554364.1 PREDICTED: Maylandia zebra serine/threonineprotein phosphatase 2B catalytic subunit alpha isoform-like (LOC101465092), transcript variant X2, mRNA	0.0142	0.0081	up	0.0117	up	0.6824	up	0.0035	up	0.6742	up	0.6707	up
MPF_ENPP1.1.2	XM_003446358.1 PREDICTED: Oreochromis niloticus ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA	0.0143	-0.6339	down	-1.5612	down	-3.8058	down	-0.9273	down	-3.1720	down	-2.2446	down
MPF_LOC101487917.3.6	XM_004572192.1 PREDICTED: Maylandia zebra PERQ amino acid-rich with GYF domain-containing protein 1-like (LOC101487917), mRNA	0.0143	0.0347	up	0.0043	up	0.9289	up	-0.0303	down	0.8942	up	0.9246	up

MPF_LOC100697044.1.1	XM_003460170.1 PREDICTED: Oreochromis niloticus myc-induced nuclear antigen-like (LOC100697044), mRNA	0.0143	0.1005	up	0.1343	up	0.8492	up	0.0338	up	0.7487	up	0.7149	up
MPF_LOC101480093.8.8	XM_004574589.1 PREDICTED: Maylandia zebra tripartite motifcontaining protein 16-like (LOC101480093), mRNA	0.0143	0.0497	up	0.1243	up	0.8154	up	0.0746	up	0.7657	up	0.6912	up
MPF_contig_009983		0.0143	0.2112	up	0.0077	up	-1.5745	down	-0.2035	down	-1.7857	down	-1.5822	down
MPF_LOC101473807.1.1	XM_004573575.1 PREDICTED: Maylandia zebra protein C-ets-1-like (LOC101473807), transcript variant X1, mRNA	0.0143	-0.1680	down	0.1626	up	1.0434	up	0.3306	up	1.2114	up	0.8808	up
MPF_LOC101471935.1.1	XM_004545975.1 PREDICTED: Maylandia zebra transcription factor MafB-like (LOC101471935), mRNA	0.0143	-0.5120	down	-1.3345	down	-3.6223	down	-0.8225	down	-3.1103	down	-2.2878	down
MPF_contig_008294		0.0143	0.0894	up	0.2423	up	0.7006	up	0.1529	up	0.6113	up	0.4584	up
MPF_contig_009977		0.0143	-0.0676	down	-0.6518	down	-1.9422	down	-0.5842	down	-1.8746	down	-1.2904	down
MPF_contig_043533		0.0143	0.0258	up	0.3281	up	0.9767	up	0.3023	up	0.9509	up	0.6486	up
MPF_LOC101063002.1.1	XP_003971894.1 PREDICTED: LOW QUALITY PROTEIN: T-cell activation Rho GTPase-activating protein-like [Takifugu rubripes]	0.0143	-0.3862	down	-0.9942	down	-3.0265	down	-0.6080	down	-2.6402	down	-2.0322	down

MPF_LOC101467998.1.1	XM_004574373.1 PREDICTED: Maylandia zebra amyloid beta A4 precursor protein-binding family A member 1-like (LOC101467998), mRNA	0.0143	0.0203	up	0.2237	up	0.9523	up	0.2035	up	0.9320	up	0.7285	up
MPF_LOC101481065.2.2	XM_004554051.1 PREDICTED: Maylandia zebra guanine nucleotidebinding protein G(s) subunit alpha-like (LOC101481065), mRNA	0.0143	-0.2878	down	-0.0493	down	0.9174	up	0.2385	up	1.2052	up	0.9667	up
MPF_LOC101477243.1.1	XM_004544896.1 PREDICTED: Maylandia zebra rho guanine nucleotide exchange factor 25-like (LOC101477243), transcript variant X3, mRNA	0.0143	-0.7834	down	-1.0417	down	-3.2091	down	-0.2583	down	-2.4257	down	-2.1674	down
MPF_LOC101473217.1.1	XM_004572509.1 PREDICTED: Maylandia zebra ventral anterior homeobox 1-like (LOC101473217), mRNA	0.0143	-0.0240	down	0.1765	up	0.8437	up	0.2005	up	0.8677	up	0.6672	up
MPF_LOC101472355.1.1	XM_004556700.1 PREDICTED: Maylandia zebra peripheral myelin protein 22-like (LOC101472355), mRNA	0.0144	-0.4302	down	-2.0633	down	-4.8534	down	-1.6330	down	-4.4232	down	-2.7901	down
MPF_contig_036796		0.0144	0.0037	up	0.3245	up	1.0411	up	0.3208	up	1.0374	up	0.7167	up
MPF_LOC100695937.1.1	XM_003449613.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100695937	0.0144	-0.5257	down	-1.1268	down	-2.7328	down	-0.6011	down	-2.2070	down	-1.6060	down

	(LOC100695937), mRNA													
MPF_LOC101484675.2.2	XM_004549119.1 PREDICTED: Maylandia zebra hepatoma-derived growth factor-like (LOC101484675), transcript variant X2, mRNA	0.0144	-0.0565	down	0.0621	up	0.6260	up	0.1186	up	0.6825	up	0.5638	up
MPF_HMGA2.2.3	NM_010441.2 Mus musculus high mobility group AT-hook 2 (Hmga2), mRNA	0.0144	-0.0347	down	-0.0068	down	0.6613	up	0.0280	up	0.6960	up	0.6680	up
MPF_LOC100697391.1.1	XP_003460149.1 PREDICTED: cystine/glutamate transporterlike [Oreochromis niloticus]	0.0144	-0.2095	down	0.1215	up	1.0013	up	0.3310	up	1.2108	up	0.8798	up
MPF_TSP_02148.1.1	XP_003377890.1 7 transmembrane receptor [Trichinella spiralis]	0.0144	-0.1826	down	-0.4091	down	-1.3846	down	-0.2265	down	-1.2020	down	-0.9755	down
MPF_contig_017922		0.0145	-0.0994	down	0.0135	up	0.5078	up	0.1129	up	0.6072	up	0.4943	up
MPF_LOC100707655.8.19	XM_003454192.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S6-like (LOC100707655), mRNA	0.0145	-0.0439	down	-0.6596	down	-2.2398	down	-0.6158	down	-2.1959	down	-1.5802	down
MPF_contig_046735		0.0145	0.0674	up	0.2005	up	1.0752	up	0.1331	up	1.0079	up	0.8747	up
MPF_contig_025533	XM_004574317.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101477091), transcript variant X4, mRNA	0.0147	-0.1425	down	-0.3801	down	-1.1824	down	-0.2376	down	-1.0399	down	-0.8023	down

MPF_contig_020382	XM_004548075.1 PREDICTED: Maylandia zebra ras-related protein Rab5A-like (LOC101476881), transcript variant X1, mRNA	0.0147	-0.1839	down	0.1533	up	1.0187	up	0.3372	up	1.2026	up	0.8654	up
MPF_LOC101479305.2.6	XM_004546110.1 PREDICTED: Maylandia zebra cytosolic sulfotransferase 3-like (LOC101479305), transcript variant X2, mRNA	0.0147	-0.1830	down	-0.2610	down	-1.3486	down	-0.0780	down	-1.1656	down	-1.0876	down
MPF_ACTBA.4.4	XM_003964421.1 PREDICTED: Takifugu rubripes actin, cytoplasmic 1like (LOC101073736), mRNA	0.0147	0.1730	up	0.3520	up	0.8047	up	0.1790	up	0.6317	up	0.4527	up
MPF_contig_015500		0.0147	-0.5099	down	-1.4952	down	-3.8176	down	-0.9852	down	-3.3077	down	-2.3225	down
MPF_contig_045038		0.0147	0.2083	up	-0.2433	down	1.2053	up	-0.4515	down	0.9971	up	1.4486	up
MPF_contig_005660		0.0147	-0.1416	down	0.1189	up	1.0220	up	0.2604	up	1.1636	up	0.9032	up
MPF_MXAN_5876.1.1	YP_634013.1 hypothetical protein MXAN_5876 [Myxococcus xanthus DK 1622]	0.0147	0.0751	up	-0.7609	down	-2.0480	down	-0.8360	down	-2.1231	down	-1.2871	down
MPF_contig_023282		0.0147	-0.0957	down	0.1415	up	0.8776	up	0.2373	up	0.9733	up	0.7361	up
MPF_contig_023989		0.0147	-0.9596	down	-1.4449	down	-3.0652	down	-0.4853	down	-2.1057	down	-1.6204	down
MPF_contig_027568		0.0147	-0.2135	down	-1.7614	down	-3.8466	down	-1.5480	down	-3.6331	down	-2.0851	down
MPF_LOC101476857.3.3	XM_004566214.1 PREDICTED: Maylandia zebra 5'-nucleotidase domaincontaining protein 1-like (LOC101476857), mRNA	0.0147	-0.0165	down	0.1083	up	0.6816	up	0.1248	up	0.6982	up	0.5733	up

MPF_contig_042890		0.0147	-0.1021	down	0.1920	up	1.2219	up	0.2941	up	1.3240	up	1.0299	up
MPF_RAMP3.1.1	RAMP3_HUMAN (sp|O60896) Receptor activity-modifying protein 3 OS=Homo sapiens GN=RAMP3 PE=2 SV=1	0.0147	-0.0723	down	0.1365	up	0.6891	up	0.2089	up	0.7614	up	0.5525	up
MPF_LOC100706363.1.1	XP_003441373.1 PREDICTED: hypothetical protein LOC100706363 [Oreochromis niloticus]	0.0147	-0.2816	down	0.1180	up	0.7739	up	0.3995	up	1.0555	up	0.6559	up
MPF_LOC101487706.1.1	XM_004565535.1 PREDICTED: Maylandia zebra cAMP-responsive element modulator-like (LOC101487706), transcript variant X2, mRNA	0.0147	-0.1217	down	-0.6970	down	-2.4215	down	-0.5752	down	-2.2998	down	-1.7245	down
MPF_LOC100698625.10.22	XM_003456694.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100698625), mRNA	0.0148	-0.3280	down	-0.3027	down	-2.0001	down	0.0253	up	-1.6721	down	-1.6974	down
MPF_LOC100707046.10.12	XM_003454686.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100707046), mRNA	0.0148	-0.1377	down	-0.1016	down	1.0020	up	0.0361	up	1.1396	up	1.1035	up
MPF_LOC100702478.4.6	XM_003453592.1 PREDICTED: Oreochromis niloticus tripartite motifcontaining protein 39-like (LOC100702478), mRNA	0.0148	0.1779	up	0.3102	up	0.8285	up	0.1323	up	0.6506	up	0.5184	up
MPF_LOC101467757.2.2	XM_004546448.1 PREDICTED: Maylandia zebra cytosolic sulfotransferase 3-like	0.0148	0.0348	up	0.1199	up	0.9248	up	0.0851	up	0.8900	up	0.8049	up

	(LOC101467757), mRNA													
MPF_LOC100699298.1.1	XP_003446682.1 PREDICTED: galectin-8-like [Oreochromis niloticus]	0.0148	-0.1986	down	-0.4303	down	1.0150	up	-0.2317	down	1.2136	up	1.4453	up
MPF_LOC100710874.10.12	XP_003453997.1 PREDICTED: hypothetical protein LOC100710874 [Oreochromis niloticus]	0.0148	-0.3758	down	-0.3325	down	-2.4626	down	0.0433	up	-2.0868	down	-2.1301	down
MPF_contig_044406		0.0148	-0.0652	down	0.1096	up	0.7168	up	0.1748	up	0.7820	up	0.6072	up
MPF_contig_043543		0.0148	0.1912	up	0.4827	up	1.4422	up	0.2915	up	1.2510	up	0.9595	up
MPF_LOC101480926.1.1	XM_004544359.1 PREDICTED: Maylandia zebra survival motor neuron protein 1-like (LOC101480926), mRNA	0.0149	0.0207	up	0.2092	up	0.8238	up	0.1885	up	0.8030	up	0.6145	up
MPF_contig_044171		0.0149	-0.1232	down	0.1470	up	0.8754	up	0.2701	up	0.9986	up	0.7284	up
MPF_contig_021708		0.0149	-0.1696	down	-0.8939	down	-2.1536	down	-0.7243	down	-1.9840	down	-1.2597	down
MPF_contig_008419		0.0150	-0.2893	down	-0.0011	down	0.9781	up	0.2882	up	1.2674	up	0.9792	up
MPF_contig_004932		0.0150	-0.0960	down	0.0752	up	0.6599	up	0.1712	up	0.7559	up	0.5847	up
MPF_contig_042705		0.0150	-0.0968	down	-0.0231	down	0.7774	up	0.0737	up	0.8742	up	0.8005	up
MPF_contig_035342		0.0150	0.1929	up	-0.7790	down	-1.7987	down	-0.9719	down	-1.9916	down	-1.0197	down
MPF_contig_013745	XM_004548188.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 12-like	0.0150	-0.2149	down	0.0606	up	0.7699	up	0.2756	up	0.9848	up	0.7092	up

	(LOC101485157), transcript variant X2, mRNA													
MPF_contig_014930	XM_004570830.1 PREDICTED: Maylandia zebra MOB kinase activator 2like (LOC101475324), transcript variant X2, mRNA	0.0150	-0.2176	down	0.0783	up	0.8465	up	0.2958	up	1.0640	up	0.7682	up
MPF_LOC100704190.2.2	XR_134884.1 PREDICTED: Oreochromis niloticus complement C4-like (LOC100704190), miscRNA	0.0150	-0.1630	down	-1.6477	down	-4.4687	down	-1.4847	down	-4.3056	down	-2.8209	down
MPF_LOC101479635.2.2	XM_004557450.1 PREDICTED: Maylandia zebra 4hydroxyphenylpyruvate dioxygenase-like (LOC101479635), mRNA	0.0150	0.0767	up	0.1049	up	0.8507	up	0.0281	up	0.7740	up	0.7459	up
MPF_contig_017190		0.0150	-0.0941	down	-1.3044	down	-3.5403	down	-1.2103	down	-3.4463	down	-2.2359	down
MPF_LOC101467665.1.2	XM_004545591.1 PREDICTED: Maylandia zebra protein RD3-like (LOC101467665), mRNA	0.0150	0.1721	up	0.3110	up	0.8782	up	0.1389	up	0.7061	up	0.5672	up
MPF_LOC101485709.2.4	XM_004548564.1 PREDICTED: Maylandia zebra synapsin-1-like (LOC101485709), mRNA	0.0150	-0.2230	down	0.1311	up	1.0369	up	0.3542	up	1.2600	up	0.9058	up
MPF_contig_036695		0.0150	-0.1555	down	0.1265	up	0.9251	up	0.2820	up	1.0806	up	0.7986	up

MPF_LOC100707166.2.2	XM_003442172.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100707166 (LOC100707166), mRNA	0.0150	0.0691	up	-0.8363	down	-2.4163	down	-0.9054	down	-2.4854	down	-1.5800	down
MPF_LOC101481680.1.1	XR_191422.1 PREDICTED: Maylandia zebra uncharacterized LOC101481680 (LOC101481680), misc_RNA	0.0150	-1.0639	down	-0.7375	down	-3.4193	down	0.3264	up	-2.3554	down	-2.6818	down
MPF_LOC101469018.2.2	XM_004563092.1 PREDICTED: Maylandia zebra arginine and glutamaterich protein 1-B-like (LOC101469018), transcript variant X2, mRNA	0.0150	-0.1531	down	0.1601	up	0.9908	up	0.3132	up	1.1439	up	0.8307	up
MPF_EIF3K.3.3	EIF3K_DANRE (sp|Q567V6) Eukaryotic translation initiation factor 3 subunit K OS=Danio rerio GN=eif3k PE=2 SV=1	0.0150	-0.4032	down	-0.7690	down	-2.3395	down	-0.3658	down	-1.9363	down	-1.5705	down
MPF_LOC101483528.1.1	XM_004542875.1 PREDICTED: Maylandia zebra epidermal growth factor receptor-like (LOC101483528), mRNA	0.0150	0.0140	up	-0.0280	down	0.9688	up	-0.0420	down	0.9548	up	0.9968	up
MPF_contig_034740		0.0150	0.0128	up	0.5465	up	0.9389	up	0.5337	up	0.9261	up	0.3924	up

MPF_SI_DKEY65L23.2.1.1	NP_001093522.1 uncharacterized protein LOC793688 [Danio rerio] ref|XP_001923659.2| PREDICTED: hypothetical protein LOC100150789 [Danio rerio] ref|XP_001922919.2| PREDICTED: hypothetical protein LOC100150626 [Danio rerio]	0.0150	-0.0646	down	0.2281	up	1.1877	up	0.2927	up	1.2523	up	0.9597	up
MPF_LOC101469549.1.2	XM_004573028.1 PREDICTED: Maylandia zebra interleukin-1 receptorlike 1-like (LOC101469549), mRNA	0.0150	-0.3538	down	-0.9646	down	-2.8565	down	-0.6108	down	-2.5027	down	-1.8919	down
MPF_LOC101169190.1.1	XP_004068046.1 PREDICTED: Usher syndrome type-1C proteinbinding protein 1-like [Oryzias latipes]	0.0150	-0.0125	down	-0.1387	down	-1.9962	down	-0.1262	down	-1.9837	down	-1.8575	down
MPF_LOC101483619.2.3	XM_004541289.1 PREDICTED: Maylandia zebra neuronal acetylcholine receptor subunit beta-2-like (LOC101483619), mRNA	0.0150	0.2225	up	0.1388	up	1.7694	up	-0.0837	down	1.5469	up	1.6306	up
MPF_LOC101471731.1.2	XM_004544422.1 PREDICTED: Maylandia zebra myocyte-specific enhancer factor 2C-like (LOC101471731), transcript variant X6, mRNA	0.0150	-1.0677	down	-2.0234	down	-3.9919	down	-0.9557	down	-2.9242	down	-1.9685	down
MPF_contig_042660		0.0150	-0.0014	down	0.1643	up	0.7395	up	0.1658	up	0.7410	up	0.5752	up

MPF_LOC101076756.1.1	XM_003972767.1 PREDICTED: Takifugu rubripes histone-lysine Nmethyltransferase MLL5-like (LOC101076756), mRNA	0.0150	-0.5266	down	-1.5782	down	-3.0446	down	-1.0516	down	-2.5179	down	-1.4663	down
MPF_contig_024386		0.0150	-0.0549	down	-1.4966	down	-3.5972	down	-1.4417	down	-3.5423	down	-2.1006	down
MPF_contig_003837		0.0150	0.4075	up	-1.8722	down	-3.8602	down	-2.2798	down	-4.2678	down	-1.9880	down
MPF_contig_028908		0.0150	0.0718	up	0.2692	up	0.7027	up	0.1974	up	0.6309	up	0.4334	up
MPF_LOC101473669.3.4	XM_004545518.1 PREDICTED: Maylandia zebra uncharacterized LOC101473669 (LOC101473669), mRNA	0.0150	-0.1245	down	0.2297	up	0.9280	up	0.3542	up	1.0525	up	0.6983	up
MPF_TBA1.1.1	TBA1_CHICK (sp|P02552) Tubulin alpha-1 chain (Fragment) OS=Gallus gallus PE=1 SV=1	0.0150	0.1674	up	0.2076	up	0.8056	up	0.0402	up	0.6382	up	0.5980	up
MPF_contig_006877		0.0151	-0.1623	down	0.1622	up	1.0253	up	0.3246	up	1.1876	up	0.8630	up
MPF_contig_026973	XM_004553863.1 PREDICTED: Maylandia zebra poly [ADP-ribose] polymerase 12-like (LOC101480887), transcript variant X1, mRNA	0.0151	0.1845	up	-1.2176	down	-2.7721	down	-1.4020	down	-2.9565	down	-1.5545	down
MPF_LOC101481842.2.8	XM_004554055.1 PREDICTED: Maylandia zebra ATP synthase subunit epsilon, mitochondrial-like (LOC101481842), transcript variant X2, mRNA	0.0152	-0.0651	down	0.1621	up	0.4485	up	0.2272	up	0.5136	up	0.2864	up

MPF_LOC101477850.7.10	XM_004575562.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12-like (LOC101477850), mRNA	0.0152	-0.0884	down	0.0118	up	0.5796	up	0.1002	up	0.6680	up	0.5678	up
MPF_LOC100692501.1.2	XM_003459223.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100692501 (LOC100692501), mRNA	0.0153	0.2346	up	-0.2960	down	-2.1804	down	-0.5305	down	-2.4149	down	-1.8844	down
MPF_LOC100695237.1.1	XR_134862.1 PREDICTED: Oreochromis niloticus UPF0765 protein C10orf58 homolog (LOC100695237), miscRNA	0.0153	0.0394	up	0.2812	up	1.1996	up	0.2418	up	1.1602	up	0.9184	up
MPF_LOC100705728.17.17	XM_003459563.1 PREDICTED: Oreochromis niloticus zinc finger protein RFP-like (LOC100705728), mRNA	0.0153	0.2184	up	0.0564	up	-0.7997	down	-0.1620	down	-1.0181	down	-0.8562	down
MPF_LOC101480238.1.1	XM_004539697.1 PREDICTED: Maylandia zebra adenylate cyclase type 2-like (LOC101480238), transcript variant X2, mRNA	0.0153	-0.1535	down	0.1594	up	0.7000	up	0.3129	up	0.8535	up	0.5406	up
MPF_contig_023955		0.0153	-0.0038	down	0.1279	up	0.8859	up	0.1316	up	0.8897	up	0.7581	up
MPF_contig_042780		0.0154	0.0396	up	0.2465	up	0.8432	up	0.2069	up	0.8035	up	0.5966	up
MPF_contig_009617		0.0154	-0.1317	down	0.2159	up	1.0405	up	0.3476	up	1.1722	up	0.8246	up
MPF_PHUM_PHUM529360.1.2	XP_002431439.1 ngd5/osm-6/ift52, putative [Pediculus humanus corporis]	0.0154	-0.7679	down	-0.7638	down	-3.1690	down	0.0040	up	-2.4012	down	-2.4052	down

MPF_LOC101481543.7.7	XM_004550249.1 PREDICTED: Maylandia zebra zinc finger BED domaincontaining protein 1-like (LOC101481543), mRNA	0.0154	-0.7258	down	-1.6661	down	-3.9211	down	-0.9404	down	-3.1954	down	-2.2550	down
MPF_LOC100698172.2.3	XP_003455687.1 PREDICTED: beta-2microglobulin-like [Oreochromis niloticus]	0.0154	-0.0490	down	0.0920	up	1.0464	up	0.1410	up	1.0954	up	0.9544	up
MPF_contig_008230		0.0154	0.0421	up	-0.7439	down	-2.9502	down	-0.7860	down	-2.9924	down	-2.2064	down
MPF_LOC100691511.1.1	XM_003460361.1 PREDICTED: Oreochromis niloticus transmembrane and ubiquitin-like domaincontaining protein 1-like (LOC100691511), partial mRNA	0.0155	-0.0892	down	-0.0452	down	0.6908	up	0.0439	up	0.7800	up	0.7360	up
MPF_LOC101482276.1.1	XM_004565422.1 PREDICTED: Maylandia zebra chromodomain- helicase-DNA-binding protein 8-like (LOC101482276), mRNA	0.0155	0.1345	up	0.0955	up	1.0821	up	-0.0390	down	0.9476	up	0.9866	up
MPF_LOC101161574.14.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.0155	0.0202	up	-1.5612	down	-4.3725	down	-1.5813	down	-4.3927	down	-2.8114	down
MPF_LOC101482235.1.2	XM_004552859.1 PREDICTED: Maylandia zebra cysteine protease ATG4B-like (LOC101482235), mRNA	0.0158	-0.1810	down	0.1204	up	1.0674	up	0.3014	up	1.2485	up	0.9470	up

MPF_contig_019367		0.0158	-0.1621	down	0.1700	up	0.8190	up	0.3322	up	0.9812	up	0.6490	up
MPF_LOC101482088.1.4	XM_004544264.1 PREDICTED: Maylandia zebra ubiquitin-conjugating enzyme E2 D4-like (LOC101482088), mRNA	0.0158	-0.0054	down	0.1283	up	0.9082	up	0.1337	up	0.9136	up	0.7799	up
MPF_LOC101477280.5.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.0158	0.0411	up	-1.7809	down	-3.5574	down	-1.8220	down	-3.5985	down	-1.7765	down
MPF_LOC100705292.1.2	XM_003439058.1 PREDICTED: Oreochromis niloticus kelch-like protein 21like (LOC100705292), mRNA	0.0159	0.1464	up	0.2675	up	0.6651	up	0.1211	up	0.5187	up	0.3976	up
MPF_LOC101476385.1.1	XM_004567688.1 PREDICTED: Maylandia zebra secretory carrierassociated membrane protein 5-like (LOC101476385), transcript variant X2, mRNA	0.0160	-0.0047	down	0.1052	up	0.7146	up	0.1099	up	0.7193	up	0.6094	up
MPF_IF4G.1.1	IF4G_SCHPO (sp|Q10475) Eukaryotic translation initiation factor 4 gamma OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tif471 PE=1 SV=1	0.0160	0.5405	up	0.2644	up	-2.7101	down	-0.2761	down	-3.2506	down	-2.9745	down
MPF_contig_043310	XM_004543936.1 PREDICTED: Maylandia zebra CMP-Nacetylneuraminate-betagalactosamide-alpha-2, 3sialyltransferase 4-like (LOC101465046), transcript variant X2, mRNA	0.0160	-0.1742	down	0.0863	up	1.0018	up	0.2604	up	1.1760	up	0.9155	up

MPF_contig_032527		0.0160	0.0081	up	-0.0217	down	0.9263	up	-0.0298	down	0.9182	up	0.9480	up
MPF_contig_009768		0.0160	-0.6241	down	-0.9545	down	-3.1517	down	-0.3304	down	-2.5276	down	-2.1972	down
MPF_contig_028429		0.0160	-0.3632	down	-1.4432	down	-3.7718	down	-1.0800	down	-3.4086	down	-2.3286	down
MPF_LOC101466590.1.1	XM_004569012.1 PREDICTED: Maylandia zebra partner and localizer of BRCA2-like (LOC101466590), transcript variant X5, mRNA	0.0160	-0.3044	down	-0.4739	down	-1.4651	down	-0.1696	down	-1.1608	down	-0.9912	down
MPF_LOC101481842.5.8	XM_004554055.1 PREDICTED: Maylandia zebra ATP synthase subunit epsilon, mitochondrial-like (LOC101481842), transcript variant X2, mRNA	0.0160	-0.0275	down	0.2504	up	0.6093	up	0.2779	up	0.6368	up	0.3589	up
MPF_LOC100692493.1.1	XP_003457870.1 PREDICTED: autophagy-related protein 16-1-like [Oreochromis niloticus]	0.0160	0.2199	up	0.3770	up	0.9792	up	0.1570	up	0.7593	up	0.6022	up
MPF_LOC101166970.1.1	XP_004073985.1 PREDICTED: uncharacterized protein LOC101166970 [Oryzias latipes]	0.0160	-1.0387	down	-1.8523	down	-4.3633	down	-0.8136	down	-3.3246	down	-2.5110	down
MPF_contig_021432		0.0160	-0.3447	down	-1.3246	down	-3.6104	down	-0.9799	down	-3.2658	down	-2.2859	down
MPF_contig_023735		0.0160	0.2291	up	0.2025	up	-1.4469	down	-0.0266	down	-1.6760	down	-1.6494	down
MPF_LOC100710612.1.1	XM_003454616.1 PREDICTED: Oreochromis niloticus macrophage mannose receptor 1-like (LOC100710612), mRNA	0.0160	-0.7295	down	-1.0414	down	-3.4247	down	-0.3120	down	-2.6952	down	-2.3832	down

MPF_LOC101474290.4.6	XM_004573400.1 PREDICTED: Maylandia zebra NHS-like protein 2-like (LOC101474290), transcript variant X4, mRNA	0.0160	-0.1697	down	0.1736	up	0.9896	up	0.3433	up	1.1593	up	0.8160	up
MPF_LOC100708352.1.2	XM_003447254.1 PREDICTED: Oreochromis niloticus sodium/hydrogen exchanger 3-like (LOC100708352), mRNA	0.0160	-0.0869	down	0.0987	up	0.8715	up	0.1857	up	0.9584	up	0.7727	up
MPF_LOC100699885.2.2	XM_003459091.1 PREDICTED: Oreochromis niloticus tripartite motifcontaining protein 16-like (LOC100699885), mRNA	0.0160	-0.0635	down	-0.1419	down	0.8513	up	-0.0784	down	0.9148	up	0.9931	up
MPF_LOC101079843.1.1	XM_003972061.1 PREDICTED: Takifugu rubripes coiled-coil and C2 domain-containing protein 1Alike (LOC101079843), mRNA	0.0160	0.2964	up	0.5235	up	1.1651	up	0.2271	up	0.8687	up	0.6416	up
MPF_contig_032693		0.0160	0.0217	up	0.1055	up	0.3900	up	0.0838	up	0.3683	up	0.2845	up
MPF_MYO1B.1.2	XP_003443378.1 PREDICTED: myosin-Ib isoform 2 [Oreochromis niloticus]	0.0160	0.2122	up	0.3658	up	1.0284	up	0.1537	up	0.8162	up	0.6625	up
MPF_LOC101474655.1.2	XM_004570828.1 PREDICTED: Maylandia zebra dual specificity protein phosphatase 8-like (LOC101474655), transcript variant X3, mRNA	0.0160	-0.0164	down	0.1062	up	0.7146	up	0.1225	up	0.7310	up	0.6084	up
MPF_contig_045499		0.0160	0.3275	up	0.6425	up	1.7487	up	0.3150	up	1.4212	up	1.1062	up

MPF_LOC101475584.3.5	XM_004561039.1 PREDICTED: Maylandia zebra thrombospondin type-1 domain-containing protein 7Alike (LOC101475584), mRNA	0.0160	-0.9975	down	-1.9184	down	-4.7065	down	-0.9209	down	-3.7090	down	-2.7881	down
MPF_LOC101173666.1.1	XP_004082016.1 PREDICTED: poliovirus receptor-related protein 2-like [Oryzias latipes]	0.0160	-0.1538	down	-1.0148	down	-3.1233	down	-0.8610	down	-2.9695	down	-2.1085	down
MPF_contig_027988	XM_004562927.1 PREDICTED: Maylandia zebra serine/threonineprotein kinase N1-like (LOC101475594), transcript variant X1, mRNA	0.0160	-0.0245	down	0.1948	up	0.9619	up	0.2192	up	0.9864	up	0.7671	up
MPF_contig_003919		0.0160	-0.1487	down	0.0501	up	0.8743	up	0.1988	up	1.0230	up	0.8242	up
MPF_LOC100691506.16.16	XM_003460016.1 PREDICTED: Oreochromis niloticus zinc finger protein RFP-like (LOC100691506), mRNA	0.0160	0.3370	up	0.0695	up	1.1549	up	-0.2675	down	0.8178	up	1.0853	up
MPF_LOC101073096.1.1	XM_003976079.1 PREDICTED: Takifugu rubripes adenosylhomocysteinase Alike (LOC101073096), mRNA	0.0160	0.1081	up	0.4727	up	1.0717	up	0.3645	up	0.9636	up	0.5991	up
MPF_LOC101480226.1.1	XM_004538168.1 PREDICTED: Maylandia zebra protein phosphatase PTC7 homolog (LOC101480226), mRNA	0.0160	0.1056	up	0.0614	up	0.8333	up	-0.0443	down	0.7276	up	0.7719	up
MPF_LOC101468090.2.6	XM_004576234.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 1like (LOC101468090), partial mRNA	0.0160	-0.6736	down	-0.6015	down	-1.7907	down	0.0721	up	-1.1171	down	-1.1891	down

MPF_LOC101483595.1.1	XM_004537989.1 PREDICTED: Maylandia zebra deleted in bladder cancer protein 1 homolog (LOC101483595), mRNA	0.0160	0.1214	up	0.1965	up	0.8121	up	0.0751	up	0.6907	up	0.6156	up
MPF_LOC101481038.1.1	XM_004548647.1 PREDICTED: Maylandia zebra cytokine-inducible SH2containing protein-like (LOC101481038), transcript variant X2, mRNA	0.0160	-0.0752	down	0.1326	up	0.9970	up	0.2079	up	1.0722	up	0.8644	up
MPF_contig_020884		0.0160	0.0434	up	0.1181	up	0.8931	up	0.0746	up	0.8497	up	0.7751	up
MPF_LOC100692095.1.1	XM_003452823.1 PREDICTED: Oreochromis niloticus aminoacyl tRNA synthase complex-interacting multifunctional protein 2-like (LOC100692095), mRNA	0.0160	0.0474	up	0.1165	up	0.7097	up	0.0691	up	0.6623	up	0.5932	up
MPF_contig_015596		0.0160	-0.5124	down	-0.4225	down	-2.6178	down	0.0899	up	-2.1054	down	-2.1953	down
MPF_LOC100696600.1.2	XM_003441455.1 PREDICTED: Oreochromis niloticus actin-related protein 2/3 complex subunit 4-like (LOC100696600), mRNA	0.0160	0.1125	up	0.1153	up	0.7827	up	0.0028	up	0.6702	up	0.6674	up
MPF_IF44L.3.4	IF44L_MOUSE (sp|Q9BDB7) Interferon-induced protein 44like OS=Mus musculus GN=Ifi44l PE=2 SV=2	0.0162	0.2488	up	-0.5780	down	-4.0528	down	-0.8268	down	-4.3015	down	-3.4747	down
MPF_CD4.1.1	NP_001072091.1 T-cell surface glycoprotein CD4 [Takifugu rubripes]	0.0164	0.1762	up	0.2087	up	0.9091	up	0.0325	up	0.7329	up	0.7004	up
MPF_contig_004176		0.0165	-0.2341	down	0.1537	up	1.1243	up	0.3878	up	1.3583	up	0.9706	up

MPF_contig_025452		0.0166	-0.5541	down	-1.5089	down	-2.4473	down	-0.9548	down	-1.8933	down	-0.9385	down
MPF_LOC101486200.2.2	XM_004548856.1 PREDICTED: Maylandia zebra sodium- and chloridedependent taurine transporterlike (LOC101486200), mRNA	0.0167	-0.0099	down	0.1063	up	0.8373	up	0.1162	up	0.8472	up	0.7310	up
MPF_contig_022315		0.0167	0.2801	up	-0.8620	down	-1.9905	down	-1.1421	down	-2.2706	down	-1.1285	down
MPF_LOC101473892.1.1	XM_004569569.1 PREDICTED: Maylandia zebra transforming growth factor beta-1-like (LOC101473892), transcript variant X2, mRNA	0.0168	-0.0132	down	-1.6324	down	-4.1849	down	-1.6192	down	-4.1718	down	-2.5525	down
MPF_contig_031900		0.0168	0.1885	up	0.1866	up	-0.9851	down	-0.0018	down	-1.1735	down	-1.1717	down
MPF_GBG12.1.1	NM_001165215.1 Oncorhynchus mykiss Guanine nucleotide-binding protein GI/GS/GO gamma-12 subunit (gbg12), mRNA gb|BT074358.1| Oncorhynchus mykiss clone omyk-evo-513-041 Guanine nucleotide-binding protein GI/GS/GO gamma-12 subunit precursor putative mRNA, complete cds	0.0169	0.0381	up	0.2000	up	0.7545	up	0.1619	up	0.7164	up	0.5545	up
MPF_LOC101471394.1.1	XM_004557138.1 PREDICTED: Maylandia zebra GS homeobox 2-like (LOC101471394), mRNA	0.0169	0.0779	up	0.0709	up	0.7677	up	-0.0070	down	0.6898	up	0.6968	up
MPF_ROBO2.1.2	ROBO2_HUMAN (sp|Q9HCK4) Roundabout homolog 2 OS=Homo sapiens GN=ROBO2 PE=1 SV=2	0.0169	0.1048	up	0.2690	up	1.0958	up	0.1642	up	0.9910	up	0.8268	up

MPF_LOC101077402.8.11	XP_003965662.1 PREDICTED: uncharacterized protein LOC101077402 [Takifugu rubripes]	0.0169	0.0460	up	0.1415	up	1.8470	up	0.0954	up	1.8009	up	1.7055	up
MPF_LOC101061679.1.1	XM_003975895.1 PREDICTED: Takifugu rubripes cAMP-responsive element modulator-like (LOC101061679), mRNA	0.0169	-0.1166	down	-0.7592	down	-2.3974	down	-0.6425	down	-2.2807	down	-1.6382	down
MPF_LOC100694289.1.1	XP_003437561.1 PREDICTED: gamma-taxilinlike [Oreochromis niloticus]	0.0169	-0.0076	down	0.2025	up	0.7732	up	0.2101	up	0.7807	up	0.5706	up
MPF_contig_025884		0.0169	-0.1653	down	0.1431	up	0.7964	up	0.3083	up	0.9616	up	0.6533	up
MPF_LOC101484172.1.1	XM_004563596.1 PREDICTED: Maylandia zebra centrosome and spindle pole-associated protein 1-like (LOC101484172), transcript variant X3, mRNA	0.0169	-0.2509	down	-0.1467	down	0.8175	up	0.1042	up	1.0684	up	0.9642	up
MPF_contig_013227	XM_004552675.1 PREDICTED: Maylandia zebra ras-associated and pleckstrin homology domainscontaining protein 1-like (LOC101482814), transcript variant X3, mRNA	0.0169	0.1187	up	-0.0714	down	1.4765	up	-0.1901	down	1.3578	up	1.5478	up
MPF_LOC101474179.2.3	XM_004568681.1 PREDICTED: Maylandia zebra nucleolin 2-like (LOC101474179), mRNA	0.0169	-0.4859	down	-1.8031	down	-4.1660	down	-1.3172	down	-3.6801	down	-2.3629	down

MPF_LOC101064585.1.2	XM_003975501.1 PREDICTED: Takifugu rubripes DEP domaincontaining protein 5-like (LOC101064585), mRNA	0.0169	0.0765	up	0.2589	up	1.0835	up	0.1824	up	1.0071	up	0.8247	up
MPF_LOC101473550.1.1	XM_004558529.1 PREDICTED: Maylandia zebra ribonuclease P/MRP protein subunit POP5-like (LOC101473550), mRNA	0.0169	0.1977	up	0.4929	up	1.4565	up	0.2952	up	1.2588	up	0.9636	up
MPF_LOC101469314.1.1	XR_190849.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 44-like (LOC101469314), transcript variant X3, misc_RNA	0.0169	-0.1129	down	0.1316	up	0.9422	up	0.2445	up	1.0551	up	0.8105	up
MPF_LOC101486063.1.1	XM_004563250.1 PREDICTED: Maylandia zebra highly divergent homeobox-like (LOC101486063), mRNA	0.0169	0.0004	up	0.2670	up	1.1949	up	0.2666	up	1.1945	up	0.9279	up
MPF_contig_016882		0.0169	0.0031	up	-0.7280	down	-2.0075	down	-0.7311	down	-2.0107	down	-1.2795	down
MPF_LOC101466706.1.1	XM_004548787.1 PREDICTED: Maylandia zebra coiled-coil domaincontaining protein 66-like (LOC101466706), transcript variant X4, mRNA	0.0170	-0.0748	down	0.0100	up	1.0439	up	0.0848	up	1.1187	up	1.0339	up
MPF_LOC101474368.1.1	XM_004567962.1 PREDICTED: Maylandia zebra integrin beta-like protein 1-like (LOC101474368), mRNA	0.0171	-0.1901	down	0.0996	up	0.9582	up	0.2897	up	1.1483	up	0.8586	up

MPF_contig_027404	XM_004568351.1 PREDICTED: Maylandia zebra protein kinase C beta type-like (LOC101478005), transcript variant X1, mRNA	0.0171	-0.0160	down	-1.0973	down	-3.5572	down	-1.0813	down	-3.5412	down	-2.4599	down
MPF_AHNAK.4.4	XP_687696.3 PREDICTED: neuroblast differentiationassociated protein AHNAK [Danio rerio]	0.0171	-0.6081	down	-2.9550	down	-5.1554	down	-2.3469	down	-4.5474	down	-2.2004	down
MPF_LOC100709368.1.1	XP_003455402.1 PREDICTED: large subunit GTPase 1 homolog [Oreochromis niloticus]	0.0171	0.0781	up	0.2340	up	1.1181	up	0.1559	up	1.0401	up	0.8842	up
MPF_LOC100708534.1.1	XM_003447507.1 PREDICTED: Oreochromis niloticus myeloid-associated differentiation marker homolog (LOC100708534), mRNA	0.0171	-0.0383	down	-2.1181	down	-5.0931	down	-2.0798	down	-5.0548	down	-2.9750	down
MPF_LOC100701013.2.2	XM_003447971.1 PREDICTED: Oreochromis niloticus CDGSH iron-sulfur domain-containing protein 3, mitochondrial-like (LOC100701013), mRNA	0.0171	-0.2000	down	0.1761	up	1.0071	up	0.3761	up	1.2071	up	0.8310	up
MPF_LOC101484170.2.2	XM_004563148.1 PREDICTED: Maylandia zebra iduronate 2-sulfataselike (LOC101484170), transcript variant X2, mRNA	0.0171	0.1028	up	0.2974	up	0.9832	up	0.1946	up	0.8804	up	0.6858	up

MPF_LOC101477320.1.1	XM_004540156.1 PREDICTED: Maylandia zebra solute carrier family 35 member G2-like (LOC101477320), mRNA	0.0171	-0.0369	down	0.0658	up	0.8806	up	0.1026	up	0.9174	up	0.8148	up
MPF_LOC101479581.1.3	XM_004543518.1 PREDICTED: Maylandia zebra uncharacterized LOC101479581 (LOC101479581), mRNA	0.0171	0.1054	up	0.2463	up	1.0934	up	0.1408	up	0.9880	up	0.8471	up
MPF_LOC101477631.1.1	XM_004548160.1 PREDICTED: Maylandia zebra syndecan-3-like (LOC101477631), mRNA	0.0171	0.0312	up	0.3859	up	0.8588	up	0.3547	up	0.8276	up	0.4729	up
MPF_LOC100709600.1.1	XM_003445263.1 PREDICTED: Oreochromis niloticus zinc-binding protein A33-like (LOC100709600), mRNA	0.0171	0.0448	up	0.1783	up	1.1849	up	0.1335	up	1.1400	up	1.0066	up
MPF_contig_015515		0.0171	0.0101	up	0.1058	up	0.3261	up	0.0957	up	0.3160	up	0.2203	up
MPF_LOC100706330.1.1	XP_003457684.1 PREDICTED: hypothetical protein LOC100706330 [Oreochromis niloticus]	0.0171	0.0154	up	-1.1031	down	-2.7709	down	-1.1185	down	-2.7862	down	-1.6677	down
MPF_LOC101466866.1.1	XM_004570172.1 PREDICTED: Maylandia zebra uncharacterized LOC101466866 (LOC101466866), mRNA	0.0171	-0.2023	down	0.1669	up	0.7854	up	0.3692	up	0.9876	up	0.6184	up

MPF_LOC100691649.1.3	XP_003449900.1 PREDICTED: low molecular weight phosphotyrosine protein phosphatase-like isoform 3 [Oreochromis niloticus] ref|XP_003449901.1| PREDICTED: low molecular weight phosphotyrosine protein phosphatase-like isoform 4 [Oreochromis niloticus]	0.0171	0.0253	up	0.2451	up	0.8200	up	0.2198	up	0.7947	up	0.5749	up
MPF_BHWA1_01395.1.1	YP_002721575.1 hypothetical protein BHWA1_01395 [Brachyspira hyodysenteriae WA1]	0.0171	-0.1750	down	-0.5839	down	-2.7414	down	-0.4089	down	-2.5664	down	-2.1575	down
MPF_contig_028735		0.0171	-1.0494	down	-0.4769	down	-2.4829	down	0.5725	up	-1.4334	down	-2.0059	down
MPF_LOC100535419.1.1	XP_003200110.1 PREDICTED: transposon TX1 uncharacterized 149 kDa protein-like [Danio rerio]	0.0171	0.3887	up	-0.5325	down	-2.9824	down	-0.9211	down	-3.3711	down	-2.4500	down
MPF_LOC100709791.1.1	XP_003448471.1 PREDICTED: tripartite motifcontaining protein 16-like [Oreochromis niloticus]	0.0171	-0.0424	down	-0.1220	down	0.6912	up	-0.0795	down	0.7337	up	0.8132	up
MPF_contig_035297		0.0171	-0.0867	down	0.2712	up	0.6721	up	0.3579	up	0.7588	up	0.4009	up
MPF_LOC100692543.1.3	XM_003449439.1 PREDICTED: Oreochromis niloticus microfibrilassociated glycoprotein 4-like (LOC100692543), mRNA	0.0171	0.4306	up	-0.1490	down	-1.6828	down	-0.5796	down	-2.1133	down	-1.5338	down

MPF_LOC100700605.10.27	XM_003458555.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100700605), mRNA	0.0171	0.0614	up	-0.6973	down	-1.9861	down	-0.7587	down	-2.0475	down	-1.2888	down
MPF_contig_009137		0.0171	-0.8271	down	-0.4132	down	-2.4347	down	0.4138	up	-1.6076	down	-2.0214	down
MPF_LOC101468521.1.1	XM_004563278.1 PREDICTED: Maylandia zebra serine/threonineprotein phosphatase 2B catalytic subunit alpha isoform-like (LOC101468521), mRNA	0.0171	-0.1863	down	0.1818	up	0.9695	up	0.3681	up	1.1557	up	0.7876	up
MPF_LOC101487549.3.9	XM_004574260.1 PREDICTED: Maylandia zebra uncharacterized LOC101487549 (LOC101487549), mRNA	0.0171	-0.1882	down	0.0977	up	0.9175	up	0.2859	up	1.1057	up	0.8198	up
MPF_LOC100696465.1.1	XP_003451072.1 PREDICTED: phosphatidylinositol 4-kinase alpha-like [Oreochromis niloticus]	0.0171	0.0585	up	0.4334	up	0.8346	up	0.3749	up	0.7761	up	0.4012	up
MPF_LOC101467579.1.1	XM_004551299.1 PREDICTED: Maylandia zebra transmembrane protein 182-like (LOC101467579), mRNA	0.0171	0.0133	up	0.0025	up	0.6456	up	-0.0108	down	0.6323	up	0.6430	up
MPF_contig_021317		0.0171	-0.0117	down	-1.2181	down	-2.6655	down	-1.2064	down	-2.6538	down	-1.4474	down
MPF_contig_008714		0.0171	-0.3639	down	-1.5249	down	-3.2130	down	-1.1610	down	-2.8491	down	-1.6881	down
MPF_LOC101478322.2.4	XM_004556897.1 PREDICTED: Maylandia zebra capZ-interacting protein-like	0.0171	-0.0138	down	0.1630	up	0.9113	up	0.1768	up	0.9251	up	0.7483	up

	(LOC101478322), mRNA													
MPF_CSF12.1.1	[BBH] CSF12_TAKRU (sp|Q8UVR8) Macrophage colony-stimulating factor 1 receptor 2 OS=Takifugu rubripes GN=csf1r2 PE=3 SV=1	0.0171	-0.1918	down	0.1744	up	1.0144	up	0.3662	up	1.2062	up	0.8400	up
MPF_contig_045417		0.0171	-0.0155	down	0.1835	up	0.9762	up	0.1990	up	0.9917	up	0.7927	up
MPF_LOC101464641.1.1	XM_004540006.1 PREDICTED: Maylandia zebra polypeptide Nacetylgalactosaminyltransferase 16-like (LOC101464641), mRNA	0.0171	-0.2263	down	0.1392	up	1.0546	up	0.3655	up	1.2809	up	0.9154	up
MPF_contig_037720		0.0171	0.1374	up	0.4977	up	1.0632	up	0.3603	up	0.9259	up	0.5656	up
MPF_LOC101463819.1.1	XM_004549502.1 PREDICTED: Maylandia zebra tetraspanin-5-like (LOC101463819), transcript variant X2, mRNA	0.0171	-1.2313	down	-1.5414	down	-4.5922	down	-0.3101	down	-3.3609	down	-3.0508	down
MPF_TNF6B.1.1	TNF6B_HUMAN (sp|O95407) Tumor necrosis factor receptor superfamily member 6B OS=Homo sapiens GN=TNFRSF6B PE=1 SV=1	0.0171	-1.4181	down	-3.1646	down	-6.0567	down	-1.7465	down	-4.6386	down	-2.8921	down
MPF_LOC101171771.1.2	XM_004077345.1 PREDICTED: Oryzias latipes uncharacterized LOC101171771 (LOC101171771), mRNA	0.0171	0.1434	up	0.0073	up	-3.0322	down	-0.1361	down	-3.1756	down	-3.0395	down

MPF_PSV.1.1	PSV_DICDI (sp|P08798) Prespore vesicle protein OS=Dictyostelium discoideum GN=psvA PE=2 SV=3	0.0171	-1.0518	down	-0.5927	down	-2.6524	down	0.4591	up	-1.6005	down	-2.0597	down
MPF_LOC100700823.1.2	XP_003446356.1 PREDICTED: hypothetical protein LOC100700823 [Oreochromis niloticus]	0.0171	-0.0210	down	0.1351	up	0.8236	up	0.1560	up	0.8446	up	0.6886	up
MPF_LOC101472851.2.2	XR_191377.1 PREDICTED: Maylandia zebra homeobox protein Hox-C4a-like (LOC101472851), transcript variant X3, misc_RNA	0.0171	-0.2498	down	0.1257	up	1.0781	up	0.3755	up	1.3279	up	0.9524	up
MPF_LOC101470261.1.1	XM_004541142.1 PREDICTED: Maylandia zebra teneurin-2-like (LOC101470261), transcript variant X2, mRNA	0.0171	-0.1270	down	0.1153	up	0.8786	up	0.2424	up	1.0056	up	0.7633	up
MPF_contig_023946		0.0171	-0.1570	down	0.2265	up	0.9927	up	0.3834	up	1.1497	up	0.7662	up
MPF_LOC101472043.11.14	XM_004573789.1 PREDICTED: Maylandia zebra tight junctionassociated protein 1-like (LOC101472043), transcript variant X4, mRNA	0.0171	-0.1118	down	-0.1889	down	-1.1278	down	-0.0771	down	-1.0159	down	-0.9389	down
MPF_contig_016131		0.0172	-0.4424	down	-1.2760	down	-3.1309	down	-0.8336	down	-2.6884	down	-1.8549	down
MPF_LOC100691043.5.5	XM_003457742.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 12-like (LOC100691043), mRNA	0.0172	-0.5518	down	-1.0129	down	-3.1059	down	-0.4611	down	-2.5542	down	-2.0931	down

MPF_LOC100702190.4.6	XM_003448143.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L10a-like (LOC100702190), mRNA	0.0172	0.2725	up	0.3983	up	0.8258	up	0.1258	up	0.5533	up	0.4275	up
MPF_LOC101477081.3.3	XM_004549844.1 PREDICTED: Maylandia zebra noelin-like (LOC101477081), transcript variant X2, mRNA	0.0172	-0.1677	down	-0.2837	down	0.6748	up	-0.1160	down	0.8425	up	0.9585	up
MPF_contig_020862		0.0172	-0.2776	down	-0.1958	down	-1.6385	down	0.0818	up	-1.3609	down	-1.4427	down
MPF_contig_029610		0.0172	-0.3097	down	-0.1300	down	-1.3740	down	0.1797	up	-1.0643	down	-1.2440	down
MPF_LOC100689954.1.2	XM_003453546.1 PREDICTED: Oreochromis niloticus carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase protein-like (LOC100689954), mRNA	0.0172	0.3231	up	0.3582	up	1.3625	up	0.0351	up	1.0394	up	1.0044	up
MPF_contig_046856		0.0172	-0.2003	down	0.3012	up	1.2430	up	0.5015	up	1.4433	up	0.9418	up
MPF_LOC100706818.2.9	XR_134822.1 PREDICTED: Oreochromis niloticus selenoprotein Pa-like (LOC100706818), miscRNA	0.0173	0.0131	up	0.3023	up	0.7618	up	0.2893	up	0.7487	up	0.4595	up
MPF_LOC100691365.1.2	XM_003446687.1 PREDICTED: Oreochromis niloticus UPF0463 transmembrane protein C6orf35 homolog (LOC100691365), mRNA	0.0173	-0.2560	down	0.0421	up	0.6347	up	0.2981	up	0.8907	up	0.5926	up
MPF_contig_045318		0.0173	-0.0947	down	0.1585	up	0.5599	up	0.2532	up	0.6545	up	0.4014	up
MPF_contig_015428		0.0173	0.0452	up	0.2528	up	0.9657	up	0.2076	up	0.9204	up	0.7128	up

MPF_contig_035511	XM_004558926.1 PREDICTED: Maylandia zebra ketohexokinase-like (LOC101480218), transcript variant X3, mRNA	0.0173	0.2340	up	-1.1526	down	-3.2048	down	-1.3866	down	-3.4387	down	-2.0522	down
MPF_contig_035510		0.0173	-0.2517	down	-0.0956	down	0.8511	up	0.1561	up	1.1028	up	0.9467	up
MPF_LOC100708213.1.1	XP_003457845.1 PREDICTED: hypothetical protein LOC100708213 [Oreochromis niloticus]	0.0173	-0.4714	down	-1.8918	down	-4.8691	down	-1.4204	down	-4.3977	down	-2.9773	down
MPF_LOC100689738.1.1	XP_003443225.1 PREDICTED: major facilitator superfamily domaincontaining protein 6-like [Oreochromis niloticus]	0.0173	-0.1791	down	0.2283	up	0.9885	up	0.4074	up	1.1676	up	0.7602	up
MPF_LOC100699721.2.2	XP_003460016.1 PREDICTED: bifunctional protein NCOAT-like, partial [Oreochromis niloticus]	0.0174	-0.1576	down	-0.5553	down	-2.9445	down	-0.3977	down	-2.7868	down	-2.3892	down
MPF_LOC101465301.1.1	XM_004538299.1 PREDICTED: Maylandia zebra procollagen galactosyltransferase 2-like (LOC101465301), mRNA	0.0174	-0.1428	down	0.2223	up	1.0010	up	0.3652	up	1.1438	up	0.7786	up
MPF_LOC100712300.2.2	XP_003452130.1 PREDICTED: sister chromatid cohesion protein DCC1-like [Oreochromis niloticus]	0.0174	0.1155	up	0.3129	up	1.2578	up	0.1974	up	1.1423	up	0.9449	up
MPF_LOC101474305.1.20	XM_004575475.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101474305), mRNA	0.0174	0.0654	up	0.1886	up	-1.2645	down	0.1233	up	-1.3299	down	-1.4532	down
MPF_contig_049020		0.0175	0.0029	up	0.1135	up	0.6968	up	0.1105	up	0.6939	up	0.5833	up

MPF_LOC100694437.1.2	XM_003451931.1 PREDICTED: Oreochromis niloticus NFU1 iron-sulfur cluster scaffold homolog, mitochondrial-like (LOC100694437), mRNA	0.0176	-0.4264	down	-0.3683	down	-2.9423	down	0.0581	up	-2.5159	down	-2.5740	down
MPF_LOC101483915.1.1	XM_004565975.1 PREDICTED: Maylandia zebra alpha-N-acetylgalactosaminide alpha2,6-sialyltransferase 2-like (LOC101483915), mRNA	0.0176	-0.1351	down	0.2338	up	0.7064	up	0.3690	up	0.8415	up	0.4725	up
MPF_LOC101074351.1.1	XP_003968494.1 PREDICTED: double-strand break repair protein MRE11Alike [Takifugu rubripes]	0.0176	0.0098	up	0.3395	up	1.0461	up	0.3297	up	1.0363	up	0.7066	up
MPF_contig_024030		0.0176	-0.5508	down	-0.2847	down	-1.6595	down	0.2662	up	-1.1086	down	-1.3748	down
MPF_IK.1.1	XM_003457013.1 PREDICTED: Oreochromis niloticus IK cytokine, downregulator of HLA II (IK), mRNA	0.0176	0.0403	up	0.2414	up	0.8994	up	0.2011	up	0.8591	up	0.6580	up
MPF_LOC101070529.1.1	XP_003970239.1 PREDICTED: glycerophosphoinositol inositolphosphodiesterase GDPD2-like [Takifugu rubripes]	0.0176	0.4797	up	-0.2927	down	1.4800	up	-0.7724	down	1.0003	up	1.7727	up
MPF_LOC101466337.11.22	XM_004575687.1 PREDICTED: Maylandia zebra prothymosin alpha-Blike (LOC101466337), mRNA	0.0176	-0.1462	down	0.2342	up	1.0488	up	0.3804	up	1.1950	up	0.8146	up
MPF_LOC101156352.1.1	XP_004077953.1	0.0176	0.5016	up	-2.0559	down	-4.2049	down	-2.5575	down	-4.7066	down	-2.1490	down

	PREDICTED: ictacalcin-like [Oryzias latipes]													
MPF_contig_029831		0.0176	-0.0912	down	-0.4309	down	-1.5432	down	-0.3397	down	-1.4520	down	-1.1123	down
MPF_CYYR1.1.19	NM_212882.1 Danio rerio cysteine and tyrosine-rich protein 1 (cyyr1), mRNA gb|BC066606.1| Danio rerio cysteine and tyrosine-rich protein 1, mRNA (cDNA clone MGC:77252 IMAGE:6963826), complete cds	0.0177	0.1409	up	0.2226	up	0.7590	up	0.0817	up	0.6181	up	0.5364	up
MPF_MIR142A.1.1	NR_030090.1 Danio rerio microRNA 142a (mir142a), microRNA	0.0178	0.2035	up	-1.4653	down	-3.2948	down	-1.6688	down	-3.4983	down	-1.8295	down
MPF_LOC101484444.1.1	XM_004563244.1 PREDICTED: Maylandia zebra uncharacterized LOC101484444 (LOC101484444), mRNA	0.0178	0.1174	up	0.0531	up	0.8048	up	-0.0643	down	0.6874	up	0.7517	up
MPF_contig_017097		0.0178	-0.3019	down	-1.5788	down	-3.7649	down	-1.2769	down	-3.4630	down	-2.1861	down
MPF_contig_005929		0.0178	-0.2789	down	0.2200	up	0.9887	up	0.4990	up	1.2677	up	0.7687	up
MPF_contig_014823		0.0178	-0.5052	down	-0.1867	down	-1.7493	down	0.3185	up	-1.2442	down	-1.5627	down
MPF_contig_028725		0.0178	0.0744	up	0.2591	up	1.0823	up	0.1847	up	1.0079	up	0.8232	up
MPF_LOC101486209.1.4	XM_004551098.1 PREDICTED: Maylandia zebra uncharacterized LOC101486209 (LOC101486209), mRNA	0.0178	0.6536	up	-1.1807	down	-3.8112	down	-1.8343	down	-4.4648	down	-2.6305	down
MPF_LOC100694797.1.2	XP_003453218.1 PREDICTED: nucleoprotein TPR-like [Oreochromis	0.0178	-0.1476	down	0.2265	up	0.8285	up	0.3741	up	0.9761	up	0.6020	up

	niloticus]													
MPF_LOC101480440.1.1	XM_004541919.1 PREDICTED: Maylandia zebra deleted in malignant brain tumors 1 protein-like (LOC101480440), mRNA	0.0178	0.0223	up	-0.5436	down	-1.1264	down	-0.5659	down	-1.1487	down	-0.5828	down
MPF_LOC101476796.1.1	XM_004548629.1 PREDICTED: Maylandia zebra vacuolar fusion protein MON1 homolog B-like (LOC101476796), transcript variant X3, mRNA	0.0178	0.0570	up	0.1792	up	0.9716	up	0.1222	up	0.9146	up	0.7924	up
MPF_LOC101479727.1.6	XM_004576138.1 PREDICTED: Maylandia zebra uncharacterized LOC101479727 (LOC101479727), mRNA	0.0180	0.2584	up	0.3639	up	0.8949	up	0.1056	up	0.6366	up	0.5310	up
MPF_LOC101467232.1.1	XM_004541226.1 PREDICTED: Maylandia zebra ceramide synthase 2like (LOC101467232), mRNA	0.0180	-0.2607	down	-1.5031	down	-3.6677	down	-1.2424	down	-3.4070	down	-2.1646	down
MPF_LOC101469738.2.2	XM_004551780.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase MSL2-like (LOC101469738), mRNA	0.0180	0.1256	up	0.0976	up	0.8817	up	-0.0280	down	0.7561	up	0.7841	up
MPF_LOC101485801.1.2	XM_004569981.1 PREDICTED: Maylandia zebra transcription factor GATA-3-like (LOC101485801), transcript variant X9, mRNA	0.0180	-0.1704	down	0.0454	up	0.8074	up	0.2158	up	0.9778	up	0.7621	up

MPF_SEL1L.1.1	XM_003440777.1 PREDICTED: Oreochromis niloticus sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA	0.0181	-0.1628	down	-0.2490	down	0.9192	up	-0.0863	down	1.0819	up	1.1682	up
MPF_contig_044606		0.0181	0.6820	up	-1.6077	down	-3.6449	down	-2.2897	down	-4.3269	down	-2.0372	down
MPF_LOC101480609.1.2	XM_004539422.1 PREDICTED: Maylandia zebra homeodomain-interacting protein kinase 3like (LOC101480609), transcript variant X2, mRNA	0.0182	-1.1349	down	-2.2824	down	-4.3889	down	-1.1475	down	-3.2540	down	-2.1065	down
MPF_G0S2.1.1	[BBH] G0S2_MOUSE (sp|Q61585) G0/G1 switch protein 2 OS=Mus musculus GN=G0s2 PE=2 SV=1	0.0182	0.1531	up	0.1094	up	1.0201	up	-0.0437	down	0.8670	up	0.9107	up
MPF_LOC101471773.1.3	XM_004553653.1 PREDICTED: Maylandia zebra dihydropteridine reductase-like (LOC101471773), mRNA	0.0182	-0.0585	down	0.0004	up	0.9797	up	0.0589	up	1.0382	up	0.9793	up
MPF_contig_010163		0.0182	0.2335	up	0.2318	up	0.7282	up	-0.0017	down	0.4947	up	0.4964	up
MPF_contig_032239		0.0182	-0.2869	down	-1.3563	down	-3.6336	down	-1.0694	down	-3.3467	down	-2.2773	down
MPF_KCC2B.1.1	[BBH] KCC2B_HUMAN (sp|Q13554) Calcium/calmodulindependent protein kinase type II subunit beta OS=Homo sapiens GN=CAMK2B PE=1 SV=3	0.0182	0.1185	up	0.3078	up	1.0424	up	0.1893	up	0.9239	up	0.7346	up

MPF_contig_002093	XM_004561062.1 PREDICTED: Maylandia zebra sentrin-specific protease 6-like (LOC101481863), transcript variant X1, mRNA	0.0182	0.2520	up	0.2518	up	0.9408	up	-0.0002	down	0.6888	up	0.6890	up
MPF_LOC101471831.1.1	XM_004545712.1 PREDICTED: Maylandia zebra sodium/hydrogen exchanger 6-like (LOC101471831), transcript variant X2, mRNA	0.0182	0.4459	up	0.7424	up	1.2699	up	0.2965	up	0.8240	up	0.5275	up

MPF_LOC101471553.1.1	XM_004572678.1 PREDICTED: Maylandia zebra protein capicua homolog (LOC101471553), transcript variant X4, mRNA	0.0183	-0.0437	down	-0.7339	down	-1.9692	down	-0.6902	down	-1.9255	down	-1.2353	down
MPF_LOC101163218.1.1	XP_004083710.1 PREDICTED: integrator complex subunit 9-like [Oryzias latipes]	0.0183	-0.0803	down	-0.9216	down	-3.2220	down	-0.8413	down	-3.1417	down	-2.3004	down
MPF_LOC101464139.1.1	XM_004553987.1 PREDICTED: Maylandia zebra protein SOGA1-like (LOC101464139), transcript variant X1, mRNA	0.0183	-0.1106	down	-0.1617	down	0.8871	up	-0.0511	down	0.9977	up	1.0488	up
MPF_contig_015096		0.0183	-0.0887	down	0.1874	up	0.8571	up	0.2761	up	0.9458	up	0.6697	up
MPF_contig_044800		0.0184	0.0332	up	0.1124	up	0.9371	up	0.0792	up	0.9038	up	0.8247	up
MPF_LOC101479577.1.1	XM_004542105.1 PREDICTED: Maylandia zebra uncharacterized LOC101479577 (LOC101479577), transcript variant X1, mRNA	0.0184	0.2760	up	0.3229	up	1.0747	up	0.0469	up	0.7987	up	0.7518	up

MPF_LOC100696784.1.1	XP_003441680.1 PREDICTED: HHIP-like protein 1-like [Oreochromis niloticus]	0.0185	-1.0814	down	-2.6619	down	-3.6515	down	-1.5805	down	-2.5701	down	-0.9896	down
MPF_LOC101476311.2.3	XM_004571250.1 PREDICTED: Maylandia zebra sodium/potassiumtransporting ATPase subunit alpha-1-like (LOC101476311), transcript variant X2, mRNA	0.0186	0.1197	up	0.3027	up	0.6624	up	0.1830	up	0.5427	up	0.3597	up
MPF_LOC101488047.1.1	XM_004561547.1 PREDICTED: Maylandia zebra calcium/calmodulindependent protein kinase type IV-like (LOC101488047), mRNA	0.0186	-0.2276	down	-0.3880	down	-2.4012	down	-0.1603	down	-2.1736	down	-2.0132	down
MPF_LOC100695839.1.1	XP_003447752.1 PREDICTED: inositolpentakisphosphate 2-kinaselike [Oreochromis niloticus]	0.0187	0.1685	up	-0.0177	down	1.2007	up	-0.1862	down	1.0322	up	1.2184	up
MPF_LOC101484118.1.2	XM_004570768.1 PREDICTED: Maylandia zebra SLIT-ROBO Rho GTPase-activating protein 1like (LOC101484118), transcript variant X4, mRNA	0.0187	-0.4947	down	-0.4206	down	-2.0095	down	0.0741	up	-1.5148	down	-1.5890	down
MPF_LOC101471012.1.1	XM_004556045.1 PREDICTED: Maylandia zebra golgin subfamily A member 4-like (LOC101471012), transcript variant X2, mRNA	0.0187	-0.0104	down	0.2705	up	1.0026	up	0.2808	up	1.0130	up	0.7321	up
MPF_contig_022962		0.0187	0.1357	up	-1.1264	down	-2.7450	down	-1.2621	down	-2.8807	down	-1.6186	down
MPF_LOC101487734.1.2	XM_004571292.1	0.0187	-0.5816	down	-1.3717	down	-3.6932	down	-0.7901	down	-3.1116	down	-2.3215	down

	PREDICTED: Maylandia zebra cytohesin-4-like (LOC101487734), mRNA													
MPF_LOC101477438.2.2	XM_004545630.1 PREDICTED: Maylandia zebra ligand of Numb protein X 2-like (LOC101477438), transcript variant X3, mRNA	0.0187	0.0272	up	0.2041	up	0.7435	up	0.1769	up	0.7163	up	0.5394	up
MPF_LOC101066223.1.1	XP_003974027.1 PREDICTED: cytochrome bc1 complex subunit 6, mitochondrial-like [Takifugu rubripes]	0.0187	0.3537	up	0.6264	up	1.4855	up	0.2727	up	1.1318	up	0.8591	up
MPF_LOC101476819.3.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0.0188	-0.3704	down	-0.3672	down	-1.9773	down	0.0032	up	-1.6069	down	-1.6101	down
MPF_LOC101475864.1.1	XM_004556346.1 PREDICTED: Maylandia zebra protein FAM83F-like (LOC101475864), mRNA	0.0188	0.1245	up	0.3511	up	1.0061	up	0.2266	up	0.8816	up	0.6550	up
MPF_LOC101474542.1.1	XM_004565746.1 PREDICTED: Maylandia zebra stathmin-4-like (LOC101474542), transcript variant X2, mRNA	0.0188	-0.1054	down	-0.1541	down	0.7960	up	-0.0488	down	0.9014	up	0.9501	up
MPF_LOC100697793.2.2	XM_003447553.1 PREDICTED: Oreochromis niloticus DNA polymerase III polC-type-like (LOC100697793), mRNA	0.0188	-0.3389	down	-1.8783	down	-4.2947	down	-1.5395	down	-3.9558	down	-2.4164	down
MPF_LOC101477280.4.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.0188	-0.1541	down	-1.5444	down	-3.4361	down	-1.3903	down	-3.2820	down	-1.8918	down

MPF_LOC100699934.1.1	XP_003448851.1 PREDICTED: probable Gprotein coupled receptor 19like [Oreochromis niloticus]	0.0189	-0.0366	down	0.1407	up	0.7915	up	0.1773	up	0.8281	up	0.6508	up
MPF_PRG4.1.4	PRG4_MOUSE (sp|Q9JM99) Proteoglycan 4 OS=Mus musculus GN=Prg4 PE=1 SV=2	0.0189	-0.0035	down	0.1425	up	0.9795	up	0.1460	up	0.9830	up	0.8369	up
MPF_LOC100699757.1.2	XP_003449595.1 PREDICTED: leucine-rich repeat and calponin homology domain-containing protein 1-like [Oreochromis niloticus]	0.0189	0.1323	up	0.2074	up	0.4148	up	0.0750	up	0.2825	up	0.2075	up
MPF_contig_037326		0.0190	-0.1393	down	0.2048	up	0.8739	up	0.3441	up	1.0132	up	0.6691	up
MPF_contig_015394		0.0190	0.0750	up	0.3743	up	1.1322	up	0.2993	up	1.0572	up	0.7579	up
MPF_contig_032524		0.0190	-0.3952	down	0.1181	up	-1.7619	down	0.5133	up	-1.3667	down	-1.8800	down
MPF_contig_010109		0.0190	0.0194	up	0.3016	up	0.6830	up	0.2821	up	0.6636	up	0.3815	up
MPF_contig_047945		0.0192	0.2461	up	0.4687	up	0.8248	up	0.2226	up	0.5787	up	0.3561	up
MPF_contig_011239	XM_004562318.1 PREDICTED: Maylandia zebra TOM1-like protein 2like (LOC101476649), transcript variant X2, mRNA	0.0193	-0.0216	down	0.1904	up	0.5899	up	0.2120	up	0.6115	up	0.3995	up
MPF_LOC101473512.1.1	XM_004573574.1 PREDICTED: Maylandia zebra retroviral integration site protein Fli-1 homolog (LOC101473512), mRNA	0.0193	-0.4713	down	-0.6197	down	-2.6411	down	-0.1485	down	-2.1698	down	-2.0213	down

MPF_HSD17B8.1.1	XM_003457993.1 PREDICTED: Oreochromis niloticus 17-beta hydroxysteroid dehydrogenase type 8 (HSD17B8), mRNA	0.0193	0.0233	up	0.4001	up	0.7322	up	0.3768	up	0.7089	up	0.3321	up
MPF_contig_028954		0.0193	-0.0309	down	0.0013	up	0.7219	up	0.0322	up	0.7528	up	0.7206	up
MPF_LOC100692440.1.1	XM_003446691.1 PREDICTED: Oreochromis niloticus disintegrin and metalloproteinase domaincontaining protein 17-like (LOC100692440), mRNA	0.0194	0.2080	up	0.3075	up	0.6742	up	0.0996	up	0.4662	up	0.3667	up
MPF_LOC101064585.2.2	XM_003975501.1 PREDICTED: Takifugu rubripes DEP domaincontaining protein 5-like (LOC101064585), mRNA	0.0194	0.0068	up	0.1735	up	0.9278	up	0.1667	up	0.9211	up	0.7544	up
MPF_contig_014852		0.0194	-0.5904	down	-0.1442	down	-1.7204	down	0.4463	up	-1.1299	down	-1.5762	down
MPF_LOC101463698.1.1	XM_004568112.1 PREDICTED: Maylandia zebra maestro heat-like repeat-containing protein family member 1-like (LOC101463698), transcript variant X3, mRNA	0.0194	0.1566	up	0.3671	up	1.3357	up	0.2105	up	1.1791	up	0.9686	up
MPF_LOC100691286.1.1	XM_003452172.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100691286 (LOC100691286), mRNA	0.0194	0.2880	up	-0.8806	down	-2.2605	down	-1.1686	down	-2.5485	down	-1.3799	down

MPF_LOC100695308.2.2	XP_003448420.1 PREDICTED: adenosylhomocysteinase Blike [Oreochromis niloticus]	0.0194	0.1320	up	0.4315	up	1.0265	up	0.2995	up	0.8945	up	0.5950	up
MPF_LOC100697750.1.3	XM_003459604.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 14-like (LOC100697750), mRNA	0.0194	-0.4528	down	-1.7260	down	-3.7582	down	-1.2732	down	-3.3054	down	-2.0322	down
MPF_TBA.2.17	TBA_LYTPI (sp|P02553) Tubulin alpha chain (Fragment) OS=Lytechinus pictus PE=3 SV=1	0.0194	0.2373	up	0.2493	up	0.8295	up	0.0121	up	0.5923	up	0.5802	up
MPF_LOC101479168.1.2	XM_004559838.1 PREDICTED: Maylandia zebra zinc finger protein ZXDC-like (LOC101479168), mRNA	0.0194	-0.0231	down	0.3147	up	0.8370	up	0.3379	up	0.8602	up	0.5223	up
MPF_contig_040915		0.0194	0.1538	up	-0.1553	down	-1.4279	down	-0.3091	down	-1.5816	down	-1.2726	down
MPF_CFAH.6.15	CFAH_HUMAN (sp|P08603) Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	0.0194	-0.5661	down	-1.6828	down	-3.5233	down	-1.1167	down	-2.9572	down	-1.8405	down
MPF_KDM2BA.6.11	NM_213167.1 Danio rerio lysine (K)-specific demethylase 2Ba (kdm2ba), mRNA gb|BC068386.1| Danio rerio zgc:85787, mRNA (cDNA clone MGC:85787 IMAGE:6961124), complete cds	0.0194	0.2352	up	0.3476	up	0.7864	up	0.1124	up	0.5512	up	0.4388	up
MPF_COLI.1.1	COLI_THUOB (sp|Q9YGK2) Pro-opiomelanocortin OS=Thunnus obesus GN=pomc PE=2 SV=1	0.0195	-0.2676	down	-0.0434	down	0.7403	up	0.2241	up	1.0079	up	0.7837	up

MPF_LOC101469799.2.5	XM_004544977.1 PREDICTED: Maylandia zebra zinc finger protein Xfinlike (LOC101469799), transcript variant X17, mRNA	0.0195	-0.1415	down	-0.0852	down	-1.4758	down	0.0563	up	-1.3343	down	-1.3906	down
MPF_contig_009512		0.0195	-0.1456	down	0.2304	up	0.9258	up	0.3760	up	1.0714	up	0.6953	up
MPF_LOC101065219.3.3	XM_003969289.1 PREDICTED: Takifugu rubripes protein S100-A1-like (LOC101065219), mRNA	0.0195	-0.6835	down	-1.5397	down	-2.9818	down	-0.8562	down	-2.2983	down	-1.4421	down
MPF_EJP617_28390.1.2	YP_005819407.1 hypothetical protein EJP617_28390 [Erwinia sp. Ejp617]	0.0195	-0.3382	down	-0.0309	down	0.8393	up	0.3074	up	1.1776	up	0.8702	up
MPF_contig_007070		0.0195	-0.1492	down	0.2270	up	1.0031	up	0.3762	up	1.1523	up	0.7761	up
MPF_contig_023611		0.0195	-0.9538	down	-0.7385	down	-3.2822	down	0.2153	up	-2.3284	down	-2.5438	down
MPF_LOC100712300.1.2	XM_003452082.1 PREDICTED: Oreochromis niloticus sister chromatid cohesion protein DCC1-like (LOC100712300), mRNA	0.0195	0.0267	up	0.4253	up	0.7810	up	0.3986	up	0.7542	up	0.3556	up
MPF_LOC100706121.1.1	XP_003446460.1 PREDICTED: histone acetyltransferase MYST2-like isoform 2 [Oreochromis niloticus]	0.0196	0.1652	up	0.3715	up	0.7646	up	0.2063	up	0.5994	up	0.3931	up
MPF_F107A.1.1	NP_001187899.1 fam107a [Ictalurus punctatus]	0.0198	0.1443	up	0.3575	up	0.8584	up	0.2133	up	0.7142	up	0.5009	up
MPF_contig_044194		0.0198	0.1749	up	-1.6463	down	-3.2384	down	-1.8212	down	-3.4133	down	-1.5921	down

MPF_LOC100707140.3.4	XP_003458392.1 PREDICTED: hypothetical protein LOC100707140 [Oreochromis niloticus]	0.0198	-0.0601	down	-0.7028	down	-2.3169	down	-0.6427	down	-2.2568	down	-1.6141	down
MPF_contig_017575		0.0198	-0.0405	down	-0.0013	down	0.6884	up	0.0391	up	0.7288	up	0.6897	up
MPF_contig_045162	XM_004548644.1 PREDICTED: Maylandia zebra hemK methyltransferase family member 1-like (LOC101480569), transcript variant X1, mRNA	0.0198	-0.0373	down	0.3697	up	0.7416	up	0.4070	up	0.7789	up	0.3719	up
MPF_LOC101467543.1.1	XM_004567935.1 PREDICTED: Maylandia zebra integrin alpha-4-like (LOC101467543), mRNA	0.0198	-0.0033	down	0.0994	up	-0.9707	down	0.1027	up	-0.9674	down	-1.0702	down
MPF_contig_013979	XM_004551640.1 PREDICTED: Maylandia zebra 40S ribosomal protein S24-like (LOC101482129), transcript variant X1, mRNA	0.0198	-0.5061	down	-1.7619	down	-3.9198	down	-1.2558	down	-3.4137	down	-2.1579	down
MPF_contig_035547		0.0199	-0.6355	down	-1.0129	down	-3.4317	down	-0.3774	down	-2.7962	down	-2.4189	down
MPF_LOC100702190.2.6	XM_003448143.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L10a-like (LOC100702190), mRNA	0.0200	0.0125	up	0.1139	up	1.1701	up	0.1015	up	1.1576	up	1.0562	up
MPF_LOC101464899.2.4	XM_004553991.1 PREDICTED: Maylandia zebra protein bassoon-like (LOC101464899), transcript variant X2, mRNA	0.0200	-0.8073	down	-0.9144	down	-3.0230	down	-0.1071	down	-2.2157	down	-2.1087	down

MPF_LOC100693237.1.1	XM_003442623.1 PREDICTED: Oreochromis niloticus catechol Omethyltransferase-like (LOC100693237), mRNA	0.0202	-0.3603	down	-1.3873	down	-3.3402	down	-1.0270	down	-2.9799	down	-1.9530	down
MPF_contig_032713		0.0202	0.1831	up	0.3345	up	0.6781	up	0.1514	up	0.4950	up	0.3436	up

MPF_LOC101467469.1.1	XM_004573106.1 PREDICTED: Maylandia zebra ras-related protein RRas-like (LOC101467469), transcript variant X2, mRNA	0.0202	-0.1241	down	0.1868	up	0.8003	up	0.3109	up	0.9245	up	0.6136	up
MPF_LOC101165910.2.2	XP_004076327.1 PREDICTED: von Willebrand factor A domain-containing protein 7-like [Oryzias latipes]	0.0202	0.0250	up	0.0698	up	1.0202	up	0.0448	up	0.9952	up	0.9504	up
MPF_LOC101474655.2.2	XM_004570828.1 PREDICTED: Maylandia zebra dual specificity protein phosphatase 8-like (LOC101474655), transcript variant X3, mRNA	0.0202	0.0289	up	0.1441	up	0.7455	up	0.1152	up	0.7166	up	0.6014	up
MPF_LOC101472286.1.1	XM_004541888.1 PREDICTED: Maylandia zebra translation initiation factor eIF-2B subunit deltalike (LOC101472286), mRNA	0.0202	0.0876	up	0.3372	up	1.3801	up	0.2496	up	1.2925	up	1.0429	up
MPF_LOC101472640.3.4	XM_004574391.1 PREDICTED: Maylandia zebra microtubule-associated serine/threonine-protein kinase 3-like (LOC101472640), transcript variant X2, mRNA	0.0202	-0.2726	down	-0.4681	down	-1.8681	down	-0.1955	down	-1.5955	down	-1.4000	down
MPF_contig_020221		0.0202	-0.0131	down	0.2638	up	0.7391	up	0.2768	up	0.7522	up	0.4753	up

MPF_LOC101469207.1.1	XM_004560645.1 PREDICTED: Maylandia zebra c-Jun-amino-terminal kinase-interacting protein 3like (LOC101469207), transcript variant X10, mRNA	0.0203	-0.3822	down	-1.2516	down	-3.0386	down	-0.8694	down	-2.6564	down	-1.7870	down
MPF_LOC100712299.1.1	XM_003451996.1 PREDICTED: Oreochromis niloticus myoferlin-like (LOC100712299), mRNA	0.0203	-0.8920	down	-1.1446	down	-3.9398	down	-0.2526	down	-3.0478	down	-2.7952	down
MPF_LOC101477684.3.4	XM_004539594.1 PREDICTED: Maylandia zebra small EDRK-rich factor 2-like (LOC101477684), mRNA	0.0204	0.1492	up	0.2297	up	0.7750	up	0.0805	up	0.6258	up	0.5454	up
MPF_LOC101484965.1.2	XM_004572913.1 PREDICTED: Maylandia zebra polyhomeotic-like protein 3-like (LOC101484965), transcript variant X2, mRNA	0.0204	-0.2566	down	0.7637	up	0.7841	up	1.0203	up	1.0407	up	0.0204	up
MPF_contig_048479		0.0204	-0.0888	down	0.1625	up	0.5762	up	0.2513	up	0.6650	up	0.4138	up
MPF_CYYR1.14.19	NM_212882.1 Danio rerio cysteine and tyrosine-rich protein 1 (cyyr1), mRNA gb|BC066606.1| Danio rerio cysteine and tyrosine-rich protein 1, mRNA (cDNA clone MGC:77252 IMAGE:6963826), complete cds	0.0205	0.1776	up	0.3806	up	0.7301	up	0.2030	up	0.5525	up	0.3496	up
MPF_contig_014917		0.0205	-0.3907	down	-0.4490	down	-2.1443	down	-0.0583	down	-1.7537	down	-1.6953	down

MPF_LOC101478678.1.2	XM_004551725.1 PREDICTED: Maylandia zebra transmembrane protein 150A-like (LOC101478678), mRNA	0.0205	0.1277	up	0.5244	up	1.0420	up	0.3967	up	0.9143	up	0.5176	up
MPF_LOC101486993.1.1	XM_004554270.1 PREDICTED: Maylandia zebra sodium-dependent neutral amino acid transporter SLC6A17-like (LOC101486993), mRNA	0.0205	-0.7473	down	-0.4157	down	-2.6494	down	0.3316	up	-1.9020	down	-2.2336	down
MPF_LOC101065219.2.3	XM_003969289.1 PREDICTED: Takifugu rubripes protein S100-A1-like (LOC101065219), mRNA	0.0206	-1.2023	down	-2.1458	down	-3.9067	down	-0.9435	down	-2.7043	down	-1.7608	down
MPF_contig_044512		0.0206	-0.0469	down	0.1433	up	1.0934	up	0.1902	up	1.1403	up	0.9501	up
MPF_contig_004895		0.0207	0.0075	up	0.0933	up	0.8495	up	0.0858	up	0.8420	up	0.7563	up
MPF_LOC101168245.2.2	XM_004079605.1 PREDICTED: Oryzias latipes ATP-binding cassette subfamily E member 1-like (LOC101168245), mRNA	0.0207	0.2975	up	0.3471	up	0.8780	up	0.0496	up	0.5804	up	0.5308	up
MPF_LOC101471721.1.1	XM_004565738.1 PREDICTED: Maylandia zebra potassium voltagegated channel subfamily G member 1-like (LOC101471721), mRNA	0.0207	-1.2717	down	0.0158	up	0.9407	up	1.2875	up	2.2124	up	0.9249	up
MPF_LOC100694953.1.2	XM_003448201.1 PREDICTED: Oreochromis niloticus troponin T, cardiac muscle isoforms-like (LOC100694953), mRNA	0.0207	-0.1988	down	-0.1718	down	0.9271	up	0.0271	up	1.1260	up	1.0989	up
MPF_LOC100708634.4.4	XP_003449376.1 PREDICTED: apolipoprotein A-I-like [Oreochromis niloticus]	0.0207	-0.2135	down	0.1533	up	0.8954	up	0.3669	up	1.1089	up	0.7420	up

MPF_MMS19.1.1	XM_003438539.1 PREDICTED: Oreochromis niloticus MMS19 nucleotide excision repair homolog (S. cerevisiae) (MMS19), mRNA	0.0208	0.0853	up	0.2286	up	0.8552	up	0.1433	up	0.7700	up	0.6266	up

MPF_LOC100709074.1.1	XM_003448084.1 PREDICTED: Oreochromis niloticus T-complex protein 1 subunit beta-like (LOC100709074), mRNA	0.0208	-0.5983	down	-1.7923	down	-3.6486	down	-1.1940	down	-3.0503	down	-1.8563	down
MPF_LOC101465079.2.2	XM_004551108.1 PREDICTED: Maylandia zebra basal cell adhesion molecule-like (LOC101465079), mRNA	0.0208	-0.6386	down	-1.3781	down	-3.6587	down	-0.7395	down	-3.0202	down	-2.2807	down
MPF_contig_025080		0.0208	-0.0218	down	0.1491	up	0.7912	up	0.1709	up	0.8130	up	0.6421	up
MPF_LOC101162518.1.1	XP_004068643.1 PREDICTED: syndecan-4-like [Oryzias latipes]	0.0208	-0.1543	down	-0.0342	down	0.7216	up	0.1201	up	0.8759	up	0.7558	up
MPF_contig_011610		0.0208	0.0320	up	0.3463	up	0.8858	up	0.3143	up	0.8538	up	0.5396	up
MPF_LOC100703964.3.3	XM_003442244.1 PREDICTED: Oreochromis niloticus cytochrome c oxidase subunit 4 isoform 1, mitochondrial-like (LOC100703964), mRNA	0.0208	-0.0192	down	0.3171	up	1.0468	up	0.3363	up	1.0660	up	0.7297	up
MPF_LOC101078556.1.1	XM_003972456.1 PREDICTED: Takifugu rubripes zinc finger protein 330-like (LOC101078556), mRNA	0.0208	-0.0275	down	0.0771	up	0.5813	up	0.1045	up	0.6088	up	0.5043	up

MPF_LOC101172433.1.1	XP_004077062.1 PREDICTED: uncharacterized protein LOC101172433 [Oryzias latipes]	0.0208	0.2017	up	0.0997	up	1.4198	up	-0.1020	down	1.2181	up	1.3201	up
MPF_LOC101064915.1.1	XM_003967542.1 PREDICTED: Takifugu rubripes thromboxane-A synthase-like (LOC101064915), mRNA	0.0208	-0.8045	down	-1.6918	down	-3.7017	down	-0.8873	down	-2.8972	down	-2.0099	down
MPF_LOC101475584.5.5	XM_004561039.1 PREDICTED: Maylandia zebra thrombospondin type-1 domain-containing protein 7Alike (LOC101475584), mRNA	0.0208	0.0931	up	0.3273	up	0.8395	up	0.2342	up	0.7464	up	0.5123	up
MPF_LOC101477056.1.1	XM_004568159.1 PREDICTED: Maylandia zebra uncharacterized LOC101477056 (LOC101477056), mRNA	0.0208	0.3413	up	0.7507	up	0.7144	up	0.4094	up	0.3731	up	-0.0363	down
MPF_LOC101475776.2.7	XM_004539154.1 PREDICTED: Maylandia zebra ATP synthase subunit d, mitochondrial-like (LOC101475776), transcript variant X2, mRNA	0.0208	-0.1718	down	0.0083	up	1.0482	up	0.1801	up	1.2200	up	1.0399	up
MPF_LOC101466612.1.2	XM_004549597.1 PREDICTED: Maylandia zebra zinc finger protein 462like (LOC101466612), transcript variant X1, mRNA	0.0208	-0.1558	down	-0.9526	down	-2.7804	down	-0.7967	down	-2.6246	down	-1.8279	down
MPF_contig_047973		0.0208	0.1699	up	0.2948	up	0.8416	up	0.1249	up	0.6718	up	0.5468	up

MPF_LOC101487672.1.1	XM_004557853.1 PREDICTED: Maylandia zebra Fanconi anemia group B protein-like (LOC101487672), mRNA	0.0208	0.0442	up	0.1863	up	0.9254	up	0.1421	up	0.8812	up	0.7391	up
MPF_contig_020368	XM_004550291.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101467183), transcript variant X2, mRNA	0.0208	-0.0481	down	-1.0893	down	-2.9905	down	-1.0412	down	-2.9424	down	-1.9012	down
MPF_LOC100712302.1.1	XP_003452302.1 PREDICTED: aminoacyl tRNA synthase complexinteracting multifunctional protein 1-like [Oreochromis niloticus]	0.0208	-0.6351	down	-1.5570	down	-3.5710	down	-0.9220	down	-2.9359	down	-2.0140	down
MPF_LOC100693585.1.1	XM_003439014.1 PREDICTED: Oreochromis niloticus ceramide synthase 5like (LOC100693585), mRNA	0.0209	0.2323	up	0.0729	up	0.9170	up	-0.1594	down	0.6847	up	0.8441	up
MPF_contig_023757		0.0210	-0.7787	down	-1.5910	down	-3.3981	down	-0.8123	down	-2.6194	down	-1.8071	down
MPF_contig_037867		0.0210	0.2016	up	0.3319	up	0.7382	up	0.1303	up	0.5367	up	0.4064	up
MPF_contig_032148		0.0210	0.2940	up	0.4117	up	1.0705	up	0.1177	up	0.7765	up	0.6588	up
MPF_LOC101482364.1.4	XM_004541093.1 PREDICTED: Maylandia zebra cytoplasmic polyadenylation elementbinding protein 4-like (LOC101482364), mRNA	0.0210	-0.0012	down	0.0153	up	0.7387	up	0.0165	up	0.7399	up	0.7234	up
MPF_ESR1.1.1	[BBH] ESR1_PAGMA (sp|O42132) Estrogen receptor OS=Pagrus major GN=esr1 PE=2 SV=1	0.0210	0.1534	up	0.2574	up	1.3985	up	0.1040	up	1.2451	up	1.1411	up
MPF_LOC101159291.2.2	XM_004078003.1 PREDICTED: Oryzias latipes sodium/potassiumtransporting ATPase subunit alpha-3-like	0.0210	-0.1922	down	-1.5956	down	-4.0005	down	-1.4034	down	-3.8084	down	-2.4049	down

	(LOC101159291), mRNA													
MPF_contig_009550		0.0210	-0.0717	down	0.0890	up	0.8302	up	0.1607	up	0.9019	up	0.7411	up
MPF_contig_020110		0.0210	-0.1505	down	-0.2954	down	-1.6625	down	-0.1449	down	-1.5120	down	-1.3671	down
MPF_LOC101484929.1.3	XM_004542976.1 PREDICTED: Maylandia zebra CMP-N-acetylneuraminate-beta-1,4galactoside alpha-2,3sialyltransferase-like (LOC101484929), mRNA	0.0210	0.0068	up	-0.5635	down	-2.1749	down	-0.5703	down	-2.1817	down	-1.6114	down
MPF_LOC101465099.1.1	XM_004557394.1 PREDICTED: Maylandia zebra moesin-like (LOC101465099), mRNA	0.0210	0.5242	up	-1.9376	down	-5.0509	down	-2.4619	down	-5.5751	down	-3.1133	down
MPF_LOC100695994.10.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.0210	-0.2226	down	0.1679	up	0.7554	up	0.3906	up	0.9780	up	0.5875	up
MPF_LOC101467829.1.2	XM_004565458.1 PREDICTED: Maylandia zebra serine/threonineprotein kinase pim-1-like (LOC101467829), mRNA	0.0210	-0.1817	down	-0.8237	down	-3.3017	down	-0.6420	down	-3.1199	down	-2.4780	down
MPF_LOC101487074.1.1	XM_004574997.1 PREDICTED: Maylandia zebra cGMP-specific 3',5'cyclic phosphodiesterase-like (LOC101487074), transcript variant X3, mRNA	0.0211	-0.1789	down	-0.0823	down	-1.2404	down	0.0966	up	-1.0615	down	-1.1581	down
MPF_FRIL1.1.1	FRIL1_MOUSE (sp|P29391) Ferritin light chain 1 OS=Mus	0.0211	-0.0686	down	-0.4306	down	1.0203	up	-0.3621	down	1.0888	up	1.4509	up

	musculus GN=Ftl1 PE=1 SV=2													
MPF_LOC101464352.1.1	XM_004538572.1 PREDICTED: Maylandia zebra uncharacterized LOC101464352 (LOC101464352), mRNA	0.0211	-0.0786	down	0.2162	up	1.0921	up	0.2948	up	1.1706	up	0.8758	up
MPF_LOC101166342.1.1	XM_004080448.1 PREDICTED: Oryzias latipes receptor-type tyrosine-protein phosphatase epsilon-like (LOC101166342), mRNA	0.0211	0.2683	up	0.3399	up	1.0568	up	0.0716	up	0.7885	up	0.7169	up
MPF_FHOD3.2.2	XP_003437785.1 PREDICTED: FH1/FH2 domain-containing protein 3 [Oreochromis niloticus]	0.0211	0.0039	up	-0.0108	down	0.7968	up	-0.0147	down	0.7928	up	0.8076	up
MPF_LOC100699821.2.2	XP_003443423.1 PREDICTED: ATP-binding cassette sub-family A member 1-like [Oreochromis niloticus]	0.0212	0.0515	up	0.3554	up	0.8446	up	0.3039	up	0.7931	up	0.4892	up
MPF_contig_018806		0.0212	0.0320	up	0.1498	up	0.7620	up	0.1178	up	0.7300	up	0.6123	up
MPF_LOC100695308.1.2	XP_003448420.1 PREDICTED: adenosylhomocysteinase Blike [Oreochromis niloticus]	0.0212	0.0576	up	0.4308	up	0.9876	up	0.3732	up	0.9300	up	0.5569	up
MPF_contig_041655		0.0212	-0.0435	down	0.1540	up	0.4510	up	0.1975	up	0.4945	up	0.2970	up
MPF_contig_017402	XM_004570830.1 PREDICTED: Maylandia zebra MOB kinase activator 2like (LOC101475324), transcript variant X2, mRNA	0.0212	-0.2082	down	-0.0430	down	0.8186	up	0.1652	up	1.0268	up	0.8616	up

MPF_LOC101483521.1.1	XM_004540909.1 PREDICTED: Maylandia zebra early growth response protein 1-like (LOC101483521), mRNA	0.0213	-0.5116	down	-2.0563	down	-4.3664	down	-1.5448	down	-3.8548	down	-2.3101	down
MPF_contig_000877		0.0213	-0.1107	down	0.1381	up	0.5253	up	0.2488	up	0.6360	up	0.3872	up
MPF_LOC101473487.3.8	XM_004568499.1 PREDICTED: Maylandia zebra Krueppel-like factor 6like (LOC101473487), mRNA	0.0213	0.1123	up	-0.1650	down	-0.5005	down	-0.2774	down	-0.6128	down	-0.3355	down
MPF_LOC100707676.3.3	XM_003458184.1 PREDICTED: Oreochromis niloticus transcription factor p65-like (LOC100707676), mRNA	0.0213	-0.1289	down	-0.1945	down	-0.9506	down	-0.0656	down	-0.8217	down	-0.7561	down
MPF_contig_004006		0.0213	-0.0488	down	0.2865	up	0.9301	up	0.3353	up	0.9789	up	0.6436	up
MPF_LOC101475225.1.1	XM_004546564.1 PREDICTED: Maylandia zebra protein phosphatase 1 regulatory subunit 16A-like (LOC101475225), mRNA	0.0213	-0.1213	down	0.1271	up	0.9289	up	0.2484	up	1.0503	up	0.8019	up
MPF_contig_003206		0.0213	0.0666	up	0.3812	up	1.0801	up	0.3146	up	1.0135	up	0.6989	up
MPF_LOC101479127.1.1	XM_004548455.1 PREDICTED: Maylandia zebra integrin-alpha FG-GAP repeat-containing protein 2like (LOC101479127), mRNA	0.0213	0.1002	up	0.1976	up	0.4997	up	0.0973	up	0.3995	up	0.3022	up
MPF_contig_034874		0.0213	0.0409	up	0.1454	up	0.5622	up	0.1045	up	0.5214	up	0.4168	up

MPF_LOC101068490.3.3	XP_003971983.1 PREDICTED: C-type lectin domain family 4 member Flike [Takifugu rubripes]	0.0213	0.0108	up	0.0822	up	0.7957	up	0.0714	up	0.7849	up	0.7135	up
MPF_RL18A.4.14	RL18A_ICTPU (sp|Q90YU9) 60S ribosomal protein L18a OS=Ictalurus punctatus GN=rpl18a PE=2 SV=1	0.0213	0.6252	up	-0.6618	down	-1.0990	down	-1.2870	down	-1.7241	down	-0.4372	down
MPF_contig_008128		0.0213	0.2078	up	0.0685	up	-1.2907	down	-0.1393	down	-1.4985	down	-1.3592	down
MPF_LOC101168228.1.1	XP_004076087.1 PREDICTED: T-cell immunoglobulin and mucin domain-containing protein 4like [Oryzias latipes]	0.0213	-0.3117	down	-1.9043	down	-3.5919	down	-1.5925	down	-3.2802	down	-1.6877	down
MPF_contig_014071	XM_004574586.1 PREDICTED: Maylandia zebra zinc finger MYND domain-containing protein 11like (LOC101478959), transcript variant X3, mRNA	0.0213	0.0549	up	0.2096	up	0.8164	up	0.1547	up	0.7615	up	0.6068	up
MPF_contig_038789		0.0213	-0.0881	down	-0.0072	down	0.8133	up	0.0809	up	0.9014	up	0.8206	up
MPF_contig_043487		0.0213	-0.4397	down	-0.5104	down	-2.0134	down	-0.0707	down	-1.5737	down	-1.5030	down
MPF_LOC100534702.2.5	XR_117879.1 PREDICTED: Danio rerio hypothetical LOC100534702 (LOC100534702), miscRNA	0.0213	0.1316	up	0.2414	up	0.7249	up	0.1098	up	0.5933	up	0.4835	up
MPF_U5S1.1.1	[BBH] U5S1_MOUSE (sp|O08810) 116 kDa U5 small nuclear ribonucleoprotein component OS=Mus musculus GN=Eftud2 PE=2 SV=1	0.0213	-0.1005	down	0.0855	up	0.8010	up	0.1860	up	0.9015	up	0.7155	up

MPF_contig_037167		0.0213	-0.0652	down	0.2440	up	0.6116	up	0.3092	up	0.6767	up	0.3675	up
MPF_contig_047601		0.0213	-0.7526	down	-1.0779	down	-3.2513	down	-0.3254	down	-2.4987	down	-2.1733	down
MPF_LOC101470455.1.1	XM_004539752.1 PREDICTED: Maylandia zebra aminopeptidase N-like (LOC101470455), mRNA	0.0213	0.2938	up	-0.8338	down	-4.4732	down	-1.1275	down	-4.7669	down	-3.6394	down
MPF_LOC101484083.3.3	XM_004539190.1 PREDICTED: Maylandia zebra ATP-binding cassette sub-family A member 1-like (LOC101484083), transcript variant X2, mRNA	0.0213	-0.1498	down	-0.8431	down	-2.2911	down	-0.6933	down	-2.1413	down	-1.4480	down
MPF_LOC101464934.2.3	XM_004565357.1 PREDICTED: Maylandia zebra matrix metalloproteinase-14-like (LOC101464934), mRNA	0.0214	0.2923	up	0.0609	up	-1.1328	down	-0.2314	down	-1.4251	down	-1.1937	down
MPF_LOC100712517.2.2	XM_003459650.1 PREDICTED: Oreochromis niloticus RNA (guanine-9-)methyltransferase domaincontaining protein 2-like (LOC100712517), mRNA	0.0214	-0.1265	down	-0.8899	down	-1.9242	down	-0.7634	down	-1.7977	down	-1.0344	down
MPF_LOC100706471.2.2	XP_003445630.1 PREDICTED: drebrin-like protein-like [Oreochromis niloticus]	0.0214	-0.1047	down	0.1621	up	0.8805	up	0.2668	up	0.9852	up	0.7184	up
MPF_LOC101474833.1.3	XM_004570025.1 PREDICTED: Maylandia zebra bcl-2-like protein 11like (LOC101474833), mRNA	0.0215	0.3644	up	-0.3857	down	-2.9678	down	-0.7501	down	-3.3322	down	-2.5821	down
MPF_ACVR2AA.1.1	NP_001103748.1 activin receptor type-2A precursor [Danio rerio]	0.0215	0.2335	up	0.5964	up	1.7890	up	0.3629	up	1.5555	up	1.1926	up

MPF_contig_019251		0.0215	0.1470	up	0.1688	up	0.8319	up	0.0218	up	0.6849	up	0.6631	up
MPF_HAGOROMO.1.1	XM_003456673.1 PREDICTED: Oreochromis niloticus F-box/WD repeatcontaining protein 4-like (LOC100691948), mRNA	0.0217	0.3832	up	0.5655	up	0.9592	up	0.1823	up	0.5760	up	0.3937	up
MPF_LOC100700318.1.1	XM_003455569.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L7-like 1-like (LOC100700318), mRNA	0.0217	-0.0102	down	0.2216	up	0.7169	up	0.2318	up	0.7271	up	0.4953	up
MPF_LOC100694290.2.2	XM_003437598.1 PREDICTED: Oreochromis niloticus cryptochrome-1-like (LOC100694290), mRNA	0.0217	-0.0949	down	0.3694	up	0.8771	up	0.4644	up	0.9721	up	0.5077	up
MPF_LOC100702052.1.1	XM_003458326.1 PREDICTED: Oreochromis niloticus myosin-XVIIIa-like (LOC100702052), mRNA	0.0217	-0.0363	down	0.0533	up	0.9166	up	0.0897	up	0.9529	up	0.8632	up
MPF_contig_023861		0.0218	-0.5016	down	-1.0908	down	-2.1468	down	-0.5892	down	-1.6453	down	-1.0561	down
MPF_LOC100712420.1.5	XP_003456711.1 PREDICTED: adenine phosphoribosyltransferaselike [Oreochromis niloticus]	0.0218	-0.4003	down	-0.6607	down	-1.8099	down	-0.2604	down	-1.4095	down	-1.1492	down
MPF_LOC100706878.2.6	XP_003458391.1 PREDICTED: hypothetical protein LOC100706878 [Oreochromis niloticus]	0.0218	-0.5158	down	-0.2146	down	-2.2932	down	0.3011	up	-1.7775	down	-2.0786	down
MPF_contig_004155		0.0218	0.0261	up	0.2239	up	0.4461	up	0.1978	up	0.4200	up	0.2221	up
MPF_contig_037988		0.0219	-0.1067	down	0.0729	up	1.4230	up	0.1795	up	1.5297	up	1.3502	up

MPF_LOC100704053.1.12	XM_003440652.1 PREDICTED: Oreochromis niloticus ubiquitin-like protein FUBI-like (LOC100704053), mRNA	0.0219	0.0478	up	-0.8906	down	-1.7268	down	-0.9385	down	-1.7747	down	-0.8362	down
MPF_LOC101068490.2.3	XP_003971983.1 PREDICTED: C-type lectin domain family 4 member Flike [Takifugu rubripes]	0.0219	0.0706	up	0.0907	up	0.8134	up	0.0200	up	0.7427	up	0.7227	up
MPF_LOC101161574.3.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.0219	-0.7546	down	-1.0711	down	-1.9485	down	-0.3165	down	-1.1939	down	-0.8774	down
MPF_LOC101472431.1.6	XM_004550961.1 PREDICTED: Maylandia zebra cytochrome P450 4B1like (LOC101472431), transcript variant X1, mRNA	0.0219	-0.5014	down	-0.0627	down	-1.8453	down	0.4387	up	-1.3439	down	-1.7826	down
MPF_LOC100700496.3.3	XM_003453022.1 PREDICTED: Oreochromis niloticus probable ribonuclease ZC3H12D-like (LOC100700496), mRNA	0.0219	-0.3355	down	-1.2051	down	-3.1841	down	-0.8695	down	-2.8486	down	-1.9791	down
MPF_contig_036406		0.0219	-0.0832	down	0.0380	up	0.8923	up	0.1212	up	0.9755	up	0.8543	up
MPF_LOC101161574.4.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0.0219	-0.3597	down	-1.3062	down	-3.2950	down	-0.9465	down	-2.9352	down	-1.9888	down

MPF_LOC101467415.3.4	XM_004562898.1 PREDICTED: Maylandia zebra lipid phosphate phosphatase-related protein type 5-like (LOC101467415), transcript variant X5, mRNA	0.0220	-0.0608	down	0.2338	up	0.8696	up	0.2947	up	0.9304	up	0.6358	up
MPF_LOC100710418.2.4	XM_003450487.1 PREDICTED: Oreochromis niloticus nucleophosmin-like (LOC100710418), mRNA	0.0220	0.0025	up	0.1441	up	1.0036	up	0.1417	up	1.0012	up	0.8595	up
MPF_LOC101075004.1.1	XM_003964966.1 PREDICTED: Takifugu rubripes uncharacterized LOC101075004 (LOC101075004), mRNA	0.0220	-0.1145	down	-2.3364	down	-4.4440	down	-2.2219	down	-4.3294	down	-2.1075	down
MPF_contig_039397		0.0220	-0.1070	down	-0.2620	down	-1.6264	down	-0.1550	down	-1.5195	down	-1.3645	down
MPF_contig_009844		0.0220	-0.0450	down	-0.2870	down	0.9912	up	-0.2419	down	1.0362	up	1.2781	up
MPF_LOC101174370.1.1	XP_004077240.1 PREDICTED: glutathione Stransferase 3-like [Oryzias latipes]	0.0220	-0.4072	down	-0.6065	down	-1.0488	down	-0.1993	down	-0.6416	down	-0.4423	down
MPF_AHNAK.3.4	XP_687696.3 PREDICTED: neuroblast differentiationassociated protein AHNAK [Danio rerio]	0.0221	-0.7972	down	-2.6168	down	-5.1158	down	-1.8196	down	-4.3186	down	-2.4990	down
MPF_LOC101163366.1.1	XM_004081463.1 PREDICTED: Oryzias latipes tetraspanin-7-like (LOC101163366), mRNA	0.0222	-0.1400	down	0.2659	up	0.9651	up	0.4059	up	1.1051	up	0.6992	up
MPF_LOC101482559.1.1	XM_004563141.1	0.0222	0.1027	up	0.1936	up	0.7947	up	0.0908	up	0.6920	up	0.6012	up

	PREDICTED: Maylandia zebra myopalladin-like (LOC101482559), mRNA												
MPF_LOC101470101.3.4	XM_004572496.1 PREDICTED: Maylandia zebra collagen alpha-1(XIII) chain-like (LOC101470101), mRNA	0.0222	-0.0201	down	0.1551	up	0.7525	up	0.1753	up	0.7726	up	0.5974	up
MPF_LOC100694405.1.2	XM_003443693.1 PREDICTED: Oreochromis niloticus uncharacterized protein C8orf76-like (LOC100694405), mRNA	0.0222	0.2245	up	0.3869	up	1.0928	up	0.1623	up	0.8682	up	0.7059	up
MPF_LOC101473955.1.1	XM_004542552.1 PREDICTED: Maylandia zebra WD repeat-containing protein 47-like (LOC101473955), mRNA	0.0222	0.2084	up	0.0246	up	1.5163	up	-0.1838	down	1.3078	up	1.4916	up

MPF_LOC101464586.2.2	XM_004571741.1 PREDICTED: Maylandia zebra tensin-3-like (LOC101464586), transcript variant X3, mRNA	0.0223	-0.0187	down	-0.4387	down	-1.7113	down	-0.4200	down	-1.6926	down	-1.2726	down
MPF_LOC100710374.1.3	XM_003459643.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100710374 (LOC100710374), mRNA	0.0223	0.3668	up	0.4048	up	0.7336	up	0.0379	up	0.3667	up	0.3288	up
MPF_LOC101156534.2.3	XR_177556.1 PREDICTED: Oryzias latipes synaptotagmin-1-like (LOC101156534), misc_RNA	0.0224	-0.0670	down	-0.1466	down	0.7802	up	-0.0796	down	0.8472	up	0.9268	up

MPF_TTC9B.1.1	NM_001078791.2 Xenopus (Silurana) tropicalis tetratricopeptide repeat domain 9B (ttc9b), mRNA	0.0224	-0.7566	down	-1.4565	down	-3.1659	down	-0.6998	down	-2.4093	down	-1.7094	down
MPF_LOC101476572.2.2	XM_004541074.1 PREDICTED: Maylandia zebra tetraspanin-17-like (LOC101476572), mRNA	0.0224	-0.9548	down	-1.7534	down	-3.9979	down	-0.7986	down	-3.0431	down	-2.2445	down
MPF_LOC101471123.1.1	XM_004562912.1 PREDICTED: Maylandia zebra choline transporter-like protein 2-like (LOC101471123), transcript variant X3, mRNA	0.0224	0.0105	up	0.2476	up	0.4817	up	0.2371	up	0.4712	up	0.2341	up
MPF_contig_010014		0.0224	-0.0877	down	0.1503	up	0.6923	up	0.2380	up	0.7800	up	0.5421	up
MPF_LOC101484122.9.9	XM_004572909.1 PREDICTED: Maylandia zebra eukaryotic translation initiation factor 5A-1-like (LOC101484122), mRNA	0.0224	0.0017	up	-0.2108	down	0.9382	up	-0.2124	down	0.9365	up	1.1489	up
MPF_LELG_02721.2.2	XP_001526163.1 hypothetical protein LELG_02721 [Lodderomyces elongisporus NRRL YB-4239]	0.0224	-0.2137	down	-0.0341	down	0.5414	up	0.1796	up	0.7551	up	0.5755	up
MPF_LOC101171896.1.1	XP_004086536.1 PREDICTED: polyadenylatebinding protein-interacting protein 2-like [Oryzias latipes]	0.0224	-0.0549	down	0.2264	up	1.2515	up	0.2813	up	1.3064	up	1.0252	up
MPF_LOC101466842.5.5	XM_004540117.1 PREDICTED: Maylandia zebra syntaxin-binding protein 5-like (LOC101466842), transcript variant X5, mRNA	0.0224	0.0575	up	0.4155	up	1.2032	up	0.3580	up	1.1457	up	0.7877	up

MPF_LOC101469368.1.2	XM_004573559.1 PREDICTED: Maylandia zebra large proline-rich protein BAG6-like (LOC101469368), mRNA	0.0224	0.2937	up	0.5814	up	0.9437	up	0.2878	up	0.6501	up	0.3623	up
MPF_contig_032146		0.0224	0.0212	up	-1.5088	down	-3.0673	down	-1.5299	down	-3.0884	down	-1.5585	down
MPF_contig_026674		0.0224	-0.0286	down	0.2542	up	0.5382	up	0.2828	up	0.5667	up	0.2840	up
MPF_LOC100711469.1.2	XM_003445853.1 PREDICTED: Oreochromis niloticus beta-synuclein-like (LOC100711469), mRNA	0.0224	-0.0033	down	-0.0173	down	0.9449	up	-0.0141	down	0.9482	up	0.9623	up
MPF_contig_015574		0.0224	0.0437	up	0.1108	up	0.8006	up	0.0671	up	0.7569	up	0.6898	up
MPF_contig_016225	XM_004558106.1 PREDICTED: Maylandia zebra phosphatidylinositolbinding clathrin assembly protein-like (LOC101478138), transcript variant X5, mRNA	0.0224	0.0751	up	0.0968	up	0.7494	up	0.0217	up	0.6743	up	0.6526	up
MPF_LOC100690591.1.2	XP_003453202.1 PREDICTED: astrotactin-1like [Oreochromis niloticus]	0.0224	-0.1719	down	0.9265	up	1.0664	up	1.0984	up	1.2383	up	0.1399	up
MPF_LOC101468583.4.7	XM_004576296.1 PREDICTED: Maylandia zebra uncharacterized LOC101468583 (LOC101468583), mRNA	0.0224	-0.5886	down	-0.7677	down	-2.7227	down	-0.1791	down	-2.1341	down	-1.9550	down
MPF_contig_036141		0.0224	0.0695	up	0.1412	up	0.8941	up	0.0718	up	0.8247	up	0.7529	up

MPF_LOC101485687.1.1	XM_004567815.1 PREDICTED: Maylandia zebra polycomb protein suz12-B-like (LOC101485687), transcript variant X1, mRNA	0.0224	0.1390	up	0.1676	up	0.7517	up	0.0286	up	0.6127	up	0.5841	up
MPF_LOC100705746.2.3	XP_003443116.1 PREDICTED: trafficking protein particle complex subunit 5-like [Oreochromis niloticus]	0.0224	0.0872	up	0.2491	up	0.4765	up	0.1619	up	0.3893	up	0.2274	up
MPF_LOC101484951.3.3	XM_004546887.1 PREDICTED: Maylandia zebra myosin regulatory light chain 2, smooth muscle minor isoform-like (LOC101484951), mRNA	0.0224	-0.1493	down	-0.3039	down	-1.7030	down	-0.1546	down	-1.5537	down	-1.3991	down
MPF_LOC101484718.1.2	XM_004561625.1 PREDICTED: Maylandia zebra UV radiation resistanceassociated gene protein-like (LOC101484718), mRNA	0.0224	0.0307	up	0.1677	up	1.0154	up	0.1370	up	0.9847	up	0.8477	up
MPF_LOC101470650.2.2	XM_004540130.1 PREDICTED: Maylandia zebra nesprin-1-like (LOC101470650), transcript variant X2, mRNA	0.0224	-0.1974	down	-0.4094	down	-1.5079	down	-0.2120	down	-1.3106	down	-1.0985	down
MPF_LOC100711656.2.2	XP_003446481.1 PREDICTED: cytosolic endobeta-Nacetylglucosaminidase-like [Oreochromis niloticus]	0.0224	-0.4076	down	-0.0196	down	-1.6055	down	0.3881	up	-1.1979	down	-1.5860	down

MPF_LOC101488105.1.1	XM_004550275.1 PREDICTED: Maylandia zebra beta-2 adrenergic receptor-like (LOC101488105), mRNA	0.0224	-0.0787	down	-0.0474	down	0.7016	up	0.0313	up	0.7803	up	0.7491	up
MPF_NEMVEDRAFT_V1 G199834.1.1	XP_001639047.1 predicted protein [Nematostella vectensis]	0.0224	-0.4779	down	-0.0449	down	0.8271	up	0.4330	up	1.3051	up	0.8720	up
MPF_BTF3.2.2	BTF3_MOUSE (sp|Q64152) Transcription factor BTF3 OS=Mus musculus GN=Btf3 PE=2 SV=3	0.0224	0.2572	up	0.5035	up	0.7322	up	0.2463	up	0.4750	up	0.2286	up
MPF_LOC101064754.2.2	XM_003964223.1 PREDICTED: Takifugu rubripes calpain-2 catalytic subunit-like (LOC101064754), mRNA	0.0224	0.0220	up	-0.4054	down	0.8963	up	-0.4274	down	0.8744	up	1.3017	up
MPF_LOC101484055.3.4	XM_004553153.1 PREDICTED: Maylandia zebra tropomyosin alpha-1 chain-like (LOC101484055), transcript variant X3, mRNA	0.0224	-0.0440	down	0.1429	up	0.7098	up	0.1869	up	0.7537	up	0.5669	up
MPF_POL.2.6	POL_FENV1 (sp|P31792) Pol polyprotein (Fragment) OS=Feline endogenous virus ECE1 GN=pol PE=3 SV=1	0.0224	0.1468	up	-1.5105	down	-4.3534	down	-1.6573	down	-4.5002	down	-2.8429	down
MPF_contig_007932		0.0224	-0.0163	down	0.2738	up	0.6439	up	0.2901	up	0.6602	up	0.3701	up
MPF_contig_020569		0.0224	-0.0702	down	0.2033	up	0.7553	up	0.2735	up	0.8255	up	0.5520	up
MPF_LOC101468789.1.2	XM_004550754.1 PREDICTED: Maylandia zebra polyhomeotic-like protein 1-like (LOC101468789), mRNA	0.0224	0.0802	up	0.5409	up	1.3083	up	0.4607	up	1.2281	up	0.7674	up

MPF_contig_010734		0.0224	0.1408	up	-0.2150	down	1.1033	up	-0.3557	down	0.9626	up	1.3183	up
MPF_LOC101467510.1.4	XM_004561752.1 PREDICTED: Maylandia zebra folliculin-interacting protein 1-like (LOC101467510), transcript variant X2, mRNA	0.0224	-0.0836	down	0.0948	up	0.5519	up	0.1785	up	0.6355	up	0.4571	up
MPF_LOC100690836.1.1	XP_003447492.1 PREDICTED: presequence protease, mitochondrial-like [Oreochromis niloticus]	0.0224	0.0262	up	0.1852	up	0.5554	up	0.1590	up	0.5292	up	0.3702	up
MPF_contig_006984		0.0224	0.0794	up	0.1874	up	0.5335	up	0.1079	up	0.4541	up	0.3461	up
MPF_LOC101487834.1.1	XM_004574180.1 PREDICTED: Maylandia zebra HAUS augmin-like complex subunit 3-like (LOC101487834), mRNA	0.0224	0.1601	up	0.5020	up	0.9888	up	0.3419	up	0.8287	up	0.4867	up
MPF_LOC100694557.5.24	XM_003458536.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100694557), mRNA	0.0224	-0.1185	down	-0.0368	down	0.6510	up	0.0817	up	0.7695	up	0.6879	up
MPF_contig_034973		0.0225	-0.0980	down	-0.1242	down	0.6774	up	-0.0261	down	0.7754	up	0.8016	up
MPF_contig_037350		0.0225	0.1424	up	0.2914	up	0.6628	up	0.1490	up	0.5204	up	0.3714	up
MPF_FA7.2.2	FA7_HUMAN (sp|P08709) Coagulation factor VII OS=Homo sapiens GN=F7 PE=1 SV=1	0.0225	-0.2720	down	0.1945	up	0.8774	up	0.4665	up	1.1494	up	0.6829	up
MPF_contig_025280		0.0225	0.0150	up	0.1964	up	0.6099	up	0.1814	up	0.5948	up	0.4135	up

MPF_LOC101475515.1.1	XM_004545728.1 PREDICTED: Maylandia zebra cleavage stimulation factor subunit 2-like (LOC101475515), transcript variant X3, mRNA	0.0225	0.0653	up	0.2431	up	0.8698	up	0.1777	up	0.8045	up	0.6267	up
MPF_contig_020270	XM_004542486.1 PREDICTED: Maylandia zebra ubiquitin-conjugating enzyme E2 R1-like (LOC101480834), transcript variant X1, mRNA	0.0225	0.6350	up	0.2238	up	1.1304	up	-0.4112	down	0.4954	up	0.9066	up
MPF_LOC101486277.2.2	XM_004568460.1 PREDICTED: Maylandia zebra uncharacterized LOC101486277 (LOC101486277), mRNA	0.0225	-0.0850	down	-0.7914	down	-2.3312	down	-0.7064	down	-2.2462	down	-1.5398	down
MPF_LOC101480516.1.2	XM_004537976.1 PREDICTED: Maylandia zebra protein phosphatase 1D-like (LOC101480516), mRNA	0.0225	-0.0226	down	-0.1433	down	1.1497	up	-0.1207	down	1.1723	up	1.2930	up
MPF_contig_027934		0.0226	0.0880	up	0.4986	up	1.4076	up	0.4106	up	1.3196	up	0.9090	up
MPF_contig_027617		0.0226	-0.5219	down	-0.5043	down	-1.9659	down	0.0176	up	-1.4440	down	-1.4616	down
MPF_AHNK.21.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiationassociated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.0226	-0.4886	down	-2.2095	down	-4.6687	down	-1.7209	down	-4.1802	down	-2.4592	down
MPF_LOC101468998.1.1	XM_004556785.1 PREDICTED: Maylandia zebra sclerostin-like	0.0227	-0.2149	down	0.0536	up	1.4283	up	0.2685	up	1.6432	up	1.3747	up

	(LOC101468998), transcript variant X2, mRNA													
MPF_LOC101464125.1.1	XM_004573638.1 PREDICTED: Maylandia zebra DNA-directed RNA polymerase I subunit RPA12like (LOC101464125), transcript variant X4, mRNA	0.0227	0.3044	up	0.7903	up	0.9594	up	0.4859	up	0.6551	up	0.1691	up
MPF_LOC100689854.4.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0.0228	0.0381	up	0.1176	up	1.0619	up	0.0796	up	1.0239	up	0.9443	up
MPF_contig_032806		0.0228	0.0678	up	0.4139	up	0.9752	up	0.3462	up	0.9075	up	0.5613	up
MPF_contig_018702		0.0228	0.2349	up	0.1952	up	0.9359	up	-0.0398	down	0.7010	up	0.7408	up
MPF_contig_034181		0.0228	-0.2297	down	-0.7409	down	-2.0263	down	-0.5113	down	-1.7967	down	-1.2854	down
MPF_contig_013127	XM_004539189.1 PREDICTED: Maylandia zebra ATP-binding cassette sub-family A member 1-like (LOC101484083), transcript variant X1, mRNA	0.0228	-0.2084	down	-0.8428	down	-2.3782	down	-0.6344	down	-2.1698	down	-1.5354	down
MPF_LOC101484448.2.3	XM_004540186.1 PREDICTED: Maylandia zebra lipid phosphate phosphatase-related protein type 3-like (LOC101484448), transcript variant X2, mRNA	0.0228	-0.0295	down	0.3791	up	1.7735	up	0.4086	up	1.8030	up	1.3944	up
MPF_contig_024093		0.0228	0.0754	up	0.1970	up	0.7095	up	0.1215	up	0.6341	up	0.5125	up

MPF_MOR1A.1.1	[BBH] MOR1A_CHICK (sp|Q2YHT7) Cell surface glycoprotein CD200 receptor 1-A OS=Gallus gallus GN=CD200R1A PE=1 SV=1	0.0228	-0.6394	down	-1.5796	down	-3.1244	down	-0.9402	down	-2.4850	down	-1.5448	down
MPF_contig_014719		0.0228	0.0672	up	0.2769	up	0.6049	up	0.2097	up	0.5377	up	0.3281	up
MPF_contig_009283		0.0228	-0.4359	down	-0.7562	down	-2.4231	down	-0.3203	down	-1.9872	down	-1.6669	down
MPF_LOC101472257.1.1	XM_004556797.1 PREDICTED: Maylandia zebra pyruvate dehydrogenase [lipoamide] kinase isozyme 2-like (LOC101472257), mRNA	0.0228	0.0347	up	0.1818	up	0.9981	up	0.1471	up	0.9634	up	0.8164	up
MPF_contig_032442		0.0228	-0.9528	down	-1.1981	down	-3.5449	down	-0.2453	down	-2.5921	down	-2.3468	down
MPF_LOC101077743.1.1	XP_003975039.1 PREDICTED: acetyl-CoA carboxylase 2-like [Takifugu rubripes]	0.0228	0.1286	up	0.3279	up	1.2224	up	0.1993	up	1.0938	up	0.8945	up
MPF_LOC101471364.1.1	XM_004549927.1 PREDICTED: Maylandia zebra tenascin-like (LOC101471364), transcript variant X5, mRNA	0.0228	-0.1255	down	-0.2846	down	-1.4321	down	-0.1591	down	-1.3065	down	-1.1475	down
MPF_LOC100698764.2.2	XM_003449126.1 PREDICTED: Oreochromis niloticus probable cationtransporting ATPase 13A2like (LOC100698764), mRNA	0.0228	0.1831	up	0.3802	up	0.7410	up	0.1971	up	0.5580	up	0.3608	up
MPF_LOC101068670.1.1	XM_003961269.1 PREDICTED: Takifugu rubripes transcription elongation factor B polypeptide 2-like	0.0228	-0.0251	down	-1.3137	down	-2.0184	down	-1.2886	down	-1.9933	down	-0.7047	down

	(LOC101068670), mRNA													
MPF_LOC100692915.1.1	XP_003453769.1 PREDICTED: probable alphaketoglutarate-dependent dioxygenase ABH4-like [Oreochromis niloticus]	0.0228	0.1974	up	0.5532	up	1.0288	up	0.3559	up	0.8315	up	0.4756	up
MPF_LOC101477342.1.3	XM_004546475.1 PREDICTED: Maylandia zebra eukaryotic translation elongation factor 1 epsilon-1like (LOC101477342), mRNA	0.0228	-0.0648	down	0.0406	up	0.6421	up	0.1053	up	0.7069	up	0.6016	up
MPF_RNA45S5.4.4	NR_046235.1 Homo sapiens RNA, 45S pre-ribosomal 5 (RNA45S5), ribosomal RNA	0.0228	0.1102	up	0.3518	up	0.7975	up	0.2416	up	0.6873	up	0.4457	up
MPF_SPCS.1.3	SPCS_DANRE (sp|Q803A7) O-phosphoseryl-tRNA(Sec) selenium transferase OS=Danio rerio GN=sepsecs PE=2 SV=1	0.0228	-0.0066	down	0.1309	up	0.7730	up	0.1375	up	0.7796	up	0.6421	up
MPF_contig_013856		0.0228	0.0876	up	0.3442	up	0.8363	up	0.2566	up	0.7487	up	0.4920	up
MPF_contig_026192		0.0228	-0.0041	down	0.1644	up	0.6811	up	0.1685	up	0.6852	up	0.5167	up
MPF_contig_034320		0.0228	-0.3499	down	0.0020	up	-1.7317	down	0.3519	up	-1.3818	down	-1.7338	down
MPF_LOC100690992.1.1	XM_003442702.1 PREDICTED: Oreochromis niloticus Rieske domaincontaining protein-like (LOC100690992), mRNA	0.0228	-0.1576	down	0.0253	up	0.5800	up	0.1828	up	0.7376	up	0.5548	up
MPF_LOC100691148.1.2	XM_003458290.1 PREDICTED: Oreochromis niloticus diacylglycerol kinase zeta-like (LOC100691148),	0.0228	0.0360	up	0.0841	up	0.7365	up	0.0482	up	0.7005	up	0.6524	up

	mRNA													
MPF_CD28.1.1	[BBH] CD28_HUMAN (sp|P10747) T-cell-specific surface glycoprotein CD28 OS=Homo sapiens GN=CD28 PE=1 SV=1	0.0228	-0.6930	down	-1.2871	down	-2.8446	down	-0.5941	down	-2.1516	down	-1.5576	down

MPF_LOC101061752.1.1	XM_003975168.1 PREDICTED: Takifugu rubripes SEC14-like protein 2like (LOC101061752), mRNA	0.0228	-0.6829	down	-1.6115	down	-3.6111	down	-0.9286	down	-2.9282	down	-1.9996	down
MPF_contig_004858		0.0228	-0.1740	down	-0.2023	down	-1.6591	down	-0.0283	down	-1.4851	down	-1.4568	down
MPF_LOC100693180.1.1	XP_003452227.1 PREDICTED: hypothetical protein LOC100693180 [Oreochromis niloticus]	0.0228	0.2062	up	0.3498	up	0.7350	up	0.1436	up	0.5288	up	0.3852	up
MPF_LOC101472211.3.4	XM_004545811.1 PREDICTED: Maylandia zebra BEN domain- containing protein 4-like (LOC101472211), mRNA	0.0228	-0.0173	down	0.1098	up	0.8016	up	0.1272	up	0.8190	up	0.6918	up
MPF_LOC101165232.1.1	XP_004070172.1 PREDICTED: N-terminal EFhand calcium-binding protein 2-like [Oryzias latipes]	0.0228	0.0567	up	-0.0604	down	0.6453	up	-0.1171	down	0.5886	up	0.7057	up
MPF_LOC100695137.3.3	XP_003447509.1 PREDICTED: high affinity immunoglobulin epsilon receptor subunit gamma-like [Oreochromis niloticus]	0.0228	0.5163	up	-1.6726	down	-4.3610	down	-2.1888	down	-4.8773	down	-2.6884	down

MPF_LOC101482781.1.4	XM_004569427.1 PREDICTED: Maylandia zebra ran-binding protein 9like (LOC101482781), mRNA	0.0228	0.0883	up	0.3419	up	1.0379	up	0.2536	up	0.9496	up	0.6960	up
MPF_contig_043323		0.0228	-0.5786	down	-0.3551	down	-1.9591	down	0.2235	up	-1.3805	down	-1.6040	down
MPF_LOC101464911.1.1	XM_004560530.1 PREDICTED: Maylandia zebra protein FAM181B-like (LOC101464911), mRNA	0.0228	0.0808	up	0.0993	up	1.6048	up	0.0185	up	1.5240	up	1.5054	up
MPF_LOC101483137.3.3	XM_004564978.1 PREDICTED: Maylandia zebra WD repeat-containing protein 62-like (LOC101483137), mRNA	0.0228	-0.0763	down	0.2432	up	0.9628	up	0.3195	up	1.0392	up	0.7197	up
MPF_contig_023437		0.0229	-0.4569	down	-0.3210	down	-2.2058	down	0.1359	up	-1.7489	down	-1.8848	down
MPF_LOC100699517.2.2	XP_003456582.1 PREDICTED: hypothetical protein LOC100699517 [Oreochromis niloticus]	0.0230	-0.0008	down	0.2528	up	1.1731	up	0.2537	up	1.1740	up	0.9203	up
MPF_contig_009706		0.0230	-1.0601	down	-0.7689	down	-3.1071	down	0.2913	up	-2.0470	down	-2.3383	down
MPF_LOC101487230.3.3	XM_004568550.1 PREDICTED: Maylandia zebra pre-B-cell leukemia transcription factor 2-like (LOC101487230), mRNA	0.0230	0.1120	up	-1.0350	down	-2.8417	down	-1.1471	down	-2.9537	down	-1.8067	down
MPF_LOC101473946.1.3	XM_004540042.1 PREDICTED: Maylandia zebra protein salvador homolog 1-like (LOC101473946), mRNA	0.0230	-0.0295	down	0.0291	up	0.6190	up	0.0586	up	0.6485	up	0.5899	up

MPF_LOC100331403.3.3	XM_003200790.1 PREDICTED: Danio rerio hypothetical protein LOC100331403 (LOC100331403), mRNA	0.0230	0.1111	up	-0.8410	down	-2.0415	down	-0.9521	down	-2.1527	down	-1.2006	down
MPF_contig_015477		0.0231	-0.3931	down	-0.1649	down	-1.5731	down	0.2282	up	-1.1800	down	-1.4082	down
MPF_contig_028664		0.0231	0.0097	up	-0.1418	down	-1.0413	down	-0.1514	down	-1.0509	down	-0.8995	down
MPF_contig_036988		0.0231	-0.0948	down	0.0766	up	0.7432	up	0.1714	up	0.8379	up	0.6665	up
MPF_contig_009685		0.0231	0.0056	up	0.2116	up	0.6397	up	0.2060	up	0.6341	up	0.4281	up
MPF_LOC101477528.1.1	XM_004568962.1 PREDICTED: Maylandia zebra uncharacterized LOC101477528 (LOC101477528), transcript variant X3, mRNA	0.0231	0.1292	up	0.0991	up	0.7613	up	-0.0300	down	0.6321	up	0.6621	up
MPF_ZN235.8.9	ZN235_HUMAN (sp|Q14590) Zinc finger protein 235 OS=Homo sapiens GN=ZNF235 PE=2 SV=3	0.0231	0.0702	up	0.2272	up	1.0490	up	0.1570	up	0.9788	up	0.8218	up
MPF_LOC101466312.1.2	XM_004569463.1 PREDICTED: Maylandia zebra protein EFR3 homolog A-like (LOC101466312), transcript variant X4, mRNA	0.0232	0.0910	up	0.1550	up	0.9530	up	0.0639	up	0.8620	up	0.7980	up
MPF_LOC101480386.1.1	XM_004574590.1 PREDICTED: Maylandia zebra E3 ubiquitin/ISG15 ligase TRIM25-like (LOC101480386), mRNA	0.0232	0.1463	up	0.3046	up	0.9862	up	0.1583	up	0.8399	up	0.6816	up

MPF_UBIQ.3.3	UBIQ_RABIT (sp|P62975) Ubiquitin OS=Oryctolagus cuniculus PE=1 SV=1	0.0232	0.3275	up	0.3745	up	0.5875	up	0.0470	up	0.2601	up	0.2130	up
MPF_LOC100693543.1.1	XP_003450393.1 PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial-like [Oreochromis niloticus]	0.0232	0.1412	up	0.1818	up	0.7814	up	0.0406	up	0.6403	up	0.5997	up
MPF_LOC100693024.1.1	XP_003456072.1 PREDICTED: ubiquitinconjugating enzyme E2 J1like isoform 2 [Oreochromis niloticus]	0.0232	0.1739	up	0.1951	up	0.6323	up	0.0212	up	0.4584	up	0.4373	up
MPF_LOC100710676.1.1	XP_003448392.1 PREDICTED: green-sensitive opsin-like [Oreochromis niloticus]	0.0232	-0.2116	down	-0.3989	down	-1.8480	down	-0.1874	down	-1.6365	down	-1.4491	down
MPF_LOC101480666.2.2	XM_004572977.1 PREDICTED: Maylandia zebra regulator of cell cycle RGCC-like (LOC101480666), mRNA	0.0232	-0.0506	down	0.2158	up	0.8940	up	0.2664	up	0.9446	up	0.6782	up
MPF_LOC100703053.1.1	XM_003440732.1 PREDICTED: Oreochromis niloticus ATP-dependent RNA helicase DDX1-like (LOC100703053), mRNA	0.0232	-0.0207	down	0.3434	up	1.1923	up	0.3641	up	1.2130	up	0.8489	up
MPF_LOC101464277.1.1	XM_004543741.1 PREDICTED: Maylandia zebra rho guanine nucleotide exchange factor 12-like (LOC101464277), transcript variant X3, mRNA	0.0232	0.0669	up	0.2645	up	0.8284	up	0.1977	up	0.7616	up	0.5639	up
MPF_contig_023668		0.0232	0.1760	up	0.3046	up	0.6725	up	0.1287	up	0.4965	up	0.3679	up

MPF_contig_046542	XP_003443377.1 PREDICTED: myosin-Ib isoform 1 [Oreochromis niloticus]	0.0232	0.2354	up	0.4508	up	0.9914	up	0.2154	up	0.7561	up	0.5407	up
MPF_contig_009278		0.0232	-0.1825	down	0.0979	up	0.6548	up	0.2803	up	0.8373	up	0.5570	up
MPF_LOC100689746.1.1	XP_003445067.1 PREDICTED: proline-rich protein 5-like [Oreochromis niloticus]	0.0232	-0.3428	down	0.0879	up	0.9769	up	0.4307	up	1.3197	up	0.8890	up
MPF_LOC101484994.2.2	XM_004555447.1 PREDICTED: Maylandia zebra UPF0524 protein C3orf70 homolog A-like (LOC101484994), mRNA	0.0233	-0.5007	down	-1.3695	down	-3.2274	down	-0.8688	down	-2.7267	down	-1.8579	down
MPF_LOC101164889.1.1	XM_004070593.1 PREDICTED: Oryzias latipes putative nuclease HARBI1like (LOC101164889), mRNA	0.0233	-0.0513	down	0.0637	up	0.6876	up	0.1150	up	0.7389	up	0.6239	up
MPF_contig_008757		0.0233	-0.0016	down	0.1482	up	0.8585	up	0.1497	up	0.8601	up	0.7103	up
MPF_LOC100706983.9.1 1	XP_003460110.1 PREDICTED: 28S ribosomal protein S28, mitochondriallike [Oreochromis niloticus]	0.0233	-0.1283	down	-0.0651	down	0.9577	up	0.0632	up	1.0860	up	1.0228	up
MPF_SIAT7BRELATED.1.1	XM_003979995.1 PREDICTED: Takifugu rubripes alpha-2,6sialyltransferase ST6GalNAc II B (siat7B-related), mRNA	0.0234	-0.0984	down	0.2132	up	0.6648	up	0.3116	up	0.7632	up	0.4516	up
MPF_LOC101167345.13.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA	0.0234	-0.2191	down	-1.8565	down	-3.1158	down	-1.6375	down	-2.8967	down	-1.2592	down

MPF_LOC101065884.1.2	XM_003965883.1 PREDICTED: Takifugu rubripes 1-acylglycerol-3phosphate O-acyltransferase ABHD5-like (LOC101065884), mRNA	0.0234	-0.1217	down	0.1027	up	0.5631	up	0.2244	up	0.6848	up	0.4604	up
MPF_LOC101061889.1.1	XP_003972358.1 PREDICTED: sorbin and SH3 domain-containing protein 2like [Takifugu rubripes]	0.0234	0.1183	up	0.2410	up	0.7197	up	0.1227	up	0.6015	up	0.4788	up
MPF_LOC101485840.1.2	XM_004561077.1 PREDICTED: Maylandia zebra uncharacterized LOC101485840 (LOC101485840), mRNA	0.0235	-0.1237	down	-0.2724	down	0.6613	up	-0.1486	down	0.7850	up	0.9337	up
MPF_RS3.2.5	RS3_RAT (sp|P62909) 40S ribosomal protein S3 OS=Rattus norvegicus GN=Rps3 PE=1 SV=1	0.0235	-0.2474	down	-0.5109	down	-1.1301	down	-0.2635	down	-0.8827	down	-0.6191	down
MPF_LOC101157594.1.1	XP_004065840.1 PREDICTED: uncharacterized protein LOC101157594 [Oryzias latipes]	0.0235	-0.2208	down	-1.3429	down	-2.4659	down	-1.1221	down	-2.2451	down	-1.1230	down
MPF_contig_028605		0.0235	-0.7413	down	-1.9554	down	-4.0581	down	-1.2141	down	-3.3169	down	-2.1027	down
MPF_LOC101478477.2.3	XM_004571884.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 39-like (LOC101478477), transcript variant X2, mRNA	0.0235	0.2458	up	0.3762	up	0.9092	up	0.1303	up	0.6634	up	0.5331	up

MPF_LOC100708198.1.1	XP_003453989.1 PREDICTED: wiskott-Aldrich syndrome protein family member 3-like [Oreochromis niloticus]	0.0236	-0.1469	down	0.0459	up	0.6122	up	0.1928	up	0.7592	up	0.5664	up
MPF_contig_048639		0.0236	0.0765	up	0.2267	up	0.7592	up	0.1501	up	0.6827	up	0.5326	up
MPF_AHNK.17.22	[BBH] AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.0237	-0.7348	down	-2.2324	down	-4.7985	down	-1.4976	down	-4.0637	down	-2.5662	down
MPF_LOC100699407.1.3	XM_003451114.1 PREDICTED: Oreochromis niloticus stress-associated endoplasmic reticulum protein 1-like (LOC100699407), mRNA	0.0237	-0.0467	down	-0.1633	down	0.9452	up	-0.1166	down	0.9919	up	1.1085	up
MPF_LOC101482551.1.1	XM_004538177.1 PREDICTED: Maylandia zebra smoothelin-like (LOC101482551), mRNA	0.0237	-0.2665	down	-0.4368	down	-1.7118	down	-0.1704	down	-1.4453	down	-1.2750	down
MPF_LOC101483152.2.3	XM_004544173.1 PREDICTED: Maylandia zebra GTPase-activating protein and VPS9 domaincontaining protein 1-like (LOC101483152), mRNA	0.0237	-0.0138	down	0.1122	up	0.9333	up	0.1260	up	0.9471	up	0.8211	up

MPF_LOC101477334.3.3	XM_004568161.1 PREDICTED: Maylandia zebra FYVE, RhoGEF and PH domain-containing protein 1-like (LOC101477334), transcript variant X2, mRNA	0.0237	-0.0053	down	0.2103	up	0.7654	up	0.2155	up	0.7706	up	0.5551	up
MPF_LOC100692921.1.1	XM_003454794.1 PREDICTED: Oreochromis niloticus P2Y purinoceptor 12like (LOC100692921), mRNA	0.0237	0.1791	up	-0.8750	down	-1.9102	down	-1.0542	down	-2.0893	down	-1.0352	down
MPF_LOC101464846.1.1	XM_004568566.1 PREDICTED: Maylandia zebra ras GTPase-activating protein SynGAP-like (LOC101464846), transcript variant X9, mRNA	0.0237	0.1584	up	0.3378	up	0.8633	up	0.1795	up	0.7050	up	0.5255	up
MPF_RT28.3.8	RT28_BOVIN (sp|P82928) 28S ribosomal protein S28, mitochondrial OS=Bos taurus GN=MRPS28 PE=1 SV=2	0.0237	-0.7886	down	-0.7597	down	-2.5643	down	0.0289	up	-1.7757	down	-1.8046	down
MPF_LOC101468994.1.1	XM_004555202.1 PREDICTED: Maylandia zebra poly [ADP-ribose] polymerase 2-like (LOC101468994), mRNA	0.0237	-0.0197	down	0.1959	up	1.0164	up	0.2156	up	1.0361	up	0.8205	up
MPF_LOC101477924.3.5	XM_004571254.1 PREDICTED: Maylandia zebra carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1-like (LOC101477924), mRNA	0.0237	0.2017	up	-0.0415	down	-1.4597	down	-0.2432	down	-1.6614	down	-1.4182	down
MPF_LOC101483247.2.2	XM_004566502.1 PREDICTED: Maylandia zebra rho guanine nucleotide exchange factor 10-like (LOC101483247), transcript variant X2, mRNA	0.0237	-0.6837	down	0.3449	up	0.9191	up	1.0286	up	1.6027	up	0.5742	up

MPF_LOC101465015.1.1	XM_004562273.1 PREDICTED: Maylandia zebra MKL/myocardin-like protein 2-like (LOC101465015), transcript variant X4, mRNA	0.0237	-0.2782	down	-0.3280	down	-1.6628	down	-0.0498	down	-1.3847	down	-1.3348	down
MPF_contig_014376	XM_004557593.1 PREDICTED: Maylandia zebra MKL/myocardin-like protein 1-like (LOC101469106), transcript variant X4, mRNA	0.0237	0.4114	up	0.4432	up	0.9637	up	0.0317	up	0.5523	up	0.5205	up
MPF_LOC101471940.1.1	XM_004570910.1 PREDICTED: Maylandia zebra TBC1 domain family member 25-like (LOC101471940), mRNA	0.0237	-0.0233	down	0.1145	up	1.5543	up	0.1377	up	1.5775	up	1.4398	up
MPF_LOC101479776.1.2	XM_004568261.1 PREDICTED: Maylandia zebra transmembrane and TPR repeat-containing protein 2-like (LOC101479776), mRNA	0.0238	-0.3123	down	0.0412	up	0.5924	up	0.3535	up	0.9047	up	0.5512	up
MPF_contig_017955		0.0239	0.3535	up	-0.6757	down	-2.2158	down	-1.0292	down	-2.5693	down	-1.5401	down
MPF_contig_015307		0.0239	0.1543	up	0.2684	up	0.5905	up	0.1141	up	0.4362	up	0.3221	up
MPF_contig_038961		0.0239	-0.0085	down	0.2338	up	0.7531	up	0.2424	up	0.7617	up	0.5193	up
MPF_contig_033609		0.0239	-0.0172	down	0.1537	up	0.9329	up	0.1708	up	0.9501	up	0.7792	up
MPF_LOC101471521.1.3	XM_004543486.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF128-like (LOC101471521), mRNA	0.0239	-0.8981	down	-1.7649	down	-3.9773	down	-0.8668	down	-3.0792	down	-2.2124	down

MPF_contig_024644		0.0239	-0.1072	down	-0.1002	down	0.6863	up	0.0070	up	0.7935	up	0.7865	up
MPF_LOC101471595.1.3	XM_004560274.1 PREDICTED: Maylandia zebra tubulin alpha-1A chainlike (LOC101471595), mRNA	0.0239	-0.0884	down	0.1078	up	0.8979	up	0.1962	up	0.9863	up	0.7901	up
MPF_LOC100691115.1.1	XP_003450716.1 PREDICTED: zinc finger protein 574-like [Oreochromis niloticus]	0.0239	-0.0131	down	0.1208	up	0.9481	up	0.1339	up	0.9612	up	0.8273	up
MPF_LOC575849.1.3	XP_781315.3 PREDICTED: protein SpAN-like [Strongylocentrotus purpuratus]	0.0239	0.0472	up	0.2916	up	0.7377	up	0.2444	up	0.6905	up	0.4461	up
MPF_contig_035190		0.0239	-0.0377	down	0.1208	up	0.5505	up	0.1586	up	0.5883	up	0.4297	up
MPF_LOC101475700.1.3	XM_004564763.1 PREDICTED: Maylandia zebra phosphate carrier protein, mitochondrial-like (LOC101475700), transcript variant X2, mRNA	0.0239	-0.8938	down	-0.6061	down	-2.8504	down	0.2878	up	-1.9566	down	-2.2443	down
MPF_RAPH1.1.2	XM_003459208.1 PREDICTED: Oreochromis niloticus Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 (RAPH1), mRNA	0.0241	-0.1867	down	-0.1978	down	0.9571	up	-0.0111	down	1.1438	up	1.1549	up
MPF_LOC100700605.2.27	XM_003458555.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100700605), mRNA	0.0241	0.0696	up	0.1636	up	0.6210	up	0.0939	up	0.5514	up	0.4575	up
MPF_LOC101470525.1.1	XM_004556790.1 PREDICTED: Maylandia zebra vesicle-fusing ATPaselike (LOC101470525), mRNA	0.0241	0.0899	up	0.3475	up	0.7999	up	0.2576	up	0.7100	up	0.4524	up

MPF_DKC1.2.3	XM_003460212.1 PREDICTED: Oreochromis niloticus dyskeratosis congenita 1, dyskerin (DKC1), mRNA	0.0241	-0.2029	down	-0.0761	down	0.9129	up	0.1268	up	1.1158	up	0.9890	up
MPF_LOC100697415.3.3	XP_003444759.1 PREDICTED: neuroblast differentiation-associated protein AHNAK-like [Oreochromis niloticus]	0.0241	-0.7949	down	-2.5086	down	-4.9532	down	-1.7137	down	-4.1582	down	-2.4446	down
MPF_LOC100693572.1.1	XM_003457590.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693572 (LOC100693572), mRNA	0.0241	-0.0690	down	0.2922	up	1.0828	up	0.3612	up	1.1518	up	0.7906	up
MPF_TCNA.2.4	TCNA_TRYCR (sp|P23253) Sialidase OS=Trypanosoma cruzi GN=TCNA PE=2 SV=1	0.0241	0.1831	up	-0.0062	down	0.8701	up	-0.1892	down	0.6870	up	0.8763	up
MPF_LOC101473901.1.2	XM_004572233.1 PREDICTED: Maylandia zebra CDC42 small effector protein 1-like (LOC101473901), transcript variant X2, mRNA	0.0241	-0.1941	down	-1.5989	down	-4.4243	down	-1.4048	down	-4.2302	down	-2.8254	down
MPF_DDA1.2.2	DDA1_DANRE (sp|Q7T2A3) DET1- and DDB1-associated protein 1 OS=Danio rerio GN=dda1 PE=2 SV=1	0.0241	0.0458	up	0.1189	up	0.6064	up	0.0731	up	0.5606	up	0.4874	up
MPF_LOC100707133.1.12	XP_003457606.1 PREDICTED: hypothetical protein LOC100707133 [Oreochromis niloticus]	0.0242	-0.4867	down	-0.4259	down	-2.2067	down	0.0608	up	-1.7200	down	-1.7808	down

MPF_RTBS.5.36	RTBS_DROME (sp|Q95SX7) Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1	0.0242	-0.4224	down	-0.2795	down	1.2396	up	0.1429	up	1.6620	up	1.5191	up
MPF_LOC101061779.1.1	XP_003964422.1 PREDICTED: pyridoxaldependent decarboxylase domain-containing protein 1like [Takifugu rubripes]	0.0242	0.0397	up	0.3183	up	0.6390	up	0.2786	up	0.5993	up	0.3207	up
MPF_LOC101478591.1.1	XM_004575412.1 PREDICTED: Maylandia zebra probable cationtransporting ATPase 13A2like (LOC101478591), transcript variant X4, mRNA	0.0242	0.1650	up	0.4394	up	0.8208	up	0.2745	up	0.6558	up	0.3814	up
MPF_contig_008194		0.0242	-0.0026	down	0.2819	up	0.7371	up	0.2846	up	0.7398	up	0.4552	up
MPF_contig_010158		0.0242	-0.3481	down	-0.1485	down	-1.5493	down	0.1996	up	-1.2012	down	-1.4008	down
MPF_contig_030749		0.0243	0.0266	up	-1.4302	down	-2.9949	down	-1.4568	down	-3.0215	down	-1.5647	down
MPF_LOC100151239.1.1	XP_001921419.1 PREDICTED: protein FAM89A-like [Danio rerio]	0.0243	-0.0045	down	0.0473	up	0.8442	up	0.0518	up	0.8486	up	0.7969	up
MPF_contig_000500		0.0243	-0.1468	down	0.3596	up	0.9434	up	0.5065	up	1.0903	up	0.5838	up
MPF_LOC101156484.2.2	XM_004067491.1 PREDICTED: Oryzias latipes CD81 antigen-like (LOC101156484), mRNA	0.0243	-0.5078	down	-1.5919	down	-3.3249	down	-1.0841	down	-2.8172	down	-1.7331	down
MPF_LOC100712012.2.3	XP_003446066.1 PREDICTED: neural cell adhesion molecule L1-like [Oreochromis niloticus]	0.0243	0.0707	up	0.0560	up	0.9561	up	-0.0147	down	0.8854	up	0.9001	up

MPF_LOC100702221.1.1	XP_003455702.1 PREDICTED: interleukin-17 receptor A-like [Oreochromis niloticus]	0.0243	-0.0542	down	0.1944	up	0.3317	up	0.2487	up	0.3859	up	0.1372	up
MPF_contig_047564		0.0243	-0.0265	down	0.1152	up	0.7541	up	0.1418	up	0.7806	up	0.6389	up
MPF_contig_032061		0.0243	-0.2426	down	0.0174	up	-1.3068	down	0.2600	up	-1.0642	down	-1.3242	down
MPF_contig_049193		0.0243	-0.3060	down	-0.6803	down	1.1053	up	-0.3743	down	1.4113	up	1.7856	up
MPF_contig_020905	XM_004557861.1 PREDICTED: Maylandia zebra F-box-like/WD repeatcontaining protein TBL1X-like (LOC101465000), transcript variant X1, mRNA	0.0243	0.0755	up	0.0876	up	1.1438	up	0.0120	up	1.0682	up	1.0562	up
MPF_LOC101482225.2.4	XM_004572985.1 PREDICTED: Maylandia zebra A-kinase anchor protein 11-like (LOC101482225), transcript variant X2, mRNA	0.0243	-0.0033	down	0.1096	up	0.8309	up	0.1129	up	0.8342	up	0.7213	up
MPF_LOC100708750.2.2	XM_003457879.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100708750), mRNA	0.0243	-0.0713	down	-0.1775	down	0.7456	up	-0.1062	down	0.8169	up	0.9231	up
MPF_LOC100705244.1.1	XM_003450063.1 PREDICTED: Oreochromis niloticus heme oxygenase 2like (LOC100705244), mRNA	0.0243	-0.0711	down	-0.6831	down	-2.8732	down	-0.6120	down	-2.8021	down	-2.1900	down
MPF_contig_026006		0.0243	0.0199	up	0.2654	up	1.0553	up	0.2455	up	1.0354	up	0.7899	up
MPF_contig_000044		0.0243	0.1952	up	0.4361	up	0.8621	up	0.2410	up	0.6669	up	0.4260	up

MPF_LOC100700436.1.1	XP_003439415.1 PREDICTED: transcriptional repressor NF-X1-like [Oreochromis niloticus]	0.0243	0.1717	up	0.0860	up	0.9616	up	-0.0857	down	0.7899	up	0.8756	up
MPF_LOC101469923.2.2	XM_004573293.1 PREDICTED: Maylandia zebra GTP cyclohydrolase 1like (LOC101469923), mRNA	0.0243	-0.0164	down	0.1852	up	0.8226	up	0.2016	up	0.8389	up	0.6374	up
MPF_contig_046713		0.0243	0.7417	up	1.4823	up	0.4848	up	0.7406	up	-0.2569	down	-0.9975	down
MPF_LOC101175629.2.2	XM_004086349.1 PREDICTED: Oryzias latipes proteasomal ubiquitin receptor ADRM1-like (LOC101175629), mRNA	0.0243	0.0556	up	0.1787	up	0.7216	up	0.1230	up	0.6660	up	0.5430	up
MPF_LOC101477137.2.2	XM_004542098.1 PREDICTED: Maylandia zebra peptidyl-prolyl cis-trans isomerase FKBP3-like (LOC101477137), mRNA	0.0243	-0.1262	down	0.1109	up	0.8532	up	0.2371	up	0.9794	up	0.7423	up
MPF_LOC101469498.4.4	XM_004560924.1 PREDICTED: Maylandia zebra dedicator of cytokinesis protein 4-like (LOC101469498), mRNA	0.0243	-0.7940	down	-0.5333	down	-1.6493	down	0.2608	up	-0.8552	down	-1.1160	down
MPF_NEMVEDRAFT_V1G152920.1.1	XP_001618924.1 hypothetical protein NEMVEDRAFT_v1g152920 [Nematostella vectensis]	0.0243	0.7476	up	0.4225	up	2.0271	up	-0.3251	down	1.2795	up	1.6046	up
MPF_LOC100693038.1.2	XP_003458500.1 PREDICTED: hypothetical protein LOC100693038 [Oreochromis niloticus]	0.0243	-0.0793	down	0.4932	up	0.3194	up	0.5725	up	0.3987	up	-0.1738	down

MPF_PIGR.3.3	XP_004177171.1 PREDICTED: polymeric immunoglobulin receptor [Taeniopygia guttata]	0.0243	-0.0287	down	0.1059	up	0.6410	up	0.1346	up	0.6697	up	0.5351	up
MPF_contig_023804		0.0243	-0.5555	down	-0.5782	down	-1.7475	down	-0.0227	down	-1.1920	down	-1.1693	down
MPF_CO8A1.4.5	CO8A1_RABIT (sp|P14282) Collagen alpha-1(VIII) chain OS=Oryctolagus cuniculus GN=COL8A1 PE=2 SV=1	0.0243	0.0089	up	0.1750	up	0.8450	up	0.1661	up	0.8361	up	0.6700	up
MPF_LOC101468141.2.4	XM_004541229.1 PREDICTED: Maylandia zebra ADAMTS-like protein 4like (LOC101468141), mRNA	0.0243	0.2882	up	0.2371	up	0.6857	up	-0.0511	down	0.3975	up	0.4486	up
MPF_LOC101079821.1.1	XP_003965751.1 PREDICTED: RING finger protein 183-like [Takifugu rubripes]	0.0243	-0.1478	down	0.6137	up	0.6097	up	0.7615	up	0.7575	up	-0.0040	down
MPF_contig_028882		0.0243	-0.0815	down	0.3231	up	0.7205	up	0.4046	up	0.8019	up	0.3974	up
MPF_LOC101480083.3.3	XM_004548835.1 PREDICTED: Maylandia zebra cytochrome c1, heme protein, mitochondrial-like (LOC101480083), mRNA	0.0243	0.1257	up	0.1185	up	0.8450	up	-0.0072	down	0.7193	up	0.7264	up
MPF_contig_048807		0.0243	0.2800	up	0.4286	up	0.8651	up	0.1485	up	0.5851	up	0.4366	up
MPF_LOC100119490.1.1	XP_001603259.2 PREDICTED: hypothetical protein LOC100119490 [Nasonia vitripennis]	0.0243	-0.2422	down	-0.1016	down	-2.6078	down	0.1406	up	-2.3657	down	-2.5063	down
MPF_contig_002650	XM_004079020.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 1 (LOC101161674), mRNA	0.0243	-0.0190	down	-1.3613	down	-3.2899	down	-1.3423	down	-3.2708	down	-1.9285	down

MPF_LOC101470938.1.1	XM_004561198.1 PREDICTED: Maylandia zebra uncharacterized LOC101470938 (LOC101470938), transcript variant X2, mRNA	0.0243	-0.0411	down	0.6054	up	1.3128	up	0.6466	up	1.3539	up	0.7073	up
MPF_SC22B.1.1	SC22B_RAT (sp|Q4KM74) Vesicle-trafficking protein SEC22b OS=Rattus norvegicus GN=Sec22b PE=1 SV=3	0.0243	0.0604	up	0.3322	up	0.7927	up	0.2719	up	0.7323	up	0.4604	up
MPF_LOC101467147.1.5	XM_004566000.1 PREDICTED: Maylandia zebra NEDD8-conjugating enzyme UBE2F-like (LOC101467147), mRNA	0.0243	0.1649	up	0.1978	up	0.6505	up	0.0329	up	0.4856	up	0.4527	up
MPF_LOC101467581.1.1	XM_004574714.1 PREDICTED: Maylandia zebra ephrin type-B receptor 4-like (LOC101467581), mRNA	0.0244	-0.0406	down	0.0369	up	1.1901	up	0.0775	up	1.2307	up	1.1532	up
MPF_LOC101463853.1.1	XM_004558959.1 PREDICTED: Maylandia zebra tRNA-splicing endonuclease subunit Sen2like (LOC101463853), mRNA	0.0244	0.2374	up	0.4186	up	1.1559	up	0.1812	up	0.9184	up	0.7373	up
MPF_B2MG.3.10	B2MG_CYPCA (sp|Q03422) Beta-2-microglobulin OS=Cyprinus carpio GN=b2m PE=3 SV=1	0.0244	-0.1544	down	-1.4669	down	-3.7125	down	-1.3125	down	-3.5581	down	-2.2456	down
MPF_contig_027603		0.0244	0.0217	up	0.2186	up	0.9862	up	0.1969	up	0.9645	up	0.7676	up

MPF_LOC101469126.1.1	XM_004562729.1 PREDICTED: Maylandia zebra monocarboxylate transporter 13-like (LOC101469126), transcript variant X5, mRNA	0.0244	0.0311	up	-0.8959	down	-2.8043	down	-0.9271	down	-2.8355	down	-1.9084	down
MPF_contig_040466		0.0244	-0.1489	down	-0.0303	down	0.2997	up	0.1186	up	0.4486	up	0.3299	up
MPF_contig_037472		0.0244	-0.0504	down	0.0970	up	0.6649	up	0.1475	up	0.7153	up	0.5679	up
MPF_LOC101473334.2.2	XM_004553568.1 PREDICTED: Maylandia zebra histone-lysine Nmethyltransferase SETD7like (LOC101473334), mRNA	0.0244	-0.3976	down	0.0874	up	1.2959	up	0.4850	up	1.6934	up	1.2084	up
MPF_LOC101473755.3.3	XM_004564853.1 PREDICTED: Maylandia zebra CCR4-NOT transcription complex subunit 2-like (LOC101473755), transcript variant X2, mRNA	0.0244	-0.5945	down	-1.3355	down	-2.6590	down	-0.7410	down	-2.0645	down	-1.3235	down
MPF_contig_007651		0.0244	0.0193	up	0.1988	up	0.5631	up	0.1795	up	0.5438	up	0.3643	up
MPF_LOC101472313.1.1	XM_004546377.1 PREDICTED: Maylandia zebra polyglutamine-binding protein 1-like (LOC101472313), transcript variant X2, mRNA	0.0244	0.2672	up	0.3523	up	1.6767	up	0.0851	up	1.4095	up	1.3244	up
MPF_contig_019120		0.0244	-0.0134	down	0.0928	up	0.6435	up	0.1062	up	0.6568	up	0.5506	up
MPF_LOC100711455.1.1	XM_003441344.1 PREDICTED: Oreochromis niloticus melanocyte protein PMEL-like (LOC100711455), mRNA	0.0244	-0.0958	down	-0.2035	down	0.7664	up	-0.1077	down	0.8622	up	0.9699	up

MPF_contig_027608		0.0245	-0.3792	down	0.3594	up	0.4833	up	0.7386	up	0.8625	up	0.1240	up
MPF_contig_023684		0.0245	0.0292	up	0.2687	up	0.5862	up	0.2395	up	0.5570	up	0.3175	up
MPF_LOC101469436.1.3	XM_004543478.1 PREDICTED: Maylandia zebra dmX-like protein 2-like (LOC101469436), transcript variant X3, mRNA	0.0245	0.0200	up	0.0854	up	0.8265	up	0.0655	up	0.8065	up	0.7410	up
MPF_LOC101478322.4.4	XM_004556897.1 PREDICTED: Maylandia zebra capZ-interacting protein-like (LOC101478322), mRNA	0.0245	-0.0264	down	0.1027	up	0.8412	up	0.1291	up	0.8676	up	0.7384	up
MPF_LOC100696099.1.3	XP_003448423.1 PREDICTED: phosphoenolpyruvate carboxykinase, cytosolic [GTP]-like [Oreochromis niloticus]	0.0246	-0.0356	down	0.3097	up	1.1281	up	0.3454	up	1.1637	up	0.8183	up
MPF_contig_016471		0.0247	-0.0165	down	0.2074	up	0.6339	up	0.2239	up	0.6504	up	0.4265	up
MPF_LOC101469304.1.8	XM_004556584.1 PREDICTED: Maylandia zebra synuclein-like (LOC101469304), mRNA	0.0247	-0.0774	down	0.0537	up	1.0730	up	0.1310	up	1.1503	up	1.0193	up
MPF_LOC101487785.1.1	XM_004539450.1 PREDICTED: Maylandia zebra mitochondrial pyruvate carrier 1-like (LOC101487785), transcript variant X1, mRNA	0.0247	0.0345	up	0.3717	up	0.8115	up	0.3372	up	0.7769	up	0.4397	up
MPF_LOC101486252.1.1	XM_004563697.1 PREDICTED: Maylandia zebra PQ-loop repeatcontaining protein 1-like (LOC101486252), transcript variant X2, mRNA	0.0247	0.3912	up	0.2608	up	1.0489	up	-0.1304	down	0.6576	up	0.7881	up

MPF_contig_018904		0.0247	-0.0627	down	0.0708	up	0.7939	up	0.1336	up	0.8567	up	0.7231	up
MPF_contig_003974		0.0247	-0.1024	down	0.2080	up	0.6369	up	0.3105	up	0.7394	up	0.4289	up
MPF_LOC100695994.17.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.0247	-0.1394	down	0.1241	up	0.7198	up	0.2635	up	0.8592	up	0.5957	up
MPF_contig_037163		0.0247	-0.0734	down	0.0417	up	0.6641	up	0.1151	up	0.7375	up	0.6224	up
MPF_LOC101477046.2.4	XM_004565575.1 PREDICTED: Maylandia zebra inhibin beta B chainlike (LOC101477046), mRNA	0.0247	-0.0682	down	-0.0586	down	0.7860	up	0.0097	up	0.8542	up	0.8446	up
MPF_contig_001917		0.0247	0.1319	up	0.3820	up	1.0398	up	0.2500	up	0.9079	up	0.6578	up
MPF_contig_019645		0.0247	0.0252	up	0.2847	up	1.0682	up	0.2596	up	1.0430	up	0.7835	up
MPF_contig_039110		0.0247	-0.2867	down	0.0953	up	0.7953	up	0.3819	up	1.0820	up	0.7001	up
MPF_contig_011517		0.0247	-0.0608	down	0.1437	up	0.6429	up	0.2045	up	0.7037	up	0.4992	up
MPF_LOC101075711.1.1	XM_003977781.1 PREDICTED: Takifugu rubripes ubiquitin carboxylterminal hydrolase 32-like (LOC101075711), mRNA	0.0248	-0.1714	down	0.0742	up	0.8539	up	0.2456	up	1.0253	up	0.7797	up
MPF_LOC101469029.1.2	XM_004540592.1 PREDICTED: Maylandia zebra inositoltetrakisphosphate 1-kinaselike (LOC101469029), mRNA	0.0248	0.1547	up	0.2245	up	0.7523	up	0.0699	up	0.5976	up	0.5278	up
MPF_LOC100700732.1.1	XM_003444889.1 PREDICTED: Oreochromis niloticus WAP four-disulfide core domain protein 3-like	0.0248	-0.2894	down	-0.2669	down	-1.5592	down	0.0225	up	-1.2697	down	-1.2922	down

	(LOC100700732), mRNA													
MPF_LOC101482897.1.9	XM_004572716.1 PREDICTED: Maylandia zebra elongation factor 1alpha-like (LOC101482897), mRNA	0.0248	0.0827	up	0.0211	up	-0.2565	down	-0.0615	down	-0.3392	down	-0.2776	down
MPF_contig_008212		0.0248	-0.0976	down	0.2163	up	0.7193	up	0.3139	up	0.8169	up	0.5031	up
MPF_LOC101464811.2.4	XM_004559330.1 PREDICTED: Maylandia zebra methionine aminopeptidase 1-like (LOC101464811), mRNA	0.0248	0.0019	up	0.1274	up	0.5471	up	0.1255	up	0.5452	up	0.4197	up
MPF_contig_026762		0.0248	-0.3081	down	-0.1802	down	0.9468	up	0.1279	up	1.2549	up	1.1270	up
MPF_contig_048139	XM_004545214.1 PREDICTED: Maylandia zebra protein FAM219A-like (LOC101484940), transcript variant X1, mRNA	0.0248	0.1302	up	-0.0435	down	1.0591	up	-0.1737	down	0.9289	up	1.1026	up
MPF_CC2D2A.1.1	XP_003439826.1 PREDICTED: coiled-coil and C2 domain-containing protein 2A [Oreochromis niloticus]	0.0250	0.2112	up	-0.0019	down	1.6979	up	-0.2131	down	1.4867	up	1.6998	up
MPF_LOC100696809.1.3	XP_003449500.1 PREDICTED: hypothetical protein LOC100696809 [Oreochromis niloticus]	0.0250	-0.0866	down	0.0565	up	0.8986	up	0.1431	up	0.9852	up	0.8421	up
MPF_contig_000345		0.0251	0.0285	up	0.2019	up	0.7071	up	0.1734	up	0.6785	up	0.5052	up

MPF_LOC100693642.1.1	XM_003454966.1 PREDICTED: Oreochromis niloticus adenylate kinase isoenzyme 1-like, transcript variant 1 (LOC100693642), mRNA	0.0251	0.0672	up	-1.3432	down	-2.9005	down	-1.4104	down	-2.9677	down	-1.5573	down
MPF_ZGC_153740.2.2	NM_001045430.1 Danio rerio zgc:153740 (zgc:153740), mRNA gb|BC122406.1| Danio rerio zgc:153740, mRNA (cDNA clone MGC:153740 IMAGE:8148169), complete cds	0.0251	-0.0909	down	0.1204	up	0.7881	up	0.2113	up	0.8789	up	0.6677	up
MPF_contig_015609		0.0252	0.1294	up	0.2867	up	0.6132	up	0.1573	up	0.4838	up	0.3265	up
MPF_LOC101477684.2.4	XM_004539594.1 PREDICTED: Maylandia zebra small EDRK-rich factor 2-like (LOC101477684), mRNA	0.0252	0.1563	up	0.1994	up	0.7773	up	0.0430	up	0.6209	up	0.5779	up
MPF_contig_029012		0.0252	-0.1883	down	-0.2017	down	-0.9938	down	-0.0134	down	-0.8055	down	-0.7921	down
MPF_LOC100709648.6.13	XM_003457730.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S4-like (LOC100709648), mRNA	0.0252	0.2007	up	0.2472	up	0.7856	up	0.0464	up	0.5849	up	0.5385	up
MPF_LOC101479905.1.2	XM_004554869.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase MARCH2-like (LOC101479905), mRNA	0.0253	-0.3386	down	0.0553	up	-0.9373	down	0.3940	up	-0.5987	down	-0.9927	down
MPF_LOC101479923.1.2	XM_004538167.1 PREDICTED: Maylandia zebra spidroin-2-like (LOC101479923), mRNA	0.0253	-0.0398	down	0.1621	up	0.7635	up	0.2018	up	0.8033	up	0.6014	up

MPF_contig_009970		0.0253	0.1487	up	0.2945	up	0.6501	up	0.1458	up	0.5014	up	0.3556	up
MPF_contig_028215		0.0253	-0.0919	down	0.1468	up	0.6485	up	0.2387	up	0.7404	up	0.5018	up
MPF_contig_010346		0.0253	-0.1713	down	-0.0475	down	0.6350	up	0.1238	up	0.8062	up	0.6825	up
MPF_LOC101472907.1.4	XM_004570821.1 PREDICTED: Maylandia zebra oxysterol-binding protein-related protein 5-like (LOC101472907), transcript variant X4, mRNA	0.0253	0.0325	up	0.0415	up	0.7895	up	0.0090	up	0.7570	up	0.7480	up
MPF_contig_035424		0.0253	-0.4408	down	-0.4316	down	-1.8354	down	0.0092	up	-1.3946	down	-1.4038	down
MPF_LOC101478245.1.1	XM_004561422.1 PREDICTED: Maylandia zebra huntingtin-interacting protein 1-like (LOC101478245), transcript variant X3, mRNA	0.0253	-0.1106	down	0.0441	up	0.9136	up	0.1547	up	1.0242	up	0.8695	up
MPF_contig_004038		0.0253	-0.4186	down	-0.4031	down	-2.1419	down	0.0155	up	-1.7233	down	-1.7388	down
MPF_LOC100693197.2.4	XP_003455593.1 PREDICTED: hypothetical protein LOC100693197 [Oreochromis niloticus]	0.0253	-0.3999	down	0.2477	up	-0.9295	down	0.6476	up	-0.5296	down	-1.1772	down
MPF_contig_037771		0.0253	-0.4459	down	-0.5804	down	-1.8114	down	-0.1345	down	-1.3655	down	-1.2310	down
MPF_SPCS.3.3	[BBH] SPCS_DANRE (sp|Q803A7) O-phosphoseryltRNA(Sec) selenium transferase OS=Danio rerio GN=sepsecs PE=2 SV=1	0.0253	-0.0503	down	0.1380	up	0.8073	up	0.1883	up	0.8576	up	0.6693	up
MPF_LOC100694733.1.1	XP_003438312.1 PREDICTED: pleckstrin-like	0.0253	-0.1668	down	-0.8912	down	-2.7478	down	-0.7244	down	-2.5810	down	-1.8566	down

	[Oreochromis niloticus]													
MPF_LOC101476538.5.1 1	XM_004575801.1 PREDICTED: Maylandia zebra 40S ribosomal protein S20-like (LOC101476538), mRNA	0.0253	-0.0338	down	0.2568	up	0.5370	up	0.2906	up	0.5708	up	0.2803	up
MPF_LOC101482740.1.1	XM_004559578.1 PREDICTED: Maylandia zebra LIM homeobox transcription factor 1-alphalike (LOC101482740), transcript variant X2, mRNA	0.0253	-0.0023	down	0.0580	up	0.8051	up	0.0603	up	0.8074	up	0.7471	up
MPF_LOC101480083.2.3	XM_004548835.1 PREDICTED: Maylandia zebra cytochrome c1, heme protein, mitochondrial-like (LOC101480083), mRNA	0.0253	-0.0250	down	-0.0018	down	0.8394	up	0.0232	up	0.8644	up	0.8412	up
MPF_NEMVEDRAFT_V1 G98162.1.1	XP_001635459.1 predicted protein [Nematostella vectensis]	0.0253	-0.1391	down	-0.0147	down	0.7467	up	0.1245	up	0.8858	up	0.7613	up
MPF_LOC101480950.1.1	XM_004572441.1 PREDICTED: Maylandia zebra chromodomain Y-like protein-like (LOC101480950), transcript variant X1, mRNA	0.0253	0.1134	up	1.0321	up	1.2469	up	0.9187	up	1.1335	up	0.2148	up
MPF_LOC101469036.1.1	XM_004542267.1 PREDICTED: Maylandia zebra platelet-activating factor acetylhydrolase-like (LOC101469036), transcript variant X1, mRNA	0.0253	0.1409	up	-0.2781	down	-3.0233	down	-0.4190	down	-3.1642	down	-2.7451	down
MPF_LOC101485903.2.2	XM_004575263.1 PREDICTED: Maylandia zebra low-density lipoprotein receptor-related protein 10like (LOC101485903), mRNA	0.0255	-0.0900	down	0.1616	up	0.5635	up	0.2516	up	0.6535	up	0.4019	up

MPF_LOC101471083.3.3	XM_004575129.1 PREDICTED: Maylandia zebra mucin-2-like (LOC101471083), mRNA	0.0255	0.3259	up	0.1233	up	1.9619	up	-0.2026	down	1.6360	up	1.8385	up
MPF_contig_022559		0.0255	-0.1288	down	0.1915	up	0.4972	up	0.3203	up	0.6260	up	0.3057	up

MPF_LOC100690512.1.1	XP_003438469.1 PREDICTED: hypothetical protein LOC100690512 [Oreochromis niloticus]	0.0256	-0.5597	down	-1.2918	down	-3.6178	down	-0.7320	down	-3.0581	down	-2.3261	down
MPF_XFIN.1.1	XFIN_XENLA (sp|P08045) Zinc finger protein Xfin OS=Xenopus laevis PE=1 SV=1	0.0256	0.1002	up	0.2657	up	1.4962	up	0.1655	up	1.3960	up	1.2305	up
MPF_contig_012813		0.0256	0.0009	up	0.3369	up	0.9135	up	0.3360	up	0.9127	up	0.5766	up
MPF_LOC101465495.1.1	XM_004538576.1 PREDICTED: Maylandia zebra lysine-specific demethylase 2B-like (LOC101465495), mRNA	0.0256	0.0156	up	0.2392	up	1.2160	up	0.2236	up	1.2004	up	0.9768	up
MPF_LOC100697077.1.1	XP_003449585.1 PREDICTED: leishmanolysinlike peptidase-like [Oreochromis niloticus]	0.0256	0.1658	up	0.4270	up	1.6115	up	0.2612	up	1.4457	up	1.1845	up
MPF_LOC101473877.1.1	XM_004541986.1 PREDICTED: Maylandia zebra cyclin-C-like (LOC101473877), mRNA	0.0256	0.2481	up	0.2335	up	1.3480	up	-0.0146	down	1.0999	up	1.1145	up
MPF_LOC101481842.1.8	XM_004554055.1 PREDICTED: Maylandia zebra ATP synthase subunit epsilon, mitochondrial-like (LOC101481842), transcript variant X2, mRNA	0.0256	0.0760	up	0.3343	up	0.6595	up	0.2583	up	0.5834	up	0.3251	up

MPF_LOC101477850.10.10	XM_004575562.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12-like (LOC101477850), mRNA	0.0256	-0.0401	down	0.1770	up	0.9196	up	0.2171	up	0.9597	up	0.7426	up
MPF_contig_023387		0.0256	-0.0109	down	0.2626	up	0.5374	up	0.2735	up	0.5483	up	0.2748	up
MPF_LOC101170275.1.4	XM_004072328.1 PREDICTED: Oryzias latipes uncharacterized LOC101170275 (LOC101170275), mRNA	0.0256	-0.0327	down	0.2822	up	1.1522	up	0.3149	up	1.1849	up	0.8700	up
MPF_LOC101464712.2.5	XM_004554817.1 PREDICTED: Maylandia zebra interferon alphainducible protein 27-like protein 2B-like (LOC101464712), transcript variant X2, mRNA	0.0256	0.0148	up	-0.1902	down	-1.5940	down	-0.2051	down	-1.6088	down	-1.4038	down
MPF_contig_006574		0.0256	0.0462	up	0.2523	up	0.4800	up	0.2061	up	0.4337	up	0.2277	up
MPF_MIR29B-2.1.1	NR_030037.1 Danio rerio microRNA 29b-2 (mir29b-2), microRNA	0.0256	-0.0254	down	0.2831	up	1.1375	up	0.3085	up	1.1629	up	0.8545	up
MPF_LOC101471856.1.1	XM_004551130.1 PREDICTED: Maylandia zebra heart- and neural crest derivatives-expressed protein 1-like (LOC101471856), mRNA	0.0256	0.2154	up	0.3859	up	0.8196	up	0.1705	up	0.6042	up	0.4337	up

MPF_RM55.1.1	[BBH] RM55_BOVIN (sp|P0C2B8) 39S ribosomal protein L55, mitochondrial OS=Bos taurus GN=MRPL55 PE=1 SV=1	0.0257	-0.0859	down	0.3025	up	0.9348	up	0.3884	up	1.0206	up	0.6322	up
MPF_contig_017839	XM_003437559.1 PREDICTED: Oreochromis niloticus cytochrome c oxidase subunit 5A, mitochondrial-like, transcript variant 1 (LOC100707142), mRNA	0.0258	0.0161	up	-0.2197	down	0.9812	up	-0.2357	down	0.9651	up	1.2009	up
MPF_contig_021053		0.0258	-0.3004	down	0.1594	up	1.9207	up	0.4597	up	2.2211	up	1.7614	up
MPF_LOC101167899.1.3	XM_004078356.1 PREDICTED: Oryzias latipes Friend leukemia integration 1 transcription factor-like (LOC101167899), mRNA	0.0258	0.8087	up	-0.0058	down	-1.1689	down	-0.8145	down	-1.9776	down	-1.1631	down
MPF_LOC101464934.1.3	XM_004565357.1 PREDICTED: Maylandia zebra matrix metalloproteinase-14-like (LOC101464934), mRNA	0.0258	-0.6006	down	-1.8331	down	-4.2830	down	-1.2325	down	-3.6825	down	-2.4499	down
MPF_LOC101472403.3.3	XM_004569122.1 PREDICTED: Maylandia zebra G1/S-specific cyclin-D2like (LOC101472403), transcript variant X2, mRNA	0.0258	0.0659	up	0.1298	up	1.4569	up	0.0639	up	1.3910	up	1.3272	up
MPF_LOC101483587.1.1	XM_004558848.1 PREDICTED: Maylandia zebra ubiquitin-conjugating enzyme E2 T-like (LOC101483587), transcript variant X2, mRNA	0.0258	0.0828	up	0.3758	up	1.2335	up	0.2931	up	1.1507	up	0.8577	up
MPF_contig_044730		0.0259	0.1291	up	0.1456	up	0.5439	up	0.0165	up	0.4147	up	0.3983	up

MPF_LOC101470907.4.4	XM_004574555.1 PREDICTED: Maylandia zebra adapter molecule crklike (LOC101470907), mRNA	0.0260	0.1818	up	0.2585	up	0.6211	up	0.0768	up	0.4393	up	0.3625	up
MPF_ZGC_110848.1.1	NM_001013329.1 Danio rerio zgc:110848 (zgc:110848), mRNA gb|BC090793.1| Danio rerio zgc:110848, mRNA (cDNA clone MGC:110848 IMAGE:7156048), complete cds	0.0260	-0.2976	down	0.0399	up	0.7289	up	0.3375	up	1.0265	up	0.6889	up
MPF_contig_018234		0.0260	-0.0217	down	0.1741	up	0.7450	up	0.1958	up	0.7667	up	0.5709	up
MPF_LOC100710653.2.2	XM_003442016.1 PREDICTED: Oreochromis niloticus prohibitin-like (LOC100710653), mRNA	0.0260	0.0612	up	0.0548	up	0.9335	up	-0.0065	down	0.8722	up	0.8787	up
MPF_LOC100692111.1.1	XP_003456389.1 PREDICTED: transmembrane protein 180-like [Oreochromis niloticus]	0.0260	-0.0323	down	0.2935	up	1.2247	up	0.3258	up	1.2570	up	0.9312	up
MPF_LOC101471788.3.4	XM_004561028.1 PREDICTED: Maylandia zebra ubiquitin-conjugating enzyme E2 E2-like (LOC101471788), mRNA	0.0260	0.2579	up	0.3661	up	0.8047	up	0.1082	up	0.5468	up	0.4386	up
MPF_LOC101467183.1.2	XM_004550296.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101467183), transcript variant X7, mRNA	0.0260	-0.3916	down	-1.0456	down	-3.0964	down	-0.6540	down	-2.7048	down	-2.0508	down
MPF_LOC100705062.1.6	XM_003446407.1 PREDICTED: Oreochromis niloticus hypothetical protein	0.0260	0.0151	up	-0.0550	down	0.8357	up	-0.0701	down	0.8206	up	0.8907	up

	LOC100705062 (LOC100705062), mRNA													
MPF_LOC101483661.2.5	XM_004572907.1 PREDICTED: Maylandia zebra traf2 and NCKinteracting protein kinase-like (LOC101483661), transcript variant X1, mRNA	0.0262	-0.0750	down	-0.0295	down	0.8153	up	0.0455	up	0.8903	up	0.8448	up
MPF_LOC101485593.1.1	XM_004543054.1 PREDICTED: Maylandia zebra protein FAM65A-like (LOC101485593), transcript variant X2, mRNA	0.0262	0.0805	up	0.0521	up	0.7799	up	-0.0284	down	0.6993	up	0.7277	up
MPF_contig_014638		0.0262	-0.2254	down	0.1351	up	-1.2649	down	0.3604	up	-1.0395	down	-1.3999	down
MPF_contig_031251		0.0262	0.0077	up	0.1805	up	0.7510	up	0.1728	up	0.7433	up	0.5704	up
MPF_LOC101483898.1.1	XM_004563146.1 PREDICTED: Maylandia zebra fragile X mental retardation protein 1-like (LOC101483898), mRNA	0.0262	0.3135	up	0.5070	up	2.1704	up	0.1935	up	1.8568	up	1.6634	up
MPF_contig_045495		0.0262	-0.1130	down	-0.1957	down	0.6305	up	-0.0827	down	0.7436	up	0.8262	up
MPF_LOC101076840.1.1	XM_003974902.1 PREDICTED: Takifugu rubripes chemokine-like receptor 1-like (LOC101076840), mRNA	0.0262	0.0215	up	-1.2688	down	-3.0280	down	-1.2903	down	-3.0495	down	-1.7592	down
MPF_LOC101064336.1.1	XP_003970294.1 PREDICTED: leucine-rich repeat neuronal protein 4-like [Takifugu rubripes]	0.0262	0.1157	up	-0.0047	down	1.0465	up	-0.1204	down	0.9308	up	1.0513	up

MPF_LOC101487136.1.3	XM_004568462.1 PREDICTED: Maylandia zebra probable serine/threonine-protein kinase kinX-like (LOC101487136), mRNA	0.0262	-0.1290	down	-0.0472	down	0.7411	up	0.0818	up	0.8701	up	0.7883	up
MPF_LOC101481552.5.41	XM_004575656.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101481552), mRNA	0.0262	-0.3659	down	-0.0169	down	0.6855	up	0.3491	up	1.0515	up	0.7024	up
MPF_LOC101474532.1.1	XM_004564475.1 PREDICTED: Maylandia zebra zinc finger protein 143like (LOC101474532), transcript variant X2, mRNA	0.0264	0.0249	up	0.0851	up	0.8225	up	0.0602	up	0.7976	up	0.7374	up
MPF_LOC101483692.1.1	XM_004555993.1 PREDICTED: Maylandia zebra protein FAM135A-like (LOC101483692), transcript variant X2, mRNA	0.0265	-0.0967	down	0.1317	up	0.7981	up	0.2284	up	0.8948	up	0.6664	up
MPF_contig_016490		0.0265	-0.0645	down	-0.1476	down	0.7082	up	-0.0831	down	0.7727	up	0.8558	up
MPF_LOC100710021.1.1	XP_003438623.1 PREDICTED: LOW QUALITY PROTEIN: BAH and coiledcoil domain-containing protein 1-like [Oreochromis niloticus]	0.0265	-0.0790	down	-0.2079	down	0.6536	up	-0.1289	down	0.7325	up	0.8615	up
MPF_LOC101473386.1.1	XM_004568854.1 PREDICTED: Maylandia zebra neurotrophin-3-like (LOC101473386), mRNA	0.0265	0.1842	up	0.4540	up	1.0216	up	0.2698	up	0.8374	up	0.5676	up
MPF_contig_016522		0.0265	-0.1661	down	0.1341	up	0.5940	up	0.3001	up	0.7601	up	0.4600	up
MPF_PRG4.3.4	PRG4_MOUSE (sp|Q9JM99) Proteoglycan 4 OS=Mus musculus GN=Prg4 PE=1 SV=2	0.0265	0.1209	up	-0.9950	down	-2.1558	down	-1.1159	down	-2.2767	down	-1.1608	down

MPF_LOC101484751.1.1	XM_004545027.1 PREDICTED: Maylandia zebra natural resistanceassociated macrophage protein 2-like (LOC101484751), transcript variant X5, mRNA	0.0265	0.1358	up	0.2639	up	1.2235	up	0.1281	up	1.0877	up	0.9596	up
MPF_LOC101074275.1.1	XP_003968653.1 PREDICTED: transforming growth factor beta-1-like [Takifugu rubripes]	0.0265	-0.4649	down	-1.8064	down	-4.0437	down	-1.3415	down	-3.5789	down	-2.2374	down
MPF_contig_019861		0.0265	-0.0345	down	0.2002	up	0.7354	up	0.2347	up	0.7699	up	0.5352	up
MPF_contig_029262		0.0265	-0.1410	down	-0.2459	down	-1.0332	down	-0.1050	down	-0.8922	down	-0.7873	down
MPF_LOC100704036.1.1	XM_003459031.1 PREDICTED: Oreochromis niloticus ADP-ribosylation factor-related protein 1-like (LOC100704036), mRNA	0.0265	-0.1067	down	0.1054	up	0.7147	up	0.2121	up	0.8214	up	0.6093	up
MPF_contig_044368		0.0265	0.0400	up	0.2840	up	0.8971	up	0.2440	up	0.8571	up	0.6131	up
MPF_contig_037880		0.0265	0.0954	up	0.1641	up	0.4667	up	0.0687	up	0.3714	up	0.3026	up
MPF_LOC101469798.3.3	XM_004544314.1 PREDICTED: Maylandia zebra ubiquitin-like protein 4A-like (LOC101469798), mRNA	0.0265	0.0568	up	0.2506	up	0.8689	up	0.1937	up	0.8121	up	0.6183	up
MPF_contig_042898		0.0265	-0.0948	down	0.0136	up	0.5377	up	0.1083	up	0.6325	up	0.5241	up
MPF_LOC101466337.8.22	XM_004575687.1 PREDICTED: Maylandia zebra prothymosin alpha-Blike (LOC101466337), mRNA	0.0265	0.0337	up	0.1775	up	0.6467	up	0.1438	up	0.6130	up	0.4692	up

MPF_contig_043407		0.0265	-0.0817	down	0.1577	up	0.9333	up	0.2395	up	1.0150	up	0.7756	up
MPF_contig_004093		0.0265	0.0326	up	0.2117	up	0.6947	up	0.1791	up	0.6621	up	0.4830	up
MPF_HECTD1.2.4	XM_003451209.1 PREDICTED: Oreochromis niloticus HECT domain containing 1 (HECTD1), mRNA	0.0265	-0.0261	down	-0.0089	down	0.8427	up	0.0173	up	0.8688	up	0.8516	up
MPF_contig_000517		0.0265	0.1009	up	0.1226	up	0.5251	up	0.0217	up	0.4242	up	0.4025	up
MPF_LOC101481957.1.1	XR_191362.1 PREDICTED: Maylandia zebra isobutyrylCoA dehydrogenase, mitochondrial-like (LOC101481957), transcript variant X2, misc_RNA	0.0265	0.0716	up	0.1477	up	0.6379	up	0.0761	up	0.5663	up	0.4902	up
MPF_LOC101154860.1.1	XP_004068951.1 PREDICTED: protein FAM107B-like [Oryzias latipes]	0.0265	0.1246	up	0.3070	up	0.8190	up	0.1824	up	0.6944	up	0.5120	up
MPF_contig_015434		0.0266	0.0031	up	0.3278	up	1.2647	up	0.3247	up	1.2617	up	0.9370	up
MPF_contig_001934		0.0266	-0.0375	down	0.2812	up	0.8659	up	0.3187	up	0.9034	up	0.5847	up
MPF_contig_032569		0.0266	0.1848	up	0.3151	up	0.6551	up	0.1304	up	0.4704	up	0.3400	up
MPF_AHNK.16.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiationassociated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.0266	-0.2709	down	-1.9671	down	-4.7746	down	-1.6963	down	-4.5038	down	-2.8075	down

MPF_LOC100702758.9.10	XM_003455412.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L27a-like (LOC100702758), mRNA	0.0266	0.0306	up	0.1660	up	0.6033	up	0.1354	up	0.5728	up	0.4374	up
MPF_LOC100692165.1.1	XP_003445661.1 PREDICTED: lysine-specific demethylase 2B-like [Oreochromis niloticus]	0.0266	-0.0298	down	-0.3793	down	0.6691	up	-0.3495	down	0.6989	up	1.0484	up
MPF_PPP6.1.1	PPP6_RAT (sp|Q64620) Serine/threonine-protein phosphatase 6 catalytic subunit OS=Rattus norvegicus GN=Ppp6c PE=2 SV=2	0.0266	0.2270	up	0.6703	up	1.1041	up	0.4434	up	0.8771	up	0.4337	up
MPF_LOC101469433.1.1	XM_004566542.1 PREDICTED: Maylandia zebra UDP-glucose 4epimerase-like (LOC101469433), transcript variant X1, mRNA	0.0266	-0.0801	down	0.3199	up	0.8126	up	0.4000	up	0.8927	up	0.4928	up
MPF_contig_035284		0.0266	-0.2164	down	0.0670	up	-0.8562	down	0.2833	up	-0.6398	down	-0.9232	down
MPF_LOC100693046.1.1	XP_003459711.1 PREDICTED: ribosome biogenesis protein bop1-like [Oreochromis niloticus]	0.0266	-0.0549	down	0.1639	up	0.7720	up	0.2189	up	0.8269	up	0.6080	up
MPF_LOC101469326.1.1	XM_004540593.1 PREDICTED: Maylandia zebra putative E3 ubiquitinprotein ligase UBR7-like (LOC101469326), mRNA	0.0266	-0.2036	down	0.2683	up	0.8423	up	0.4719	up	1.0458	up	0.5739	up
MPF_LOC100708025.2.2	XM_003456564.1 PREDICTED: Oreochromis niloticus cytohesin-4-like	0.0266	-0.7909	down	-1.1993	down	-3.5044	down	-0.4084	down	-2.7135	down	-2.3051	down

	(LOC100708025), mRNA													
MPF_LOC101465867.1.3	XM_004556121.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase TRIM21-like (LOC101465867), mRNA	0.0266	0.2745	up	0.4446	up	0.8780	up	0.1701	up	0.6036	up	0.4335	up
MPF_LOC100693225.1.1	XM_003440194.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693225 (LOC100693225), mRNA	0.0266	-0.1299	down	0.0408	up	0.7340	up	0.1707	up	0.8638	up	0.6931	up
MPF_contig_023395		0.0266	-1.2933	down	-1.0699	down	-1.9746	down	0.2233	up	-0.6814	down	-0.9047	down
MPF_LOC101175132.1.2	XP_004085856.1 PREDICTED: beta-enolaselike isoform 2 [Oryzias latipes]	0.0266	-0.0520	down	0.2175	up	0.9716	up	0.2695	up	1.0236	up	0.7541	up
MPF_LOC100691095.1.2	XM_003446686.1 PREDICTED: Oreochromis niloticus AT-rich interactive domain-containing protein 1Blike (LOC100691095), mRNA	0.0266	0.0054	up	0.2057	up	0.8365	up	0.2004	up	0.8311	up	0.6307	up
MPF_COG8.1.1	XM_003437743.1 PREDICTED: Oreochromis niloticus component of oligomeric golgi complex 8 (COG8), mRNA	0.0267	0.2217	up	0.1358	up	0.9655	up	-0.0859	down	0.7438	up	0.8297	up
MPF_LOC100695229.4.4	XM_003450269.1 PREDICTED: Oreochromis niloticus induced myeloid leukemia cell differentiation protein Mcl-1 homolog (LOC100695229), mRNA	0.0267	-0.0288	down	0.0434	up	0.7149	up	0.0722	up	0.7437	up	0.6715	up

MPF_contig_034807		0.0267	0.1715	up	0.3064	up	0.6342	up	0.1349	up	0.4628	up	0.3278	up
MPF_contig_036894		0.0267	0.1378	up	0.3227	up	0.8967	up	0.1848	up	0.7589	up	0.5741	up

MPF_CELF2.7.8	XM_003786821.1 PREDICTED: Otolemur garnettii CUGBP, Elav-like family member 2, transcript variant 4 (CELF2), mRNA	0.0267	0.0646	up	0.2338	up	0.8670	up	0.1691	up	0.8024	up	0.6333	up
MPF_LOC101074317.1.1	XP_003977744.1 PREDICTED: thrombospondin type-1 domain-containing protein 7Alike [Takifugu rubripes]	0.0267	-0.0450	down	0.3222	up	1.2116	up	0.3672	up	1.2566	up	0.8894	up
MPF_LOC100534480.2.2	XM_003447448.1 PREDICTED: Oreochromis niloticus inducible cAMP early repressor (LOC100534480), mRNA	0.0267	-0.1566	down	-0.5260	down	-1.9393	down	-0.3695	down	-1.7828	down	-1.4133	down
MPF_LOC101474085.1.2	XM_004568504.1 PREDICTED: Maylandia zebra cyclin-Y-like (LOC101474085), transcript variant X4, mRNA	0.0267	-0.0112	down	0.1741	up	0.6267	up	0.1853	up	0.6379	up	0.4526	up
MPF_LOC100084244.1.1	XP_001514751.2 PREDICTED: beta-arrestin-1like, partial [Ornithorhynchus anatinus]	0.0267	-0.0994	down	0.4154	up	0.7053	up	0.5148	up	0.8048	up	0.2899	up
MPF_LOC101465348.1.6	XM_004570620.1 PREDICTED: Maylandia zebra protein ZNF365-like (LOC101465348), transcript variant X2, mRNA	0.0267	0.0379	up	0.1960	up	0.6081	up	0.1581	up	0.5702	up	0.4121	up
MPF_LOC101482217.1.2	XM_004571183.1 PREDICTED: Maylandia zebra G protein pathway suppressor 2-like	0.0267	0.1163	up	0.4174	up	0.8534	up	0.3011	up	0.7371	up	0.4360	up

	(LOC101482217), mRNA													
MPF_LOC100695658.1.1	XP_003446751.1 PREDICTED: pleckstrin homology domain-containing family G member 3-like [Oreochromis niloticus]	0.0267	-0.1538	down	0.5148	up	1.4565	up	0.6686	up	1.6103	up	0.9417	up
MPF_LOC101478931.1.1	XM_004546204.1 PREDICTED: Maylandia zebra collagen alpha-3(IX) chain-like (LOC101478931), mRNA	0.0267	-0.0612	down	-0.1907	down	0.9391	up	-0.1295	down	1.0003	up	1.1298	up
MPF_ZO71.3.10	ZO71_XENLA (sp|P18751) Oocyte zinc finger protein XlCOF7.1 (Fragment) OS=Xenopus laevis PE=2 SV=1	0.0267	-0.0569	down	0.3164	up	1.1797	up	0.3733	up	1.2366	up	0.8634	up
MPF_LOC101169385.1.3	XP_004077303.1 PREDICTED: zinc finger protein 318-like [Oryzias latipes]	0.0267	-0.0228	down	0.0858	up	1.0294	up	0.1086	up	1.0522	up	0.9436	up
MPF_LOC101474972.2.4	XM_004576316.1 PREDICTED: Maylandia zebra zinc finger protein 771like (LOC101474972), partial mRNA	0.0267	0.1606	up	0.2185	up	0.6466	up	0.0579	up	0.4860	up	0.4281	up
MPF_LOC101163553.1.1	XP_004066464.1 PREDICTED: zinc finger protein 658-like [Oryzias latipes]	0.0268	0.0789	up	0.1097	up	1.2431	up	0.0308	up	1.1642	up	1.1335	up

MPF_ADH.1.1	ADH_SULAC (sp|Q4J781) NAD-dependent alcohol dehydrogenase OS=Sulfolobus acidocaldarius (strain ATCC 33909 / DSM 639 / JCM 8929 / NBRC 15157 / NCIMB 11770) GN=adh PE=3 SV=1	0.0268	0.2151	up	0.4332	up	1.0909	up	0.2181	up	0.8759	up	0.6578	up
MPF_contig_045562		0.0268	0.1369	up	0.3847	up	1.0014	up	0.2478	up	0.8645	up	0.6166	up
MPF_contig_024095		0.0268	-0.0005	down	0.2684	up	-1.0180	down	0.2689	up	-1.0175	down	-1.2863	down
MPF_contig_026229	XM_004562887.1 PREDICTED: Maylandia zebra ras-related protein Rab3D-like (LOC101465588), transcript variant X1, mRNA	0.0268	0.1597	up	0.3832	up	1.0982	up	0.2234	up	0.9384	up	0.7150	up
MPF_LOC101478422.1.2	XM_004560767.1 PREDICTED: Maylandia zebra parvalbumin-7-like (LOC101478422), transcript variant X2, mRNA	0.0268	0.0306	up	0.1272	up	0.7890	up	0.0966	up	0.7583	up	0.6617	up
MPF_LOC101465129.16.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNAbinding protein A-like (LOC101465129), transcript variant X4, mRNA	0.0268	-0.1350	down	0.1473	up	1.0569	up	0.2823	up	1.1920	up	0.9097	up
MPF_LOC101471973.1.1	XM_004554015.1 PREDICTED: Maylandia zebra uncharacterized LOC101471973 (LOC101471973), mRNA	0.0268	0.1276	up	0.3203	up	0.6287	up	0.1928	up	0.5012	up	0.3084	up
MPF_LOC101485262.1.1	XM_004572362.1 PREDICTED: Maylandia zebra membrane-spanning 4domains subfamily A member 12-like (LOC101485262),	0.0268	-0.5153	down	-1.3526	down	-3.2836	down	-0.8373	down	-2.7684	down	-1.9311	down

	mRNA													
MPF_LOC101469939.1.2	XM_004552621.1 PREDICTED: Maylandia zebra peripheral plasma membrane protein CASK-like (LOC101469939), transcript variant X3, mRNA	0.0268	-0.0619	down	-0.0665	down	1.3115	up	-0.0047	down	1.3734	up	1.3780	up
MPF_contig_043293		0.0268	-0.1122	down	0.0525	up	0.7542	up	0.1646	up	0.8663	up	0.7017	up
MPF_LOC100709543.1.1	XP_003454327.1 PREDICTED: cortactinbinding protein 2-like [Oreochromis niloticus]	0.0268	0.0977	up	0.1762	up	0.7661	up	0.0785	up	0.6685	up	0.5899	up
MPF_LOC100706818.1.9	XR_134822.1 PREDICTED: Oreochromis niloticus selenoprotein Pa-like (LOC100706818), miscRNA	0.0268	-0.0291	down	0.3023	up	1.1626	up	0.3313	up	1.1917	up	0.8604	up
MPF_LOC100690938.3.3	XP_003451378.1 PREDICTED: microtubuleassociated protein 1B-like [Oreochromis niloticus]	0.0268	-0.0814	down	0.1024	up	0.7911	up	0.1837	up	0.8725	up	0.6888	up
MPF_contig_033110		0.0269	0.0065	up	0.2129	up	0.8784	up	0.2063	up	0.8719	up	0.6655	up
MPF_LOC100697918.2.2	XP_003438738.1 PREDICTED: nuclear prelamin A recognition factorlike [Oreochromis niloticus]	0.0269	-0.0071	down	0.2958	up	1.6737	up	0.3028	up	1.6808	up	1.3779	up
MPF_contig_034209	XM_003198881.1 PREDICTED: Danio rerio retrotransposable element Tf2 155 kDa protein type 1like (LOC100535308), mRNA	0.0269	-0.7790	down	-0.5041	down	-2.6174	down	0.2749	up	-1.8384	down	-2.1133	down

MPF_LOC101471764.1.1	XM_004575032.1 PREDICTED: Maylandia zebra tripartite motifcontaining protein 16-like (LOC101471764), mRNA	0.0269	0.2732	up	0.5058	up	0.8937	up	0.2326	up	0.6205	up	0.3879	up
MPF_LOC100710715.2.3	XM_003458665.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100710715 (LOC100710715), mRNA	0.0269	0.0695	up	0.2284	up	0.7282	up	0.1589	up	0.6587	up	0.4998	up
MPF_LOC100696287.1.2	XP_003450735.1 PREDICTED: C-type lectin domain family 9 member Alike isoform 1 [Oreochromis niloticus]	0.0269	-0.3181	down	-2.1708	down	-4.6485	down	-1.8527	down	-4.3304	down	-2.4777	down
MPF_LOC100708209.1.1	XP_003456856.1 PREDICTED: NACHT, LRR and PYD domains-containing protein 3-like [Oreochromis niloticus]	0.0269	0.1342	up	0.2385	up	0.9308	up	0.1043	up	0.7966	up	0.6924	up
MPF_LOC101480883.1.1	XM_004553334.1 PREDICTED: Maylandia zebra choline kinase alphalike (LOC101480883), mRNA	0.0269	0.0900	up	0.1405	up	0.6125	up	0.0505	up	0.5226	up	0.4721	up
MPF_ACTB2.1.2	ACTB2_TAKRU (sp|P53485) Actin, cytoplasmic 2 OS=Takifugu rubripes GN=actbb PE=3 SV=1	0.0269	-0.2344	down	-0.3426	down	-1.1405	down	-0.1082	down	-0.9060	down	-0.7979	down
MPF_contig_007138	XM_004574682.1 PREDICTED: Maylandia zebra synaptogyrin-1-like (LOC101484327), transcript variant X1, mRNA	0.0269	0.0096	up	0.4206	up	1.6280	up	0.4110	up	1.6184	up	1.2074	up

MPF_contig_010587	XM_004538157.1 PREDICTED: Maylandia zebra AP2-associated protein kinase 1-like (LOC101477308), transcript variant X1, mRNA	0.0269	-0.2827	down	0.6093	up	0.5403	up	0.8920	up	0.8230	up	-0.0690	down
MPF_LOC101487747.1.2	XM_004573537.1 PREDICTED: Maylandia zebra membrane-spanning 4domains subfamily A member 15-like (LOC101487747), transcript variant X3, mRNA	0.0269	0.6401	up	-0.5856	down	-2.9920	down	-1.2257	down	-3.6321	down	-2.4064	down
MPF_LOC101468249.1.2	XM_004541040.1 PREDICTED: Maylandia zebra clathrin light chain Blike (LOC101468249), transcript variant X2, mRNA	0.0269	-0.0492	down	0.2654	up	1.0925	up	0.3146	up	1.1416	up	0.8271	up
MPF_LOC100698283.1.1	XP_003438995.1 PREDICTED: NEDD8-activating enzyme E1 catalytic subunit-like isoform 2 [Oreochromis niloticus]	0.0269	0.0395	up	0.4124	up	0.6879	up	0.3729	up	0.6484	up	0.2755	up
MPF_LOC101160483.1.1	XP_004071578.1 PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 1like [Oryzias latipes]	0.0269	0.1809	up	0.2843	up	0.6148	up	0.1034	up	0.4339	up	0.3305	up
MPF_contig_009893		0.0270	-0.7640	down	-0.2375	down	-2.1772	down	0.5265	up	-1.4132	down	-1.9397	down
MPF_LOC101478384.1.1	XM_004547890.1 PREDICTED: Maylandia zebra coiled-coil domaincontaining protein 126-like (LOC101478384), transcript variant X3, mRNA	0.0270	0.0294	up	0.1350	up	1.1311	up	0.1056	up	1.1017	up	0.9960	up
MPF_contig_032690		0.0270	-0.1354	down	0.0320	up	-1.9389	down	0.1674	up	-1.8035	down	-1.9709	down

MPF_LOC101467046.1.1	XM_004543467.1 PREDICTED: Maylandia zebra lysM and putative peptidoglycan-binding domain-containing protein 2like (LOC101467046), mRNA	0.0270	-0.0906	down	0.1860	up	1.0886	up	0.2766	up	1.1792	up	0.9026	up
MPF_LOC101486255.2.2	XM_004540470.1 PREDICTED: Maylandia zebra mitochondrial fission regulator 1-like (LOC101486255), mRNA	0.0270	-0.1979	down	0.1248	up	0.7913	up	0.3227	up	0.9892	up	0.6665	up
MPF_LOC101468249.2.2	XM_004541040.1 PREDICTED: Maylandia zebra clathrin light chain Blike (LOC101468249), transcript variant X2, mRNA	0.0270	-0.0363	down	0.2468	up	1.0655	up	0.2831	up	1.1018	up	0.8187	up
MPF_LOC101164389.1.1	XP_004067408.1 PREDICTED: ATPdependent RNA helicase SUPV3L1, mitochondrial-like [Oryzias latipes]	0.0270	0.2187	up	0.3869	up	1.3251	up	0.1682	up	1.1064	up	0.9383	up
MPF_LOC101474259.2.2	XM_004541897.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF19B-like (LOC101474259), transcript variant X2, mRNA	0.0270	-0.5059	down	-1.5300	down	-3.1176	down	-1.0241	down	-2.6117	down	-1.5876	down
MPF_contig_032817		0.0270	0.0068	up	0.1579	up	0.9141	up	0.1511	up	0.9072	up	0.7562	up
MPF_contig_045428		0.0270	0.2104	up	0.2744	up	1.0462	up	0.0640	up	0.8358	up	0.7718	up
MPF_LOC100705473.1.1	XM_003439642.1 PREDICTED: Oreochromis niloticus probable ATPdependent RNA helicase YTHDC2-like	0.0270	-0.0056	down	0.1117	up	0.5820	up	0.1172	up	0.5876	up	0.4703	up

	(LOC100705473), mRNA													
MPF_LOC101484769.1.1	XM_004571907.1 PREDICTED: Maylandia zebra transcription factor MafB-like (LOC101484769), mRNA	0.0270	-0.5551	down	-1.5757	down	-4.0126	down	-1.0207	down	-3.4576	down	-2.4369	down
MPF_LOC100711421.1.1	XM_003456495.1 PREDICTED: Oreochromis niloticus 3-oxo-5-alphasteroid 4-dehydrogenase 2like (LOC100711421), mRNA	0.0270	0.0721	up	0.1978	up	0.9980	up	0.1257	up	0.9259	up	0.8002	up
MPF_contig_036071		0.0270	-0.0410	down	-0.0659	down	0.7987	up	-0.0249	down	0.8397	up	0.8646	up
MPF_LOC101487935.1.1	XM_004551853.1 PREDICTED: Maylandia zebra myelomaoverexpressed gene 2 protein homolog (LOC101487935), mRNA	0.0270	0.2885	up	0.4212	up	1.3016	up	0.1327	up	1.0131	up	0.8804	up
MPF_contig_015549		0.0270	-0.4037	down	-0.5389	down	-1.8545	down	-0.1352	down	-1.4508	down	-1.3156	down
MPF_LOC101486956.2.2	XM_004570349.1 PREDICTED: Maylandia zebra caskin-1-like (LOC101486956), transcript variant X6, mRNA	0.0270	0.1339	up	0.1732	up	1.1055	up	0.0392	up	0.9715	up	0.9323	up
MPF_contig_017040		0.0270	-0.0984	down	0.1001	up	0.6957	up	0.1985	up	0.7941	up	0.5956	up
MPF_contig_034180		0.0270	-0.3925	down	-0.1209	down	-1.4125	down	0.2716	up	-1.0201	down	-1.2917	down

MPF_LOC100709671.1.2	XM_003460204.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100709671 (LOC100709671), mRNA	0.0270	-1.0162	down	-0.4313	down	-2.3850	down	0.5849	up	-1.3688	down	-1.9537	down
MPF_LOC100702868.3.3	XM_003439549.1 PREDICTED: Oreochromis niloticus protein FAM169Blike (LOC100702868), mRNA	0.0270	0.0002	up	0.0087	up	0.8650	up	0.0085	up	0.8648	up	0.8563	up
MPF_CYYR1.18.19	NM_212882.1 Danio rerio cysteine and tyrosine-rich protein 1 (cyyr1), mRNA gb|BC066606.1| Danio rerio cysteine and tyrosine-rich protein 1, mRNA (cDNA clone MGC:77252 IMAGE:6963826), complete cds	0.0270	0.0238	up	0.1786	up	0.6220	up	0.1548	up	0.5981	up	0.4433	up
MPF_contig_020212		0.0270	-0.3088	down	-1.8353	down	-4.8756	down	-1.5265	down	-4.5667	down	-3.0402	down
MPF_RS7.7.10	RS7_TAKRU (sp|P50894) 40S ribosomal protein S7 OS=Takifugu rubripes GN=rps7 PE=3 SV=1	0.0270	0.2169	up	-1.0560	down	-2.3646	down	-1.2730	down	-2.5815	down	-1.3086	down
MPF_contig_023785		0.0270	-0.0127	down	0.2745	up	0.7563	up	0.2872	up	0.7691	up	0.4818	up
MPF_LOC101481390.1.1	XM_004561963.1 PREDICTED: Maylandia zebra protein phosphatase inhibitor 2-like (LOC101481390), mRNA	0.0270	-0.0855	down	0.2348	up	0.7881	up	0.3202	up	0.8736	up	0.5533	up
MPF_UBIQP.10.13	UBIQP_XENLA (sp|P62972) Polyubiquitin (Fragment) OS=Xenopus laevis PE=1	0.0270	0.3489	up	0.3696	up	0.5859	up	0.0208	up	0.2371	up	0.2163	up

	SV=2													
MPF_LOC101471171.1.1	XM_004549062.1 PREDICTED: Maylandia zebra dolichol-phosphate mannosyltransferase subunit 3-like (LOC101471171), mRNA	0.0270	0.0256	up	0.0739	up	0.6414	up	0.0483	up	0.6158	up	0.5675	up
MPF_LOC101482643.1.4	XM_004563682.1 PREDICTED: Maylandia zebra importin subunit alpha-7-like (LOC101482643), mRNA	0.0270	-0.0464	down	0.0281	up	0.9962	up	0.0746	up	1.0426	up	0.9680	up
MPF_LOC101472300.1.1	XM_004568586.1 PREDICTED: Maylandia zebra uncharacterized LOC101472300 (LOC101472300), mRNA	0.0270	-0.0366	down	-1.8389	down	-4.6327	down	-1.8023	down	-4.5961	down	-2.7939	down
MPF_contig_026907		0.0270	0.2041	up	-1.7240	down	-3.6869	down	-1.9281	down	-3.8910	down	-1.9629	down
MPF_LOC101168697.1.1	XP_004068278.1 PREDICTED: zinc finger CCCH domain-containing protein 3-like [Oryzias latipes]	0.0270	-0.0049	down	0.1266	up	0.9002	up	0.1315	up	0.9051	up	0.7736	up
MPF_PDK2.2.4	PDK2_HUMAN (sp|Q15119) [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial OS=Homo sapiens GN=PDK2 PE=1 SV=2	0.0270	-0.0009	down	0.1380	up	0.9158	up	0.1389	up	0.9167	up	0.7778	up
MPF_contig_019917		0.0270	-0.2452	down	-1.3476	down	-2.6916	down	-1.1025	down	-2.4464	down	-1.3439	down

MPF_LOC101473100.1.1	XM_004547401.1 PREDICTED: Maylandia zebra plasma membrane calcium-transporting ATPase 1-like (LOC101473100), transcript variant X3, mRNA	0.0270	0.0108	up	0.3849	up	0.9032	up	0.3740	up	0.8924	up	0.5183	up
MPF_LOC100707167.1.1	XM_003442256.1 PREDICTED: Oreochromis niloticus calretinin-like (LOC100707167), mRNA	0.0270	-0.2858	down	-0.0698	down	0.6493	up	0.2160	up	0.9351	up	0.7191	up
MPF_contig_011614	XM_004547127.1 PREDICTED: Maylandia zebra RING finger protein 165-like (LOC101475525), transcript variant X2, mRNA	0.0270	0.3888	up	0.3189	up	1.1157	up	-0.0699	down	0.7269	up	0.7968	up
MPF_LOC101485781.1.4	XM_004542132.1 PREDICTED: Maylandia zebra bromo adjacent homology domain-containing 1 protein-like (LOC101485781), mRNA	0.0270	0.4707	up	0.2963	up	0.9440	up	-0.1744	down	0.4733	up	0.6477	up
MPF_LOC101463863.1.2	XR_190895.1 PREDICTED: Maylandia zebra palmitoyltransferase ZDHHC7-like (LOC101463863), transcript variant X2, misc_RNA	0.0270	-0.1483	down	0.0420	up	0.6936	up	0.1903	up	0.8419	up	0.6516	up
MPF_DHR13.1.1	DHR13_BOVIN (sp|Q17QU7) Dehydrogenase/reductase SDR family member 13 OS=Bos taurus GN=DHRS13 PE=2 SV=1	0.0270	-0.0231	down	0.1504	up	0.8636	up	0.1736	up	0.8867	up	0.7132	up
MPF_contig_032499		0.0270	-0.0704	down	0.1197	up	0.7117	up	0.1901	up	0.7821	up	0.5920	up

MPF_LOC101478079.1.1	XM_004542100.1 PREDICTED: Maylandia zebra pre-mRNA-processing factor 39-like (LOC101478079), transcript variant X1, mRNA	0.0270	-0.1575	down	0.4796	up	0.7714	up	0.6372	up	0.9289	up	0.2917	up
MPF_LOC101485691.1.3	XM_004568633.1 PREDICTED: Maylandia zebra homeobox protein HoxB4a-like (LOC101485691), mRNA	0.0270	-0.0099	down	-0.0353	down	0.8807	up	-0.0255	down	0.8905	up	0.9160	up
MPF_contig_002690		0.0271	0.0095	up	0.1315	up	0.8125	up	0.1219	up	0.8029	up	0.6810	up
MPF_APOC2.2.2	XP_003450543.1 PREDICTED: hypothetical protein LOC100712561 [Oreochromis niloticus]	0.0271	-0.1593	down	-0.2499	down	0.6475	up	-0.0906	down	0.8068	up	0.8974	up
MPF_contig_023846		0.0272	-0.1093	down	0.2509	up	0.5543	up	0.3601	up	0.6636	up	0.3034	up
MPF_LOC101480983.1.1	XM_004556365.1 PREDICTED: Maylandia zebra S-modulin-like (LOC101480983), mRNA	0.0272	-0.1842	down	0.2621	up	0.9393	up	0.4463	up	1.1235	up	0.6772	up
MPF_LOC101486758.1.1	XM_004545478.1 PREDICTED: Maylandia zebra reticulon-4 receptorlike 2-like (LOC101486758), mRNA	0.0272	-0.2019	down	0.3491	up	0.8996	up	0.5510	up	1.1015	up	0.5504	up
MPF_LOC100705821.1.1	XM_003459705.1 PREDICTED: Oreochromis niloticus RWD domaincontaining protein 4-like (LOC100705821), mRNA	0.0272	0.0918	up	0.2311	up	0.9742	up	0.1393	up	0.8824	up	0.7431	up

MPF_LOC100710728.2.5	XM_003438906.1 PREDICTED: Oreochromis niloticus CD63 antigen-like (LOC100710728), mRNA	0.0272	-0.1111	down	-0.0008	down	0.7855	up	0.1102	up	0.8965	up	0.7863	up
MPF_contig_038752		0.0272	-0.0504	down	-0.0508	down	1.0193	up	-0.0003	down	1.0697	up	1.0701	up
MPF_contig_000319		0.0272	-0.0944	down	0.0336	up	0.8596	up	0.1280	up	0.9540	up	0.8260	up
MPF_LOC100707106.1.1	XP_003451942.1 PREDICTED: recombining binding protein suppressor of hairless-like protein-like [Oreochromis niloticus]	0.0274	-0.1006	down	-0.3093	down	1.0768	up	-0.2087	down	1.1774	up	1.3861	up
MPF_LOC101482884.1.3	XM_004547433.1 PREDICTED: Maylandia zebra pantothenate kinase 4like (LOC101482884), transcript variant X2, mRNA	0.0274	0.0096	up	0.3530	up	1.0857	up	0.3434	up	1.0761	up	0.7326	up
MPF_LOC101464358.1.2	XM_004563987.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 20like (LOC101464358), mRNA	0.0275	0.0214	up	0.2601	up	0.7595	up	0.2388	up	0.7382	up	0.4994	up
MPF_LOC100689854.6.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0.0275	-0.0297	down	0.2688	up	1.0583	up	0.2985	up	1.0880	up	0.7894	up
MPF_LOC101482669.1.1	XM_004545112.1 PREDICTED: Maylandia zebra guanine nucleotidebinding protein-like 3-like (LOC101482669), mRNA	0.0275	-0.0953	down	0.0917	up	0.5995	up	0.1870	up	0.6947	up	0.5078	up
MPF_contig_018804		0.0275	0.0224	up	0.0921	up	0.7502	up	0.0697	up	0.7278	up	0.6581	up
MPF_LOC101071928.1.1	XP_003978669.1 PREDICTED: uncharacterized protein LOC101071928 [Takifugu	0.0275	-0.7436	down	-2.1023	down	-3.5240	down	-1.3587	down	-2.7803	down	-1.4217	down

	rubripes]													

MPF_LOC100712490.2.2	XM_003454128.1 PREDICTED: Oreochromis niloticus T-complex protein 1 subunit delta-like (LOC100712490), mRNA	0.0275	0.0491	up	0.1138	up	0.6827	up	0.0647	up	0.6336	up	0.5689	up
MPF_contig_046428		0.0276	0.1345	up	0.3571	up	0.9665	up	0.2225	up	0.8320	up	0.6095	up
MPF_LOC100692410.1.1	XP_003440487.1 PREDICTED: calcium and integrin-binding family member 2-like [Oreochromis niloticus]	0.0276	-0.0462	down	0.1919	up	0.8287	up	0.2381	up	0.8749	up	0.6368	up
MPF_LOC101467846.6.1 1	XM_004567936.1 PREDICTED: Maylandia zebra 60S ribosomal protein L8-like (LOC101467846), mRNA	0.0276	0.1751	up	0.3372	up	1.2556	up	0.1621	up	1.0805	up	0.9184	up
MPF_LOC100694073.1.1	XM_003449692.1 PREDICTED: Oreochromis niloticus oxysterol-binding protein 1-like (LOC100694073), mRNA	0.0277	0.2105	up	0.4461	up	0.9471	up	0.2355	up	0.7366	up	0.5011	up
MPF_LOC100707625.1.1	XP_003447875.1 PREDICTED: coiled-coil domain-containing protein 28B-like [Oreochromis niloticus]	0.0277	-0.0156	down	0.2968	up	0.6418	up	0.3123	up	0.6573	up	0.3450	up

MPF_LOC101161674.1.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA	0.0277	-0.0858	down	-1.3362	down	-3.1229	down	-1.2504	down	-3.0370	down	-1.7867	down
MPF_LOC101476994.3.3	XM_004574797.1 PREDICTED: Maylandia zebra myotubularin-like (LOC101476994), mRNA	0.0277	-0.0935	down	0.1324	up	0.4425	up	0.2258	up	0.5359	up	0.3101	up
MPF_contig_021764		0.0277	0.0025	up	0.1257	up	1.1021	up	0.1232	up	1.0996	up	0.9764	up
MPF_LOC569742.1.1	XP_698239.5 PREDICTED: hypothetical protein LOC569742 [Danio rerio]	0.0277	-0.4946	down	-0.3927	down	-2.0082	down	0.1019	up	-1.5136	down	-1.6155	down
MPF_LOC101066707.1.1	XM_003965418.1 PREDICTED: Takifugu rubripes zinc finger FYVE domain-containing protein 16like (LOC101066707), mRNA	0.0277	-0.1946	down	0.1710	up	0.8475	up	0.3655	up	1.0420	up	0.6765	up
MPF_LOC101483327.1.1	XM_004541476.1 PREDICTED: Maylandia zebra chromobox protein homolog 3-like (LOC101483327), transcript variant X2, mRNA	0.0277	0.0171	up	0.1176	up	0.8077	up	0.1005	up	0.7906	up	0.6901	up
MPF_LOC101076641.1.1	XP_003964552.1 PREDICTED: epidermal growth factor receptor kinase substrate 8-like protein 1-like [Takifugu rubripes]	0.0277	-0.0339	down	0.3296	up	1.1645	up	0.3635	up	1.1984	up	0.8350	up
MPF_LOC101478094.1.1	XM_004569499.1 PREDICTED: Maylandia zebra matrix	0.0277	0.0633	up	0.1075	up	0.5854	up	0.0442	up	0.5222	up	0.4780	up

	metalloproteinase-16-like (LOC101478094), transcript variant X1, mRNA													
MPF_contig_035389	XM_003441012.1 PREDICTED: Oreochromis niloticus proactivator polypeptide-like, transcript variant 1 (LOC100689911), mRNA	0.0277	-0.0016	down	0.3281	up	1.0827	up	0.3298	up	1.0843	up	0.7545	up
MPF_LOC101477280.6.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.0277	0.2832	up	-1.1217	down	-3.2688	down	-1.4050	down	-3.5520	down	-2.1471	down
MPF_LOC101477354.1.1	XM_004572334.1 PREDICTED: Maylandia zebra terminal uridylyltransferase 4-like (LOC101477354), mRNA	0.0277	-0.1230	down	-0.1420	down	0.8363	up	-0.0190	down	0.9593	up	0.9783	up
MPF_HMGA1B.1.6	NM_001077276.1 Danio rerio high mobility group AT-hook 1b (hmga1b), mRNA	0.0277	0.1357	up	0.2953	up	0.8459	up	0.1596	up	0.7102	up	0.5506	up
MPF_contig_031602		0.0277	0.0002	up	0.1637	up	0.9120	up	0.1635	up	0.9118	up	0.7483	up
MPF_LOC101473402.1.1	XM_004548338.1 PREDICTED: Maylandia zebra protein kinase C and casein kinase substrate in neurons protein 2-like (LOC101473402), transcript variant X3, mRNA	0.0277	-0.2410	down	-0.3783	down	-1.9752	down	-0.1373	down	-1.7342	down	-1.5969	down
MPF_contig_024013		0.0277	-0.1200	down	-0.2300	down	0.6928	up	-0.1100	down	0.8128	up	0.9229	up

MPF_LOC100698243.1.1	XR_134871.1 PREDICTED: Oreochromis niloticus hypothetical LOC100698243 (LOC100698243), miscRNA	0.0277	-0.2893	down	0.1449	up	-0.6178	down	0.4342	up	-0.3285	down	-0.7627	down
MPF_contig_021825		0.0277	-0.0737	down	-0.0653	down	1.2746	up	0.0084	up	1.3483	up	1.3399	up
MPF_LOC100534962.1.1	XP_003201578.1 PREDICTED: oocyte zinc finger protein XlCOF6-like [Danio rerio]	0.0277	-0.0211	down	0.2179	up	1.2568	up	0.2390	up	1.2779	up	1.0389	up
MPF_MYHM2126-2.1.3	XP_003975582.1 PREDICTED: myosin-7 [Takifugu rubripes]	0.0277	-1.0026	down	-1.2635	down	-3.3041	down	-0.2609	down	-2.3015	down	-2.0406	down
MPF_LOC100695307.3.3	XM_003448117.1 PREDICTED: Oreochromis niloticus enoyl-CoA hydratase domain-containing protein 3, mitochondrial-like (LOC100695307), mRNA	0.0277	0.0040	up	0.1563	up	0.9790	up	0.1523	up	0.9750	up	0.8227	up
MPF_LOC100704588.1.1	XP_003440203.1 PREDICTED: ATPdependent RNA helicase DQX1-like [Oreochromis niloticus]	0.0277	-0.1460	down	0.2493	up	0.8540	up	0.3953	up	1.0000	up	0.6047	up
MPF_contig_001020	XM_004563222.1 PREDICTED: Maylandia zebra CCR4-NOT transcription complex subunit 7-like (LOC101478719), transcript variant X1, mRNA	0.0277	0.2654	up	0.5335	up	1.0140	up	0.2680	up	0.7486	up	0.4805	up
MPF_contig_032639		0.0277	0.0774	up	0.2799	up	0.9036	up	0.2025	up	0.8262	up	0.6238	up
MPF_contig_025758		0.0277	-0.1439	down	-0.1878	down	0.5966	up	-0.0440	down	0.7404	up	0.7844	up

MPF_LOC100691609.1.1	XP_003441572.1 PREDICTED: guanine nucleotide-binding proteinlike 3-like [Oreochromis niloticus]	0.0277	-0.0630	down	-0.0680	down	0.6121	up	-0.0050	down	0.6751	up	0.6801	up
MPF_LOC101472829.1.1	XM_004552259.1 PREDICTED: Maylandia zebra max-like protein X-like (LOC101472829), mRNA	0.0277	-0.0226	down	0.2363	up	0.8032	up	0.2589	up	0.8258	up	0.5668	up
MPF_LOC100711254.1.1	XM_003438413.1 PREDICTED: Oreochromis niloticus wings apart-like protein homolog (LOC100711254), mRNA	0.0277	-0.0043	down	-0.0315	down	0.7638	up	-0.0271	down	0.7681	up	0.7952	up
MPF_contig_019979		0.0277	-0.1404	down	-0.7854	down	-2.7514	down	-0.6449	down	-2.6110	down	-1.9661	down
MPF_LOC100697415.2.3	XP_003444759.1 PREDICTED: neuroblast differentiation-associated protein AHNAK-like [Oreochromis niloticus]	0.0277	-0.0760	down	0.0921	up	0.6247	up	0.1681	up	0.7007	up	0.5326	up
MPF_contig_018625		0.0277	-0.2130	down	-0.0789	down	1.1904	up	0.1341	up	1.4033	up	1.2692	up
MPF_LOC101074182.1.1	XP_003965497.1 PREDICTED: E3 ubiquitinprotein ligase MARCH5-like [Takifugu rubripes]	0.0277	-0.0299	down	0.2757	up	0.6899	up	0.3056	up	0.7198	up	0.4141	up
MPF_LOC101485446.1.1	XM_004550723.1 PREDICTED: Maylandia zebra visinin-like (LOC101485446), mRNA	0.0277	-0.0287	down	0.2636	up	1.0773	up	0.2924	up	1.1060	up	0.8137	up
MPF_LOC101484297.1.2	XM_004567347.1 PREDICTED: Maylandia zebra pyrroline-5-carboxylate reductase 3-like (LOC101484297), mRNA	0.0277	-0.0557	down	-0.0227	down	0.7647	up	0.0330	up	0.8204	up	0.7874	up

MPF_TASP1.1.2	XM_003441024.1 PREDICTED: Oreochromis niloticus taspase, threonine aspartase, 1 (TASP1), mRNA	0.0277	-0.2885	down	-0.3886	down	1.0250	up	-0.1001	down	1.3135	up	1.4136	up
MPF_LOC100700827.1.1	XM_003446806.1 PREDICTED: Oreochromis niloticus uncharacterized protein C21orf59 homolog (LOC100700827), mRNA	0.0277	0.1979	up	0.2652	up	0.9946	up	0.0673	up	0.7967	up	0.7294	up
MPF_LOC100689854.5.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0.0277	-0.0608	down	0.2810	up	1.1730	up	0.3419	up	1.2338	up	0.8919	up
MPF_MYO16.1.1	XM_003452934.1 PREDICTED: Oreochromis niloticus myosin XVI (MYO16), mRNA	0.0277	0.0243	up	0.1901	up	0.6042	up	0.1658	up	0.5799	up	0.4141	up
MPF_LOC101477539.2.2	XM_004570211.1 PREDICTED: Maylandia zebra transmembrane protein 47-like (LOC101477539), mRNA	0.0277	-0.0369	down	0.1102	up	0.6060	up	0.1471	up	0.6430	up	0.4959	up
MPF_contig_011356	XM_004540345.1 PREDICTED: Maylandia zebra phospholipase DDHD1like (LOC101479185), transcript variant X1, mRNA	0.0277	-0.3619	down	-0.0632	down	0.9226	up	0.2987	up	1.2845	up	0.9858	up
MPF_LOC100697337.2.4	XP_003446015.1 PREDICTED: hypothetical protein LOC100697337 [Oreochromis niloticus]	0.0277	-0.2390	down	-0.5912	down	-2.0145	down	-0.3522	down	-1.7755	down	-1.4233	down
MPF_NEMVEDRAFT_V1G88915.1.1	XP_001638721.1 predicted protein [Nematostella vectensis]	0.0277	0.2127	up	0.2996	up	1.3291	up	0.0869	up	1.1164	up	1.0295	up

MPF_contig_044192	XM_004557088.1 PREDICTED: Maylandia zebra cytoplasmic polyadenylation elementbinding protein 2-like (LOC101483979), transcript variant X1, mRNA	0.0277	-0.3741	down	-0.1933	down	0.7536	up	0.1808	up	1.1277	up	0.9469	up
MPF_LOC101075879.1.1	XP_003961756.1 PREDICTED: leucine-rich repeat-containing protein 58like [Takifugu rubripes]	0.0277	0.1031	up	0.1719	up	0.8331	up	0.0687	up	0.7300	up	0.6613	up
MPF_LOC100699885.1.2	XP_003459139.1 PREDICTED: tripartite motifcontaining protein 16-like [Oreochromis niloticus]	0.0277	-0.1066	down	-0.1132	down	0.6331	up	-0.0066	down	0.7397	up	0.7463	up
MPF_contig_034908		0.0277	-0.0845	down	0.2748	up	1.0623	up	0.3593	up	1.1468	up	0.7874	up
MPF_LOC101159641.5.35	XM_004085298.1 PREDICTED: Oryzias latipes tenascin-like (LOC101159641), mRNA	0.0277	-0.2269	down	-0.8919	down	-2.3230	down	-0.6650	down	-2.0961	down	-1.4311	down
MPF_LOC101474181.1.1	XM_004568858.1 PREDICTED: Maylandia zebra phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform-like (LOC101474181), transcript variant X3, mRNA	0.0277	-0.0474	down	0.2152	up	0.6805	up	0.2626	up	0.7279	up	0.4653	up
MPF_LOC101484306.1.1	XM_004545559.1 PREDICTED: Maylandia zebra integrator complex subunit 5-like (LOC101484306), mRNA	0.0277	-0.0790	down	0.0614	up	0.9615	up	0.1405	up	1.0405	up	0.9001	up

MPF_contig_007433	XM_004571883.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 39-like (LOC101478477), transcript variant X1, mRNA	0.0277	0.2678	up	0.4071	up	0.8905	up	0.1393	up	0.6227	up	0.4834	up
MPF_contig_029353		0.0277	0.4472	up	0.5990	up	1.5251	up	0.1518	up	1.0779	up	0.9261	up
MPF_LOC101476936.1.1	XM_004565493.1 PREDICTED: Maylandia zebra peptidyl-prolyl cis-trans isomerase FKBP1A-like (LOC101476936), mRNA	0.0277	-0.0340	down	-1.0258	down	-2.5857	down	-0.9919	down	-2.5517	down	-1.5599	down
MPF_LOC101474833.3.3	XM_004570025.1 PREDICTED: Maylandia zebra bcl-2-like protein 11like (LOC101474833), mRNA	0.0277	0.1106	up	-0.5456	down	-2.5892	down	-0.6562	down	-2.6998	down	-2.0436	down
MPF_LOC100695519.2.3	XM_003458222.1 PREDICTED: Oreochromis niloticus zinc finger protein 92-like (LOC100695519), mRNA	0.0277	0.1198	up	0.1719	up	0.9876	up	0.0521	up	0.8679	up	0.8157	up
MPF_SGS4.8.10	SGS4_DROME (sp|Q00725) Salivary glue protein Sgs-4 OS=Drosophila melanogaster GN=Sgs4 PE=2 SV=1	0.0278	-0.0477	down	0.1032	up	0.4559	up	0.1509	up	0.5036	up	0.3527	up
MPF_LOC101476311.3.3	XM_004571250.1 PREDICTED: Maylandia zebra sodium/potassiumtransporting ATPase subunit alpha-1-like (LOC101476311), transcript variant X2, mRNA	0.0278	-0.0170	down	0.1902	up	0.6281	up	0.2072	up	0.6451	up	0.4379	up

MPF_contig_005188	XM_004567422.1 PREDICTED: Maylandia zebra band 4.1-like protein 1like (LOC101479109), transcript variant X4, mRNA	0.0278	0.0339	up	0.3816	up	1.1777	up	0.3477	up	1.1438	up	0.7961	up
MPF_contig_000813		0.0278	-0.0320	down	0.2614	up	0.6111	up	0.2935	up	0.6431	up	0.3496	up
MPF_LOC101468502.1.1	XM_004555833.1 PREDICTED: Maylandia zebra copper homeostasis protein cutC homolog (LOC101468502), transcript variant X3, mRNA	0.0278	0.0034	up	0.1271	up	0.7053	up	0.1237	up	0.7019	up	0.5781	up
MPF_LOC101488132.1.2	XM_004557568.1 PREDICTED: Maylandia zebra cdc42 effector protein 1-like (LOC101488132), mRNA	0.0278	0.1061	up	0.6494	up	1.8582	up	0.5434	up	1.7521	up	1.2087	up
MPF_contig_024222		0.0278	0.0111	up	0.1924	up	0.4633	up	0.1812	up	0.4522	up	0.2709	up
MPF_LOC100700807.1.1	XP_003441694.1 PREDICTED: cytoplasmic dynein 2 heavy chain 1-like [Oreochromis niloticus]	0.0278	0.1019	up	0.4019	up	1.1376	up	0.3000	up	1.0357	up	0.7357	up
MPF_contig_018921		0.0278	-0.4523	down	-0.5699	down	-2.5163	down	-0.1176	down	-2.0640	down	-1.9464	down
MPF_LOC101483666.3.3	XM_004550438.1 PREDICTED: Maylandia zebra TATA box-binding protein-associated factor RNA polymerase I subunit Alike (LOC101483666), transcript variant X3, mRNA	0.0278	-0.4644	down	-0.6636	down	-2.9734	down	-0.1992	down	-2.5090	down	-2.3097	down
MPF_LOC101469089.3.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA	0.0279	0.1124	up	-0.3467	down	-1.7584	down	-0.4591	down	-1.8708	down	-1.4116	down

MPF_contig_000157	XM_004564005.1 PREDICTED: Maylandia zebra zinc finger Ychromosomal protein 1-like (LOC101469595), transcript variant X1, mRNA	0.0279	0.5603	up	0.5797	up	1.4045	up	0.0194	up	0.8443	up	0.8248	up
MPF_LOC100691787.1.1	XP_003441155.1 PREDICTED: zinc finger protein 511-like [Oreochromis niloticus]	0.0279	0.3125	up	0.1434	up	0.9343	up	-0.1691	down	0.6219	up	0.7909	up
MPF_contig_007919		0.0279	-0.8994	down	-0.5006	down	-2.5074	down	0.3988	up	-1.6080	down	-2.0068	down
MPF_LOC101074307.1.1	XM_003975871.1 PREDICTED: Takifugu rubripes Golgi reassemblystacking protein 2-like (LOC101074307), mRNA	0.0280	0.0551	up	0.2095	up	0.8216	up	0.1544	up	0.7665	up	0.6121	up
MPF_LOC101473855.11.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA	0.0280	-0.4631	down	-0.7136	down	-1.2432	down	-0.2505	down	-0.7801	down	-0.5296	down
MPF_contig_035773	XM_004539186.1 PREDICTED: Maylandia zebra tropomodulin-1-like (LOC101483315), transcript variant X1, mRNA	0.0281	-0.0369	down	0.2709	up	1.0591	up	0.3079	up	1.0961	up	0.7882	up
MPF_contig_029562	XM_004575516.1 PREDICTED: Maylandia zebra protein FAM222B-like (LOC101485279), transcript variant X1, mRNA	0.0281	-0.0008	down	0.0678	up	0.8754	up	0.0686	up	0.8762	up	0.8076	up
MPF_LOC101476666.3.3	XM_004541357.1 PREDICTED: Maylandia zebra epithelial splicing regulatory protein 1-like (LOC101476666), transcript variant X2, mRNA	0.0282	0.2528	up	-0.0263	down	1.2691	up	-0.2791	down	1.0164	up	1.2954	up

MPF_LOC101468537.2.3	XM_004566359.1 PREDICTED: Maylandia zebra ADAMTS-like protein 5like (LOC101468537), transcript variant X2, mRNA	0.0282	-0.0543	down	0.1413	up	0.5245	up	0.1957	up	0.5788	up	0.3832	up
MPF_LOC101471611.1.1	XM_004564014.1 PREDICTED: Maylandia zebra serine/arginine repetitive matrix protein 2-like (LOC101471611), transcript variant X2, mRNA	0.0283	-0.0615	down	0.1954	up	0.7870	up	0.2569	up	0.8485	up	0.5916	up
MPF_LOC101067829.1.1	XM_003962145.1 PREDICTED: Takifugu rubripes G-protein coupled receptor 39-like (LOC101067829), mRNA	0.0283	-0.1631	down	-0.1929	down	-1.0011	down	-0.0298	down	-0.8380	down	-0.8082	down
MPF_LOC101465317.1.5	XM_004564258.1 PREDICTED: Maylandia zebra ankyrin-2-like (LOC101465317), transcript variant X5, mRNA	0.0283	-0.0772	down	-0.2795	down	1.1906	up	-0.2023	down	1.2677	up	1.4700	up
MPF_AGL.1.1	XM_003459407.1 PREDICTED: Oreochromis niloticus amylo-alpha-1, 6glucosidase, 4-alphaglucanotransferase (AGL), mRNA	0.0285	-0.0455	down	0.2236	up	0.6923	up	0.2691	up	0.7378	up	0.4687	up
MPF_LOC101473936.1.1	XM_004559270.1 PREDICTED: Maylandia zebra PQ-loop repeatcontaining protein 3-like (LOC101473936), mRNA	0.0285	-0.1000	down	0.0077	up	0.5931	up	0.1078	up	0.6931	up	0.5854	up

MPF_contig_014026	XM_004549368.1 PREDICTED: Maylandia zebra ras GTPase-activating protein-binding protein 2-like (LOC101479323), transcript variant X1, mRNA	0.0285	-0.0314	down	0.2649	up	1.0809	up	0.2964	up	1.1124	up	0.8160	up
MPF_TYRO3.2.2	NM_131432.1 Danio rerio TYRO3 protein tyrosine kinase (tyro3), mRNA gb|AF021344.1|AF021344 Danio rerio developmental receptor tyrosine kinase (Dtk) mRNA, complete cds	0.0285	-0.2890	down	0.0859	up	0.9871	up	0.3749	up	1.2761	up	0.9012	up
MPF_LOC101064289.1.1	XM_003978509.1 PREDICTED: Takifugu rubripes ketohexokinase-like (LOC101064289), mRNA	0.0285	-0.1279	down	-0.1436	down	0.4957	up	-0.0157	down	0.6236	up	0.6393	up
MPF_LOC101473623.3.9	XM_004576627.1 PREDICTED: Maylandia zebra ferritin, middle subunitlike (LOC101473623), mRNA	0.0286	-0.0056	down	0.1377	up	0.5750	up	0.1433	up	0.5806	up	0.4374	up
MPF_LOC100694528.1.1	XP_003452879.1 PREDICTED: probable alphaketoglutarate-dependent dioxygenase ABH7-like [Oreochromis niloticus]	0.0286	0.2512	up	0.4482	up	0.9713	up	0.1970	up	0.7202	up	0.5232	up
MPF_LOC101476666.2.3	XM_004541357.1 PREDICTED: Maylandia zebra epithelial splicing regulatory protein 1-like (LOC101476666), transcript variant X2, mRNA	0.0286	0.2730	up	-0.0192	down	1.2788	up	-0.2921	down	1.0058	up	1.2979	up
MPF_LOC101172475.2.2	XM_004086336.1 PREDICTED: Oryzias latipes serine/threonine-protein kinase pim-2-like (LOC101172475), mRNA	0.0286	-0.1037	down	0.4534	up	0.9814	up	0.5571	up	1.0851	up	0.5280	up

MPF_contig_043196		0.0286	-0.0666	down	0.3050	up	1.0801	up	0.3717	up	1.1467	up	0.7751	up
MPF_LOC101483869.1.1	XM_004574429.1 PREDICTED: Maylandia zebra coiled-coil domaincontaining protein 130 homolog (LOC101483869), mRNA	0.0286	-0.0138	down	0.0413	up	0.9548	up	0.0550	up	0.9686	up	0.9136	up
MPF_LOC101465228.1.1	XM_004565359.1 PREDICTED: Maylandia zebra sal-like protein 2-like (LOC101465228), transcript variant X2, mRNA	0.0286	-0.0868	down	0.1247	up	0.9047	up	0.2115	up	0.9915	up	0.7800	up
MPF_LOC100697193.1.1	XM_003454893.1 PREDICTED: Oreochromis niloticus phosducin-like protein 3-like (LOC100697193), mRNA	0.0286	0.2561	up	0.0637	up	1.2970	up	-0.1925	down	1.0408	up	1.2333	up
MPF_EOS1.1.1	XP_004068609.1 PREDICTED: zinc finger protein Eos-like [Oryzias latipes]	0.0286	-0.2115	down	0.2023	up	1.2164	up	0.4138	up	1.4279	up	1.0142	up
MPF_contig_010802		0.0287	-0.0748	down	0.1600	up	0.9650	up	0.2348	up	1.0398	up	0.8050	up
MPF_contig_032974		0.0287	-0.1089	down	0.0476	up	0.7390	up	0.1565	up	0.8479	up	0.6914	up
MPF_LOC101482884.3.3	XM_004547433.1 PREDICTED: Maylandia zebra pantothenate kinase 4like (LOC101482884), transcript variant X2, mRNA	0.0287	0.1031	up	0.3976	up	1.0835	up	0.2945	up	0.9804	up	0.6859	up
MPF_LOC101468855.3.3	XM_004569017.1 PREDICTED: Maylandia zebra protein tweety homolog 3-like (LOC101468855), transcript variant X1, mRNA	0.0287	-0.1815	down	-0.9102	down	-3.1461	down	-0.7287	down	-2.9647	down	-2.2360	down

MPF_LOC100698172.1.3	XP_003455687.1 PREDICTED: beta-2microglobulin-like [Oreochromis niloticus]	0.0287	0.0472	up	0.4480	up	0.7858	up	0.4009	up	0.7386	up	0.3377	up
MPF_LOC101475646.3.5	XM_004550973.1 PREDICTED: Maylandia zebra metal regulatory transcription factor 1-like (LOC101475646), mRNA	0.0287	-0.1177	down	0.0562	up	0.4650	up	0.1739	up	0.5827	up	0.4088	up
MPF_ZN121.2.3	ZN121_HUMAN (sp|P58317) Zinc finger protein 121 OS=Homo sapiens GN=ZNF121 PE=2 SV=2	0.0287	0.0678	up	0.1646	up	0.8932	up	0.0968	up	0.8254	up	0.7285	up
MPF_LOC100697348.1.1	XM_003449454.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100697348 (LOC100697348), mRNA	0.0287	0.0525	up	-0.0666	down	-1.4488	down	-0.1191	down	-1.5013	down	-1.3822	down
MPF_LOC101483926.1.2	XM_004546690.1 PREDICTED: Maylandia zebra ubiquitin carboxylterminal hydrolase 12-like (LOC101483926), mRNA	0.0287	0.0169	up	0.1126	up	0.7076	up	0.0957	up	0.6907	up	0.5950	up
MPF_LOC101477280.2.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.0287	-0.0861	down	-1.6077	down	-3.5294	down	-1.5217	down	-3.4434	down	-1.9217	down
MPF_LOC100709350.3.3	XP_003449297.1 PREDICTED: cryptochrome-2like [Oreochromis niloticus]	0.0287	-0.1773	down	0.0342	up	1.1894	up	0.2114	up	1.3666	up	1.1552	up
MPF_LOC101466459.8.29	XM_004554283.1	0.0287	-0.0399	down	0.0138	up	0.8065	up	0.0537	up	0.8465	up	0.7928	up

	PREDICTED: Maylandia zebra semaphorin-3G-like (LOC101466459), mRNA													
MPF_LOC100708166.1.1	XP_003446628.1 PREDICTED: SH3 domain-binding protein 4-A-like [Oreochromis niloticus]	0.0287	-0.2323	down	0.1487	up	0.7989	up	0.3810	up	1.0312	up	0.6502	up
MPF_contig_030877		0.0287	-0.0068	down	0.1671	up	0.8918	up	0.1739	up	0.8986	up	0.7247	up
MPF_LOC100690282.1.1	XP_003445069.1 PREDICTED: tripartite motifcontaining protein 39-like [Oreochromis niloticus]	0.0287	0.2678	up	-0.6234	down	-1.2575	down	-0.8912	down	-1.5253	down	-0.6341	down
MPF_contig_024441		0.0287	-0.0483	down	0.1651	up	0.8459	up	0.2133	up	0.8942	up	0.6808	up
MPF_CNDH2.1.1	[BBH] CNDH2_DANRE (sp|Q5RH01) Condensin-2 complex subunit H2 OS=Danio rerio GN=ncaph2 PE=2 SV=1	0.0287	0.1740	up	0.1182	up	1.0558	up	-0.0558	down	0.8818	up	0.9376	up
MPF_COX1.2.7	COX1_LATCH (sp|O03167) Cytochrome c oxidase subunit 1 OS=Latimeria chalumnae GN=MT-CO1 PE=3 SV=1	0.0287	0.1527	up	-0.1263	down	1.3110	up	-0.2790	down	1.1583	up	1.4373	up
MPF_contig_001047	XM_004559756.1 PREDICTED: Maylandia zebra vitrin-like (LOC101482458), transcript variant X1, mRNA	0.0288	-0.1977	down	-0.0453	down	1.0782	up	0.1524	up	1.2759	up	1.1235	up
MPF_LOC101464726.1.4	XM_004561458.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase TRIP12-like (LOC101464726), mRNA	0.0288	0.0524	up	0.2131	up	1.0274	up	0.1607	up	0.9750	up	0.8143	up

MPF_LOC101156990.1.1	XM_004074357.1 PREDICTED: Oryzias latipes upstream-binding protein 1like (LOC101156990), mRNA	0.0288	0.1048	up	0.1310	up	1.0503	up	0.0263	up	0.9455	up	0.9192	up
MPF_LOC100705885.1.1	XM_003453768.1 PREDICTED: Oreochromis niloticus Fc receptor-like protein 3-like (LOC100705885), mRNA	0.0288	-0.0082	down	0.1703	up	0.7891	up	0.1785	up	0.7973	up	0.6188	up
MPF_LOC100709351.6.10	XM_003449499.1 PREDICTED: Oreochromis niloticus integral membrane protein 2B-like (LOC100709351), mRNA	0.0288	-0.0788	down	0.3279	up	1.1163	up	0.4067	up	1.1951	up	0.7884	up
MPF_LOC101068250.1.2	XM_003969609.1 PREDICTED: Takifugu rubripes guanosine-3',5'bis(diphosphate) 3'pyrophosphohydrolase MESH1-like (LOC101068250), mRNA	0.0288	-1.0119	down	0.0871	up	-2.2406	down	1.0990	up	-1.2287	down	-2.3276	down
MPF_LOC100712114.2.2	XM_003449341.1 PREDICTED: Oreochromis niloticus LSM domaincontaining protein 1-like (LOC100712114), mRNA	0.0288	0.2239	up	0.7536	up	0.8842	up	0.5297	up	0.6604	up	0.1307	up
MPF_GABP2.1.1	GABP2_BOVIN (sp|Q0V8G2) GA-binding protein subunit beta-2 OS=Bos taurus GN=GABPB2 PE=2 SV=2	0.0288	0.0031	up	0.1549	up	1.1073	up	0.1517	up	1.1041	up	0.9524	up
MPF_LOC101470485.1.3	XM_004545890.1 PREDICTED: Maylandia zebra uncharacterized LOC101470485	0.0288	-0.1691	down	0.1721	up	0.9372	up	0.3412	up	1.1063	up	0.7651	up

	(LOC101470485), mRNA													
MPF_contig_048489		0.0288	-0.0997	down	-0.0300	down	0.6042	up	0.0697	up	0.7040	up	0.6343	up
MPF_ZG57.4.12	ZG57_XENLA (sp|P18729) Gastrula zinc finger protein XlCGF57.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.0288	-0.4786	down	-0.5635	down	-1.3503	down	-0.0849	down	-0.8717	down	-0.7868	down
MPF_KIF18A.1.1	XM_003445746.1 PREDICTED: Oreochromis niloticus kinesin family member 18A (KIF18A), mRNA	0.0289	0.0266	up	0.1452	up	0.9887	up	0.1187	up	0.9621	up	0.8435	up
MPF_contig_028378		0.0289	-0.0059	down	0.2185	up	0.6195	up	0.2244	up	0.6254	up	0.4010	up
MPF_SSGZ1_0670.2.2	YP_006074071.1 TPR repeat protein [Streptococcus suis GZ1]	0.0289	0.1293	up	0.2201	up	1.0150	up	0.0908	up	0.8857	up	0.7949	up
MPF_contig_044388		0.0289	-0.0187	down	0.1160	up	0.7012	up	0.1347	up	0.7199	up	0.5852	up
MPF_ZN271.18.19	ZN271_PONAB (sp|Q5R5U3) Zinc finger protein 271 OS=Pongo abelii GN=ZNF271 PE=2 SV=1	0.0289	0.0030	up	0.3702	up	1.0163	up	0.3671	up	1.0133	up	0.6461	up
MPF_LOC101485221.2.2	XM_004541104.1 PREDICTED: Maylandia zebra disintegrin and metalloproteinase domaincontaining protein 19-like (LOC101485221), mRNA	0.0289	-0.6449	down	-1.7719	down	-2.8615	down	-1.1271	down	-2.2166	down	-1.0895	down

MPF_LOC101486367.1.1	XM_004543922.1 PREDICTED: Maylandia zebra transforming growth factor beta regulator 1-like (LOC101486367), transcript variant X1, mRNA	0.0289	-0.0221	down	-0.0171	down	0.7614	up	0.0050	up	0.7835	up	0.7784	up
MPF_LOC101474220.1.1	XM_004554937.1 PREDICTED: Maylandia zebra serine/threonineprotein kinase NIM1-like (LOC101474220), mRNA	0.0289	0.1870	up	0.2883	up	0.6038	up	0.1013	up	0.4168	up	0.3155	up
MPF_LOC101465258.1.1	XM_004572743.1 PREDICTED: Maylandia zebra transmembrane and coiled-coil domain-containing protein 4-like (LOC101465258), transcript variant X2, mRNA	0.0289	0.0327	up	0.1960	up	1.6102	up	0.1633	up	1.5775	up	1.4142	up
MPF_contig_043008		0.0289	-0.0114	down	0.1928	up	1.1285	up	0.2042	up	1.1399	up	0.9357	up
MPF_contig_043102		0.0289	0.0585	up	0.1887	up	0.5415	up	0.1302	up	0.4830	up	0.3528	up
MPF_contig_009192		0.0289	-0.0533	down	0.3523	up	1.2674	up	0.4056	up	1.3207	up	0.9151	up
MPF_LOC100694731.1.1	XP_003438055.1 PREDICTED: potassium voltage-gated channel subfamily V member 2-like [Oreochromis niloticus]	0.0290	-0.0521	down	0.0503	up	0.6515	up	0.1023	up	0.7036	up	0.6012	up
MPF_LOC101472043.8.14	XM_004573789.1 PREDICTED: Maylandia zebra tight junctionassociated protein 1-like (LOC101472043), transcript variant X4, mRNA	0.0290	-1.0207	down	-0.6182	down	-2.9853	down	0.4025	up	-1.9646	down	-2.3671	down

MPF_LOC101465948.3.3	XM_004549509.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily A member 1-like (LOC101465948), mRNA	0.0290	0.3463	up	-0.3197	down	0.5535	up	-0.6660	down	0.2072	up	0.8731	up
MPF_LOC101481888.1.1	XM_004542490.1 PREDICTED: Maylandia zebra BTB/POZ domaincontaining protein 2-like (LOC101481888), mRNA	0.0290	-0.1066	down	0.2148	up	1.0626	up	0.3215	up	1.1692	up	0.8478	up
MPF_contig_021847		0.0290	-0.0245	down	0.1804	up	0.8543	up	0.2049	up	0.8789	up	0.6740	up
MPF_LOC101478994.1.1	XM_004537971.1 PREDICTED: Maylandia zebra fatty aldehyde dehydrogenase-like (LOC101478994), transcript variant X2, mRNA	0.0290	-0.0397	down	0.1884	up	0.7068	up	0.2280	up	0.7464	up	0.5184	up
MPF_contig_043941		0.0290	0.2766	up	0.3714	up	0.8585	up	0.0948	up	0.5819	up	0.4871	up
MPF_contig_024216		0.0290	0.0255	up	0.3473	up	-0.8598	down	0.3218	up	-0.8854	down	-1.2071	down
MPF_LOC100698899.1.1	XM_003457691.1 PREDICTED: Oreochromis niloticus protein PAT1 homolog 1-like (LOC100698899), mRNA	0.0290	0.4354	up	0.4915	up	1.3987	up	0.0561	up	0.9633	up	0.9072	up
MPF_LOC101484703.2.2	XM_004555446.1 PREDICTED: Maylandia zebra transmembrane protein 41A-A-like (LOC101484703), mRNA	0.0290	-0.8888	down	-1.9021	down	-3.3928	down	-1.0133	down	-2.5040	down	-1.4907	down
MPF_LOC100709926.1.1	XP_003437949.1 PREDICTED: vacuolar protein sorting-associated protein 4B-like [Oreochromis niloticus]	0.0290	-0.0379	down	0.2035	up	0.7782	up	0.2414	up	0.8161	up	0.5747	up

MPF_LOC101465998.2.3	XM_004541412.1 PREDICTED: Maylandia zebra serum amyloid Pcomponent-like (LOC101465998), mRNA	0.0290	-0.1814	down	-1.5714	down	-2.7124	down	-1.3900	down	-2.5310	down	-1.1409	down
MPF_LOC101485482.1.1	XM_004563248.1 PREDICTED: Maylandia zebra POU domain, class 3, transcription factor 4-like (LOC101485482), mRNA	0.0290	-0.3121	down	-0.1018	down	0.6272	up	0.2104	up	0.9394	up	0.7290	up
MPF_LOC101487290.1.1	XM_004559498.1 PREDICTED: Maylandia zebra meteorin-like proteinlike (LOC101487290), mRNA	0.0290	0.0855	up	0.1030	up	0.8669	up	0.0175	up	0.7814	up	0.7639	up
MPF_AHNK.7.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiationassociated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.0290	0.0670	up	0.1732	up	0.8744	up	0.1062	up	0.8074	up	0.7013	up
MPF_LOC100701946.1.1	XP_003453886.1 PREDICTED: uncharacterized protein KIAA1143 homolog [Oreochromis niloticus]	0.0290	0.3032	up	0.1322	up	0.8338	up	-0.1710	down	0.5306	up	0.7016	up
MPF_contig_033779	XM_004541356.1 PREDICTED: Maylandia zebra epithelial splicing regulatory protein 1-like (LOC101476666), transcript variant X1, mRNA	0.0290	0.2580	up	-0.0289	down	1.2582	up	-0.2869	down	1.0002	up	1.2871	up
MPF_contig_031909	XM_004555771.1 PREDICTED: Maylandia zebra metal transporter CNNM4-like (LOC101472255), transcript variant X2, mRNA	0.0290	-0.1239	down	0.1008	up	0.7195	up	0.2247	up	0.8434	up	0.6187	up

MPF_contig_019024	XM_004572984.1 PREDICTED: Maylandia zebra A-kinase anchor protein 11-like (LOC101482225), transcript variant X1, mRNA	0.0290	-0.0171	down	0.1043	up	0.8093	up	0.1214	up	0.8264	up	0.7050	up
MPF_BTNL2.7.7	BTNL2_MOUSE (sp|O70355) Butyrophilin-like protein 2 OS=Mus musculus GN=Btnl2 PE=2 SV=2	0.0290	-0.0585	down	0.2876	up	1.1064	up	0.3462	up	1.1649	up	0.8188	up

MPF_FRIM.1.1	FRIM_SALSA (sp|P49947) Ferritin, middle subunit OS=Salmo salar PE=2 SV=1	0.0290	0.0221	up	0.1382	up	0.5777	up	0.1161	up	0.5557	up	0.4396	up
MPF_contig_044768		0.0290	-0.1789	down	0.0823	up	0.5657	up	0.2613	up	0.7446	up	0.4834	up
MPF_LOC101163898.1.2	XP_004070391.1 PREDICTED: ATP synthase subunit epsilon, mitochondrial-like [Oryzias latipes]	0.0290	-0.0615	down	0.2217	up	0.4836	up	0.2832	up	0.5451	up	0.2619	up
MPF_LOC100698023.1.1	XP_003440180.1 PREDICTED: endophilin-B2like isoform 1 [Oreochromis niloticus]	0.0290	-0.2269	down	0.5948	up	0.8006	up	0.8218	up	1.0275	up	0.2058	up
MPF_MK14.1.1	MK14_MOUSE (sp|P47811) Mitogen-activated protein kinase 14 OS=Mus musculus GN=Mapk14 PE=1 SV=3	0.0291	0.1586	up	0.2404	up	1.3856	up	0.0819	up	1.2270	up	1.1451	up
MPF_contig_008143		0.0291	0.1118	up	0.0805	up	0.7447	up	-0.0313	down	0.6329	up	0.6642	up

MPF_LOC101474457.1.1	XM_004568682.1 PREDICTED: Maylandia zebra abhydrolase domaincontaining protein FAM108C1-like (LOC101474457), transcript variant X1, mRNA	0.0292	-0.0387	down	0.2601	up	0.8627	up	0.2988	up	0.9014	up	0.6026	up
MPF_contig_024164		0.0292	-0.0637	down	0.1755	up	0.5588	up	0.2392	up	0.6225	up	0.3832	up
MPF_contig_020638		0.0292	0.1602	up	0.0616	up	1.5613	up	-0.0986	down	1.4011	up	1.4998	up
MPF_contig_024447		0.0292	-0.1587	down	0.2503	up	0.9958	up	0.4090	up	1.1545	up	0.7455	up
MPF_LOC100707931.1.1	XM_003454934.1 PREDICTED: Oreochromis niloticus myosin-XV-like (LOC100707931), mRNA	0.0292	0.0011	up	0.1079	up	0.4046	up	0.1067	up	0.4035	up	0.2968	up
MPF_LOC101486055.1.1	XM_004562353.1 PREDICTED: Maylandia zebra Fanconi anemiaassociated protein of 100 kDa-like (LOC101486055), mRNA	0.0292	-0.0377	down	0.2857	up	0.9671	up	0.3233	up	1.0047	up	0.6814	up
MPF_LOC101473667.1.2	XM_004568855.1 PREDICTED: Maylandia zebra stress response protein nst1-like (LOC101473667), mRNA	0.0293	-0.0828	down	0.0647	up	0.3693	up	0.1474	up	0.4520	up	0.3046	up
MPF_LOC100706818.3.9	XR_134822.1 PREDICTED: Oreochromis niloticus selenoprotein Pa-like (LOC100706818), miscRNA	0.0293	0.1712	up	0.1819	up	0.5632	up	0.0106	up	0.3920	up	0.3813	up
MPF_LOC101482028.1.1	XM_004551087.1 PREDICTED: Maylandia zebra WD repeat-containing protein 73-like (LOC101482028), mRNA	0.0293	0.0888	up	0.5514	up	0.9847	up	0.4626	up	0.8959	up	0.4334	up

MPF_LOC100696456.3.3	XP_003448503.1 PREDICTED: cathepsin Zlike [Oreochromis niloticus]	0.0293	0.0256	up	-0.5782	down	-1.9016	down	-0.6038	down	-1.9272	down	-1.3234	down
MPF_LOC100695990.1.1	XP_003440919.1 PREDICTED: GDP- Man:Man(3)GlcNAc(2)-PPDol alpha-1,2mannosyltransferase-like [Oreochromis niloticus]	0.0293	-0.1376	down	0.2303	up	0.8279	up	0.3680	up	0.9656	up	0.5976	up
MPF_LOC101483308.3.3	XM_004559856.1 PREDICTED: Maylandia zebra lysine-specific demethylase phf2-like (LOC101483308), transcript variant X3, mRNA	0.0293	0.0157	up	0.0788	up	0.7969	up	0.0631	up	0.7812	up	0.7181	up
MPF_contig_029035		0.0293	-0.3168	down	-0.5082	down	-2.7878	down	-0.1914	down	-2.4710	down	-2.2796	down
MPF_LOC101471848.1.1	XM_004573568.1 PREDICTED: Maylandia zebra putative pre-mRNAsplicing factor ATPdependent RNA helicase DHX16-like (LOC101471848), transcript variant X1, mRNA	0.0293	-0.1196	down	0.1308	up	0.8120	up	0.2504	up	0.9316	up	0.6812	up
MPF_SGS4.9.10	SGS4_DROME (sp|Q00725) Salivary glue protein Sgs-4 OS=Drosophila melanogaster GN=Sgs4 PE=2 SV=1	0.0293	-0.0603	down	0.1070	up	0.6893	up	0.1673	up	0.7496	up	0.5824	up
MPF_LOC101478686.3.4	XM_004553326.1 PREDICTED: Maylandia zebra SH3 and multiple ankyrin repeat domains protein 3-like (LOC101478686), transcript variant X2, mRNA	0.0293	-0.0497	down	0.1331	up	0.8896	up	0.1828	up	0.9393	up	0.7565	up
MPF_contig_012354		0.0293	-0.0134	down	0.1595	up	0.8546	up	0.1729	up	0.8681	up	0.6952	up

MPF_PSD12.1.1	PSD12_BOVIN (sp|Q2KJ25) 26S proteasome non-ATPase regulatory subunit 12 OS=Bos taurus GN=PSMD12 PE=2 SV=3	0.0293	-0.0128	down	0.1341	up	0.9273	up	0.1469	up	0.9401	up	0.7932	up
MPF_EIF4A2.1.1	NM_001102893.1 Xenopus (Silurana) tropicalis eukaryotic translation initiation factor 4A2 (eif4a2), mRNA gb|BC135871.1| Xenopus tropicalis hypothetical protein LOC100124955, mRNA (cDNA clone MGC:121826 IMAGE:7637784), complete cds	0.0293	-0.3938	down	-0.1767	down	-2.0341	down	0.2171	up	-1.6403	down	-1.8574	down

MPF_contig_037633		0.0293	-0.0513	down	0.3079	up	1.1738	up	0.3592	up	1.2251	up	0.8659	up
MPF_PRR21.2.3	PRR21_HUMAN (sp|Q8WXC7) Putative proline-rich protein 21 OS=Homo sapiens GN=PRR21 PE=5 SV=1	0.0293	0.1561	up	0.2358	up	0.9136	up	0.0797	up	0.7576	up	0.6779	up
MPF_LOC100699178.1.1	XM_003438369.1 PREDICTED: Oreochromis niloticus inositol 1,4,5triphosphate receptorinteracting protein-like (LOC100699178), mRNA	0.0293	0.1504	up	-0.8906	down	-3.4640	down	-1.0410	down	-3.6143	down	-2.5733	down
MPF_LOC101469226.1.1	XM_004541233.1 PREDICTED: Maylandia zebra uncharacterized LOC101469226	0.0294	0.2169	up	0.0986	up	0.9997	up	-0.1183	down	0.7828	up	0.9010	up

	(LOC101469226), mRNA													
MPF_contig_028959		0.0294	0.0923	up	0.3519	up	0.7740	up	0.2595	up	0.6817	up	0.4221	up
MPF_LOC100694496.1.1	XP_003443317.1 PREDICTED: homeobox protein Hox-A1-like [Oreochromis niloticus]	0.0294	-0.2998	down	-0.5835	down	0.8441	up	-0.2837	down	1.1439	up	1.4277	up
MPF_contig_008114		0.0294	-0.0440	down	0.0551	up	0.6872	up	0.0991	up	0.7312	up	0.6321	up
MPF_contig_041220		0.0294	-0.0544	down	0.2851	up	1.1535	up	0.3395	up	1.2079	up	0.8684	up
MPF_LOC101469398.1.2	XM_004555590.1 PREDICTED: Maylandia zebra LIM and senescent cell antigen-like-containing domain protein 1-like (LOC101469398), transcript variant X6, mRNA	0.0294	0.0568	up	0.1019	up	0.5592	up	0.0452	up	0.5024	up	0.4573	up
MPF_LOC101482035.1.1	XM_004552295.1 PREDICTED: Maylandia zebra histone acetyltransferase KAT2A-like (LOC101482035), transcript variant X3, mRNA	0.0294	0.0876	up	0.4150	up	1.2213	up	0.3274	up	1.1337	up	0.8063	up
MPF_LOC101477280.1.6	XM_004552473.1 PREDICTED: Maylandia zebra coronin-1A-like (LOC101477280), mRNA	0.0294	-0.0208	down	-1.3768	down	-3.1977	down	-1.3560	down	-3.1769	down	-1.8210	down
MPF_contig_037084		0.0294	-0.0789	down	0.0784	up	0.4363	up	0.1572	up	0.5152	up	0.3580	up
MPF_LOC100702318.5.5	XP_003458375.1 PREDICTED: galectin-9-like [Oreochromis niloticus]	0.0294	0.3001	up	-1.3881	down	-2.7496	down	-1.6882	down	-3.0497	down	-1.3615	down

MPF_LOC101069016.2.2	XM_003977363.1 PREDICTED: Takifugu rubripes synapse-associated protein 1-like (LOC101069016), mRNA	0.0294	-0.0152	down	0.1476	up	0.8479	up	0.1628	up	0.8630	up	0.7002	up
MPF_LOC101471011.1.2	XM_004555841.1 PREDICTED: Maylandia zebra LIM domain-binding protein 1-like (LOC101471011), transcript variant X1, mRNA	0.0294	0.0439	up	0.1171	up	0.8272	up	0.0732	up	0.7833	up	0.7101	up

MPF_CD48.2.4	CD48_MOUSE (sp|P18181) CD48 antigen OS=Mus musculus GN=Cd48 PE=1 SV=1	0.0294	-0.5166	down	-1.2597	down	-3.3872	down	-0.7431	down	-2.8706	down	-2.1275	down
MPF_contig_003321		0.0294	0.1637	up	-0.0837	down	0.9349	up	-0.2475	down	0.7712	up	1.0186	up
MPF_contig_013591		0.0294	0.0590	up	0.4181	up	0.8681	up	0.3590	up	0.8091	up	0.4500	up
MPF_contig_008912		0.0294	0.0164	up	0.3013	up	0.5939	up	0.2850	up	0.5775	up	0.2926	up
MPF_RPS7.5.12	XM_003971400.1 PREDICTED: Takifugu rubripes 40S ribosomal protein S7-like (LOC101073757), mRNA	0.0294	0.0326	up	-1.7841	down	-2.9869	down	-1.8167	down	-3.0195	down	-1.2027	down
MPF_LOC100696002.1.1	XM_003445297.1 PREDICTED: Oreochromis niloticus carbamoylphosphate synthase [ammonia], mitochondrial-like (LOC100696002), mRNA	0.0295	0.1340	up	0.0904	up	0.6317	up	-0.0437	down	0.4976	up	0.5413	up
MPF_LOC101472431.2.6	XM_004550961.1 PREDICTED: Maylandia zebra cytochrome P450 4B1like (LOC101472431), transcript variant X1, mRNA	0.0295	-0.0526	down	-0.3750	down	0.9658	up	-0.3224	down	1.0184	up	1.3408	up

MPF_contig_023818		0.0295	-0.6444	down	-0.1946	down	-1.7899	down	0.4498	up	-1.1455	down	-1.5954	down
MPF_ZN135.2.6	ZN135_BOVIN (sp|Q08DG8) Zinc finger protein 135 OS=Bos taurus GN=ZNF135 PE=2 SV=1	0.0295	0.0545	up	0.4470	up	1.2449	up	0.3925	up	1.1904	up	0.7979	up
MPF_LOC100703752.1.1	XP_003456347.1 PREDICTED: glia-derived nexin-like [Oreochromis niloticus]	0.0295	-0.4076	down	-0.4020	down	-2.3768	down	0.0056	up	-1.9692	down	-1.9748	down
MPF_FZD6.7.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440 IMAGE:6971142), complete cds	0.0295	-0.0901	down	-0.2502	down	-1.1759	down	-0.1600	down	-1.0858	down	-0.9257	down
MPF_LOC100700248.2.5	XP_003459295.1 PREDICTED: butyrophilinlike protein 2-like [Oreochromis niloticus]	0.0296	-0.1846	down	-0.8950	down	-2.0082	down	-0.7104	down	-1.8237	down	-1.1133	down
MPF_RIR2.1.1	[BBH] RIR2_DANRE (sp|P79733) Ribonucleosidediphosphate reductase subunit M2 OS=Danio rerio GN=rrm2 PE=1 SV=1	0.0297	-0.0161	down	0.1960	up	0.6756	up	0.2121	up	0.6917	up	0.4796	up
MPF_LOC101158190.1.1	XP_004069427.1 PREDICTED: mitochondrial inner membrane protease subunit 2-like [Oryzias latipes]	0.0298	-0.1031	down	0.0455	up	1.0463	up	0.1486	up	1.1494	up	1.0008	up

MPF_LOC101485374.1.1	XM_004557191.1 PREDICTED: Maylandia zebra ubiquitin carboxylterminal hydrolase 24-like (LOC101485374), transcript variant X2, mRNA	0.0299	0.1257	up	0.1376	up	0.8726	up	0.0118	up	0.7469	up	0.7351	up
MPF_LOC101475623.1.1	XM_004546388.1 PREDICTED: Maylandia zebra double-strand-break repair protein rad21 homolog (LOC101475623), transcript variant X1, mRNA	0.0299	0.0756	up	0.2687	up	0.6421	up	0.1931	up	0.5666	up	0.3735	up
MPF_contig_015446		0.0299	0.1454	up	0.2750	up	0.5041	up	0.1296	up	0.3587	up	0.2291	up
MPF_LOC101160514.1.1	XM_004080908.1 PREDICTED: Oryzias latipes MAGUK p55 subfamily member 7-like (LOC101160514), mRNA	0.0299	-0.0328	down	0.3280	up	1.1341	up	0.3608	up	1.1669	up	0.8061	up
MPF_LOC101163236.2.2	XP_004066987.1 PREDICTED: MAP kinaseactivating death domain protein-like [Oryzias latipes]	0.0300	-0.4626	down	-0.0250	down	0.4762	up	0.4376	up	0.9388	up	0.5012	up
MPF_LOC101472669.1.3	XM_004560278.1 PREDICTED: Maylandia zebra ganglioside-induced differentiation-associated protein 1-like 1-like (LOC101472669), mRNA	0.0300	0.0994	up	0.2778	up	0.4131	up	0.1783	up	0.3136	up	0.1353	up
MPF_LOC100708083.1.1	XM_003447253.1 PREDICTED: Oreochromis niloticus hormone-sensitive lipase-like (LOC100708083), mRNA	0.0300	0.0174	up	0.2761	up	0.8708	up	0.2587	up	0.8535	up	0.5948	up
MPF_COX1.5.7	[BBH] COX1_SALSA (sp|Q9ZZM6) Cytochrome c oxidase subunit 1 OS=Salmo salar GN=mt-co1 PE=3 SV=1	0.0301	0.0926	up	0.1566	up	1.6479	up	0.0640	up	1.5553	up	1.4913	up

MPF_LOC101487734.2.2	XM_004571292.1 PREDICTED: Maylandia zebra cytohesin-4-like (LOC101487734), mRNA	0.0301	-0.1959	down	-0.9597	down	-3.0131	down	-0.7638	down	-2.8172	down	-2.0534	down
MPF_LOC101474741.1.1	XM_004570654.1 PREDICTED: Maylandia zebra zinc transporter 6-like (LOC101474741), mRNA	0.0301	-0.3554	down	0.2983	up	1.0261	up	0.6537	up	1.3815	up	0.7278	up
MPF_contig_020773		0.0301	-0.0538	down	0.1440	up	0.4959	up	0.1977	up	0.5496	up	0.3519	up
MPF_LOC101482458.3.3	XM_004559758.1 PREDICTED: Maylandia zebra vitrin-like (LOC101482458), transcript variant X3, mRNA	0.0301	-0.2785	down	-0.1264	down	1.0012	up	0.1520	up	1.2797	up	1.1277	up
MPF_LOC100693387.2.2	XP_003457557.1 PREDICTED: coiled-coil-helixcoiled-coil-helix domaincontaining protein 7-like isoform 2 [Oreochromis niloticus]	0.0301	0.1454	up	0.1959	up	0.8031	up	0.0505	up	0.6577	up	0.6072	up
MPF_LOC101469586.1.1	XM_004560825.1 PREDICTED: Maylandia zebra striatin-interacting protein 1 homolog (LOC101469586), transcript variant X3, mRNA	0.0301	-0.0405	down	0.2653	up	1.1043	up	0.3058	up	1.1448	up	0.8391	up
MPF_LOC100174885.1.1	NM_001267644.1 Gasterosteus aculeatus ASPIP (LOC100174885), mRNA gb|DQ351706.1| Gasterosteus aculeatus cartilage acidic protein 2 (CRTAC-2) mRNA, complete cds	0.0301	0.1403	up	0.4247	up	1.1240	up	0.2844	up	0.9837	up	0.6993	up

MPF_LOC100694516.1.1	XP_003449159.1 PREDICTED: copine-9-like [Oreochromis niloticus]	0.0301	-0.3363	down	-0.3391	down	1.1426	up	-0.0028	down	1.4789	up	1.4817	up
MPF_contig_008297		0.0301	-0.0751	down	0.1240	up	0.4562	up	0.1991	up	0.5313	up	0.3322	up
MPF_contig_031699		0.0302	0.2223	up	0.6400	up	1.1797	up	0.4177	up	0.9574	up	0.5397	up
MPF_LOC101169293.7.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.0302	-0.2589	down	0.2756	up	-1.4399	down	0.5345	up	-1.1810	down	-1.7156	down
MPF_CAM-D.4.4	XM_004082666.1 PREDICTED: Oryzias latipes calmodulin (cam-d), mRNA	0.0302	-0.0601	down	0.2731	up	0.6895	up	0.3331	up	0.7496	up	0.4165	up
MPF_contig_030411		0.0302	-0.0060	down	0.2894	up	0.6620	up	0.2954	up	0.6680	up	0.3726	up
MPF_contig_015541		0.0302	-0.0364	down	0.2700	up	1.0707	up	0.3064	up	1.1071	up	0.8007	up
MPF_LOC100698716.2.2	XM_003438022.1 PREDICTED: Oreochromis niloticus glomulin-like (LOC100698716), mRNA	0.0302	0.1935	up	0.4391	up	0.8356	up	0.2456	up	0.6420	up	0.3965	up
MPF_GABPB2B.1.1	NP_001070620.1 GA repeat binding protein, beta 2b [Danio rerio]	0.0302	0.0840	up	0.2339	up	0.7304	up	0.1499	up	0.6464	up	0.4965	up
MPF_contig_044061		0.0302	-0.6898	down	-0.6839	down	-2.4720	down	0.0059	up	-1.7822	down	-1.7880	down
MPF_contig_000001		0.0302	-0.0151	down	0.2477	up	0.8268	up	0.2627	up	0.8418	up	0.5791	up
MPF_ASGL1.1.1	[BBH] ASGL1_DANRE (sp|Q5BKW9) Isoaspartyl peptidase/L-asparaginase OS=Danio rerio GN=asrgl1 PE=2 SV=1	0.0303	-0.0834	down	0.2023	up	0.7873	up	0.2857	up	0.8708	up	0.5850	up

MPF_ZN583.1.1	ZN583_MOUSE (sp|Q3V080) Zinc finger protein 583 OS=Mus musculus GN=Znf583 PE=2 SV=1	0.0303	0.0217	up	0.2880	up	1.0170	up	0.2663	up	0.9953	up	0.7290	up

MPF_SH3GL3B.1.1	NP_956475.2 SH3-domain GRB2-like 3b [Danio rerio]	0.0303	-0.1146	down	-0.0199	down	0.7795	up	0.0947	up	0.8940	up	0.7993	up
MPF_LOC100700355.1.1	XM_003442562.1 PREDICTED: Oreochromis niloticus serine/threonineprotein kinase NLK2-like (LOC100700355), mRNA	0.0303	-0.0149	down	0.4533	up	1.1303	up	0.4682	up	1.1452	up	0.6769	up
MPF_contig_008932		0.0303	-0.1291	down	0.2159	up	0.8467	up	0.3450	up	0.9758	up	0.6308	up
MPF_contig_011185		0.0303	-0.2583	down	0.5380	up	-1.5286	down	0.7963	up	-1.2702	down	-2.0665	down
MPF_LOC101465466.1.1	XM_004553276.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily A member 2-like (LOC101465466), mRNA	0.0303	0.0032	up	0.1741	up	0.6523	up	0.1710	up	0.6491	up	0.4782	up
MPF_contig_004458		0.0303	-0.2928	down	0.2373	up	1.1796	up	0.5301	up	1.4724	up	0.9423	up
MPF_LOC100709533.3.3	XM_003452328.1 PREDICTED: Oreochromis niloticus E3 ubiquitin-protein ligase FANCL-like (LOC100709533), mRNA	0.0303	-0.1336	down	0.6756	up	1.1959	up	0.8092	up	1.3295	up	0.5203	up
MPF_COX7R.3.3	COX7R_BOVIN (sp|Q3T061) Cytochrome c oxidase subunit 7A-related protein, mitochondrial OS=Bos taurus GN=COX7A2L PE=3 SV=1	0.0303	0.0230	up	-0.3364	down	0.5246	up	-0.3594	down	0.5017	up	0.8611	up

MPF_LOC101486061.1.1	XM_004563154.1 PREDICTED: Maylandia zebra protein FAM199X-like (LOC101486061), transcript variant X1, mRNA	0.0303	0.0536	up	0.4753	up	0.8791	up	0.4217	up	0.8255	up	0.4038	up
MPF_contig_028953		0.0303	-0.0469	down	0.2790	up	1.0617	up	0.3259	up	1.1085	up	0.7826	up
MPF_contig_021760		0.0303	-0.4737	down	-0.2983	down	-1.9722	down	0.1753	up	-1.4985	down	-1.6738	down
MPF_LOC101487021.1.1	XM_004540761.1 PREDICTED: Maylandia zebra thrombospondin-1-like (LOC101487021), transcript variant X2, mRNA	0.0303	-0.7313	down	-2.9891	down	-5.3941	down	-2.2578	down	-4.6628	down	-2.4050	down
MPF_LOC101484994.1.2	XM_004555447.1 PREDICTED: Maylandia zebra UPF0524 protein C3orf70 homolog A-like (LOC101484994), mRNA	0.0303	-0.2114	down	-1.2408	down	-2.8929	down	-1.0294	down	-2.6816	down	-1.6522	down
MPF_LOC101485630.2.2	XM_004552028.1 PREDICTED: Maylandia zebra transcription factor COE3-like (LOC101485630), transcript variant X3, mRNA	0.0303	0.0437	up	0.1126	up	0.6620	up	0.0689	up	0.6183	up	0.5494	up
MPF_LOC100695994.3.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.0304	0.0338	up	0.1289	up	1.0369	up	0.0952	up	1.0032	up	0.9080	up
MPF_LOC101476666.1.3	XM_004541357.1 PREDICTED: Maylandia zebra epithelial splicing regulatory protein 1-like (LOC101476666), transcript variant X2, mRNA	0.0304	0.2531	up	-0.0300	down	1.2582	up	-0.2831	down	1.0050	up	1.2882	up

MPF_LOC101473818.3.3	XM_004575140.1 PREDICTED: Maylandia zebra metallophosphoesterase MPPED2-like (LOC101473818), transcript variant X2, mRNA	0.0304	-0.0476	down	0.2979	up	1.0955	up	0.3455	up	1.1430	up	0.7975	up
MPF_contig_032770		0.0304	-0.0375	down	-0.2562	down	0.7875	up	-0.2187	down	0.8251	up	1.0437	up
MPF_LOC101167561.1.2	XP_004075784.1 PREDICTED: uncharacterized protein LOC101167561 [Oryzias latipes]	0.0304	-0.0370	down	0.3010	up	1.1384	up	0.3380	up	1.1754	up	0.8374	up
MPF_LOC101481821.1.3	XM_004550250.1 PREDICTED: Maylandia zebra DNA-directed RNA polymerase III subunit RPC9like (LOC101481821), mRNA	0.0304	-0.0358	down	-0.0397	down	1.0887	up	-0.0039	down	1.1245	up	1.1285	up
MPF_contig_020623		0.0304	-0.3891	down	0.0835	up	-1.2202	down	0.4726	up	-0.8311	down	-1.3037	down
MPF_contig_008263		0.0304	0.1517	up	0.0394	up	0.8033	up	-0.1123	down	0.6516	up	0.7638	up
MPF_LOC100712234.1.1	XM_003457656.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100712234 (LOC100712234), mRNA	0.0304	0.0679	up	-0.3457	down	-1.6976	down	-0.4136	down	-1.7655	down	-1.3519	down
MPF_NU1M.1.2	NU1M_DANRE (sp|Q9MIZ0) NADH-ubiquinone oxidoreductase chain 1 OS=Danio rerio GN=mt-nd1 PE=3 SV=1	0.0304	0.1243	up	0.3815	up	1.5339	up	0.2572	up	1.4096	up	1.1524	up
MPF_LOC101463996.1.2	XM_004569096.1 PREDICTED: Maylandia	0.0304	-0.1054	down	0.1833	up	0.8240	up	0.2886	up	0.9294	up	0.6408	up

	zebra zinc finger protein 850like (LOC101463996), mRNA													
MPF_LOC101482981.2.5	XM_004545657.1 PREDICTED: Maylandia zebra ras-related protein Rab6B-like (LOC101482981), transcript variant X6, mRNA	0.0304	0.0238	up	0.2136	up	0.6843	up	0.1897	up	0.6605	up	0.4707	up
MPF_LOC101469667.2.2	XM_004557497.1 PREDICTED: Maylandia zebra V-set and transmembrane domaincontaining protein 4-like (LOC101469667), mRNA	0.0304	-0.0334	down	0.0678	up	0.8247	up	0.1012	up	0.8581	up	0.7570	up
MPF_LOC100700648.1.1	XP_003447359.1 PREDICTED: pyruvate dehydrogenase [lipoamide] kinase isozyme 1-like [Oreochromis niloticus]	0.0305	0.1931	up	0.0072	up	0.9663	up	-0.1860	down	0.7731	up	0.9591	up
MPF_contig_019843		0.0305	-0.2384	down	-0.2615	down	-1.3697	down	-0.0230	down	-1.1312	down	-1.1082	down
MPF_LOC100690117.1.1	XP_003448481.1 PREDICTED: metastasis suppressor protein 1-like [Oreochromis niloticus]	0.0305	-0.1935	down	0.0623	up	0.7042	up	0.2558	up	0.8977	up	0.6419	up
MPF_LOC101475010.2.2	XM_004540426.1 PREDICTED: Maylandia zebra arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2like (LOC101475010), mRNA	0.0305	0.1176	up	0.4839	up	1.2054	up	0.3663	up	1.0878	up	0.7215	up
MPF_LECG.1.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.0306	-0.0040	down	0.2266	up	0.9656	up	0.2307	up	0.9696	up	0.7389	up

MPF_contig_002574		0.0306	-0.1100	down	0.1917	up	1.1126	up	0.3017	up	1.2226	up	0.9208	up
MPF_contig_026633	XM_004549165.1 PREDICTED: Maylandia zebra neurocalcin-delta Blike (LOC101473406), transcript variant X2, mRNA	0.0306	0.1471	up	0.4595	up	1.6584	up	0.3124	up	1.5113	up	1.1989	up
MPF_LOC101156833.2.4	XM_004074189.1 PREDICTED: Oryzias latipes fatty acid-binding protein, heart-like (LOC101156833), mRNA	0.0306	-0.1391	down	0.2158	up	0.7233	up	0.3549	up	0.8625	up	0.5076	up
MPF_LOC101467147.3.5	XM_004566000.1 PREDICTED: Maylandia zebra NEDD8-conjugating enzyme UBE2F-like (LOC101467147), mRNA	0.0306	-0.0198	down	0.2357	up	0.9402	up	0.2555	up	0.9601	up	0.7046	up
MPF_LOC101479692.1.1	XM_004570130.1 PREDICTED: Maylandia zebra FERM, RhoGEF and pleckstrin domain-containing protein 1-like (LOC101479692), transcript variant X1, mRNA	0.0306	-0.0713	down	0.1821	up	0.7433	up	0.2534	up	0.8146	up	0.5612	up
MPF_CYYR1.3.19	NM_212882.1 Danio rerio cysteine and tyrosine-rich protein 1 (cyyr1), mRNA gb|BC066606.1| Danio rerio cysteine and tyrosine-rich protein 1, mRNA (cDNA clone MGC:77252 IMAGE:6963826), complete cds	0.0307	0.0661	up	0.1193	up	0.6405	up	0.0532	up	0.5744	up	0.5213	up
MPF_contig_035356		0.0307	-0.3696	down	0.1286	up	-1.0812	down	0.4982	up	-0.7116	down	-1.2098	down
MPF_LOC101466862.1.1	XM_004569189.1 PREDICTED: Maylandia	0.0307	-0.1014	down	0.0859	up	0.6704	up	0.1874	up	0.7719	up	0.5845	up

	zebra zinc finger protein 40like (LOC101466862), mRNA													
MPF_contig_015103		0.0307	0.1313	up	0.3525	up	1.2107	up	0.2211	up	1.0794	up	0.8583	up
MPF_LOC100702049.1.1	XP_003458060.1 PREDICTED: major histocompatibility complex class I-related gene proteinlike [Oreochromis niloticus]	0.0307	0.0047	up	0.0735	up	0.4921	up	0.0688	up	0.4873	up	0.4185	up
MPF_LOC101471000.1.1	XM_004575946.1 PREDICTED: Maylandia zebra rap1 GTPase-GDP dissociation stimulator 1-like (LOC101471000), transcript variant X2, mRNA	0.0307	-0.1212	down	0.0569	up	0.4941	up	0.1780	up	0.6153	up	0.4372	up
MPF_contig_009499		0.0307	-0.0539	down	0.3127	up	1.0122	up	0.3666	up	1.0661	up	0.6995	up
MPF_LOC101484776.1.1	XM_004550365.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF14-like (LOC101484776), transcript variant X5, mRNA	0.0307	-0.0650	down	-0.0266	down	0.6239	up	0.0384	up	0.6889	up	0.6505	up
MPF_LOC101470425.2.2	XM_004554009.1 PREDICTED: Maylandia zebra monoglyceride lipaselike (LOC101470425), mRNA	0.0307	0.0320	up	0.3449	up	0.8742	up	0.3129	up	0.8422	up	0.5293	up
MPF_LOC101470505.1.1	XM_004550481.1 PREDICTED: Maylandia zebra mRNA-capping enzyme-like (LOC101470505), mRNA	0.0307	0.0112	up	0.2732	up	1.0105	up	0.2620	up	0.9993	up	0.7373	up
MPF_contig_033848		0.0308	-0.1908	down	0.0038	up	0.7172	up	0.1946	up	0.9080	up	0.7134	up

MPF_LOC101475041.3.3	XM_004549542.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 7-like (LOC101475041), transcript variant X2, mRNA	0.0308	0.1491	up	-1.2242	down	-3.5763	down	-1.3733	down	-3.7253	down	-2.3520	down
MPF_LOC100689830.1.6	XM_003442440.1 PREDICTED: Oreochromis niloticus mediator of RNA polymerase II transcription subunit 15-like (LOC100689830), mRNA	0.0308	-0.0861	down	0.2507	up	0.8683	up	0.3368	up	0.9544	up	0.6176	up
MPF_LOC101476265.1.2	XM_004560017.1 PREDICTED: Maylandia zebra protein LYRIC-like (LOC101476265), mRNA	0.0308	0.0340	up	0.3049	up	0.9631	up	0.2709	up	0.9292	up	0.6583	up
MPF_LOC101481552.13.41	XM_004575656.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101481552), mRNA	0.0308	-0.3202	down	0.0161	up	0.7039	up	0.3363	up	1.0241	up	0.6878	up
MPF_LOC101466337.6.22	XM_004575687.1 PREDICTED: Maylandia zebra prothymosin alpha-Blike (LOC101466337), mRNA	0.0308	0.0703	up	0.1623	up	0.6539	up	0.0920	up	0.5836	up	0.4916	up
MPF_LOC101472088.1.1	XR_190951.1 PREDICTED: Maylandia zebra uncharacterized LOC101472088 (LOC101472088), misc_RNA	0.0308	-0.2375	down	-0.0919	down	0.5776	up	0.1456	up	0.8151	up	0.6696	up
MPF_LOC101464852.2.3	XM_004569454.1 PREDICTED: Maylandia zebra unconventional myosinX-like (LOC101464852), mRNA	0.0308	0.0384	up	0.3202	up	0.8326	up	0.2818	up	0.7942	up	0.5124	up

MPF_IFIT5.6.9	NM_001142188.1 Xenopus (Silurana) tropicalis interferoninduced protein with tetratricopeptide repeats 5 (ifit5), mRNA gb|BC168560.1| Xenopus tropicalis cDNA clone MGC:184922 IMAGE:7678513, complete cds	0.0308	0.0471	up	0.2787	up	1.1327	up	0.2316	up	1.0855	up	0.8539	up
MPF_LOC100709113.1.1	XP_003458707.1 PREDICTED: E3 ubiquitinprotein ligase RNF130-like [Oreochromis niloticus]	0.0308	0.1754	up	0.4604	up	1.0916	up	0.2850	up	0.9161	up	0.6311	up
MPF_LOC101469812.1.2	XM_004571140.1 PREDICTED: Maylandia zebra polycomb group RING finger protein 3-like (LOC101469812), mRNA	0.0308	0.1194	up	0.1696	up	0.5016	up	0.0502	up	0.3823	up	0.3320	up
MPF_LOC100696885.2.2	XM_003446045.1 PREDICTED: Oreochromis niloticus C-type lectin domain family 10 member A-like (LOC100696885), mRNA	0.0308	1.1159	up	-0.9531	down	-2.6642	down	-2.0689	down	-3.7801	down	-1.7111	down
MPF_TNFAIP8L2A.1.2	NM_001045301.1 Danio rerio tumor necrosis factor, alphainduced protein 8, like 2a (tnfaip8l2a), mRNA gb|BC117652.1| Danio rerio zgc:136816, mRNA (cDNA clone MGC:136816 IMAGE:7258718), complete cds	0.0308	0.1516	up	0.2334	up	0.7003	up	0.0817	up	0.5486	up	0.4669	up
MPF_contig_047119		0.0308	-0.1218	down	-0.3020	down	-1.8190	down	-0.1802	down	-1.6971	down	-1.5169	down

MPF_LOC101483950.1.2	XM_004549875.1 PREDICTED: Maylandia zebra FCH domain only protein 2-like (LOC101483950), transcript variant X3, mRNA	0.0308	-0.0586	down	-0.0352	down	0.6511	up	0.0233	up	0.7097	up	0.6864	up
MPF_LOC101467030.1.1	XM_004563996.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 31-like (LOC101467030), mRNA	0.0308	-0.5122	down	-0.5295	down	-2.6386	down	-0.0174	down	-2.1264	down	-2.1090	down
MPF_LOC587493.3.4	XP_792312.2 PREDICTED: uncharacterized protein LOC587493 [Strongylocentrotus purpuratus]	0.0308	-0.1326	down	0.1060	up	0.6709	up	0.2386	up	0.8034	up	0.5648	up
MPF_contig_011640		0.0308	0.2897	up	-1.7535	down	-3.7130	down	-2.0432	down	-4.0028	down	-1.9595	down
MPF_LOC101477730.1.1	XM_004549268.1 PREDICTED: Maylandia zebra oxysterol-binding protein 1-like (LOC101477730), transcript variant X2, mRNA	0.0308	0.1840	up	0.4488	up	0.9235	up	0.2648	up	0.7394	up	0.4746	up
MPF_K1C18.1.2	K1C18_DANRE (sp|Q7ZTS4) Keratin, type I cytoskeletal 18 OS=Danio rerio GN=krt18 PE=1 SV=2	0.0308	-0.7460	down	-2.7377	down	-4.7676	down	-1.9916	down	-4.0216	down	-2.0299	down
MPF_LOC101470218.1.1	XM_004574288.1 PREDICTED: Maylandia zebra biotin--protein ligaselike (LOC101470218), transcript variant X1, mRNA	0.0308	0.0366	up	0.1775	up	0.6679	up	0.1409	up	0.6313	up	0.4904	up

MPF_LOC101469505.1.1	XM_004563094.1 PREDICTED: Maylandia zebra ephrin-B2a-like (LOC101469505), transcript variant X2, mRNA	0.0308	-0.5043	down	-1.4222	down	-3.4828	down	-0.9179	down	-2.9785	down	-2.0606	down
MPF_LOC101483611.1.1	XM_004563878.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF167-like (LOC101483611), transcript variant X4, mRNA	0.0309	0.1794	up	0.2463	up	0.6378	up	0.0669	up	0.4584	up	0.3915	up
MPF_LOC101479500.1.2	XM_004544158.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 34like (LOC101479500), transcript variant X2, mRNA	0.0309	0.3285	up	0.3020	up	1.0889	up	-0.0265	down	0.7604	up	0.7869	up
MPF_contig_019819		0.0309	0.0896	up	0.1847	up	0.8552	up	0.0950	up	0.7655	up	0.6705	up
MPF_LOC101063580.1.1	XP_003966085.1 PREDICTED: syndecan-2-like [Takifugu rubripes]	0.0309	-0.0584	down	-0.7518	down	-2.2666	down	-0.6934	down	-2.2082	down	-1.5148	down
MPF_LOC101064281.1.1	XP_003976694.1 PREDICTED: uncharacterized protein LOC101064281 [Takifugu rubripes]	0.0309	-0.0966	down	0.1348	up	0.7044	up	0.2314	up	0.8010	up	0.5696	up
MPF_LOC100705639.1.1	XP_003458308.1 PREDICTED: arachidonate 5lipoxygenase-activating protein-like isoform 1 [Oreochromis niloticus]	0.0309	0.0229	up	0.1313	up	0.6611	up	0.1084	up	0.6382	up	0.5299	up
MPF_contig_013416	XM_004574108.1 PREDICTED: Maylandia zebra alpha-actinin-4-like (LOC101467576), transcript variant X2, mRNA	0.0309	-0.1413	down	-0.2471	down	1.1686	up	-0.1057	down	1.3099	up	1.4156	up

MPF_LOC101067996.1.1	XP_003964368.1 PREDICTED: caskin-1-like [Takifugu rubripes]	0.0309	-0.0815	down	0.0514	up	0.7148	up	0.1329	up	0.7963	up	0.6634	up
MPF_RPL10A.1.1	NM_199636.1 Danio rerio ribosomal protein L10a (rpl10a), mRNA gb|BC059454.1| Danio rerio ribosomal protein L10a, mRNA (cDNA clone MGC:73082 IMAGE:4199288), complete cds	0.0309	-0.0542	down	0.1849	up	0.7000	up	0.2390	up	0.7542	up	0.5152	up
MPF_LOC100696926.1.1	XM_003454892.1 PREDICTED: Oreochromis niloticus pleckstrin homology domain-containing family M member 3-like (LOC100696926), mRNA	0.0309	0.0338	up	0.5153	up	0.9974	up	0.4815	up	0.9637	up	0.4822	up
MPF_LOC101477975.1.1	XM_004538253.1 PREDICTED: Maylandia zebra RIMS-binding protein 2like (LOC101477975), transcript variant X3, mRNA	0.0309	-0.1981	down	0.1424	up	0.7617	up	0.3405	up	0.9598	up	0.6193	up
MPF_COX2.4.4	[BBH] COX2_GADMO (sp|Q37741) Cytochrome c oxidase subunit 2 OS=Gadus morhua GN=mt-co2 PE=3 SV=1	0.0310	0.0379	up	0.0263	up	1.4389	up	-0.0116	down	1.4010	up	1.4126	up
MPF_OSTC.2.3	OSTC_DANRE (sp|Q7ZWJ3) Oligosaccharyltransferase complex subunit ostc OS=Danio rerio GN=ostc PE=2 SV=1	0.0310	-0.3212	down	-1.0718	down	-2.1123	down	-0.7506	down	-1.7911	down	-1.0405	down

MPF_LOC101475206.2.4	XR_191621.1 PREDICTED: Maylandia zebra uncharacterized LOC101475206 (LOC101475206), transcript variant X2, misc_RNA	0.0310	-0.0161	down	0.1645	up	1.0345	up	0.1806	up	1.0506	up	0.8699	up
MPF_CDC20.1.1	NP_001133251.1 cell division cycle protein 20 homolog [Salmo salar]	0.0310	-0.1741	down	0.2394	up	0.7630	up	0.4135	up	0.9371	up	0.5236	up
MPF_contig_028671		0.0310	-0.1444	down	-0.1817	down	0.6759	up	-0.0373	down	0.8203	up	0.8577	up
MPF_LOC101476926.1.1	XM_004540524.1 PREDICTED: Maylandia zebra uncharacterized LOC101476926 (LOC101476926), transcript variant X1, mRNA	0.0311	-0.0181	down	0.3740	up	0.7736	up	0.3921	up	0.7917	up	0.3997	up
MPF_contig_030509	XM_004568369.1 PREDICTED: Maylandia zebra arfaptin-1-like (LOC101482665), transcript variant X2, mRNA	0.0311	-0.0014	down	0.1683	up	0.7885	up	0.1697	up	0.7899	up	0.6202	up
MPF_LOC101469573.1.1	XM_004555762.1 PREDICTED: Maylandia zebra RING finger protein 214-like (LOC101469573), mRNA	0.0311	-0.0290	down	0.1236	up	0.8892	up	0.1526	up	0.9181	up	0.7656	up
MPF_LOC101463781.1.1	XM_004541855.1 PREDICTED: Maylandia zebra dihydrolipoyllysineresidue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial-like (LOC101463781), mRNA	0.0311	0.0251	up	0.1632	up	0.9478	up	0.1381	up	0.9226	up	0.7846	up

MPF_CRE_23222.1.2	XP_003089877.1 hypothetical protein CRE_23222 [Caenorhabditis remanei]	0.0311	-0.5578	down	-0.4422	down	-1.6007	down	0.1156	up	-1.0429	down	-1.1585	down
MPF_LOC100700215.1.1	XM_003451785.1 PREDICTED: Oreochromis niloticus E3 ubiquitin-protein ligase synoviolin-like (LOC100700215), mRNA	0.0311	-0.2818	down	-0.0493	down	0.6121	up	0.2325	up	0.8939	up	0.6613	up
MPF_LOC101476131.1.1	XM_004550034.1 PREDICTED: Maylandia zebra thrombospondin type-1 domain-containing protein 1like (LOC101476131), mRNA	0.0311	-0.1845	down	0.0865	up	0.5821	up	0.2710	up	0.7666	up	0.4956	up
MPF_LOC100709351.3.10	XM_003449499.1 PREDICTED: Oreochromis niloticus integral membrane protein 2B-like (LOC100709351), mRNA	0.0312	-0.0498	down	0.3142	up	1.0514	up	0.3640	up	1.1012	up	0.7372	up
MPF_LOC101485244.1.1	XM_004568719.1 PREDICTED: Maylandia zebra zinc transporter 1-like (LOC101485244), mRNA	0.0312	-0.2718	down	-1.0625	down	-2.4877	down	-0.7907	down	-2.2159	down	-1.4252	down
MPF_contig_016528		0.0313	-0.1708	down	-0.1585	down	0.3739	up	0.0123	up	0.5447	up	0.5324	up
MPF_LOC100712519.4.4	XP_003439047.1 PREDICTED: cytosolic sulfotransferase 3-like [Oreochromis niloticus]	0.0313	-0.0540	down	0.3134	up	-1.9215	down	0.3674	up	-1.8675	down	-2.2349	down
MPF_ALDOAA.1.1	NP_919358.2 fructosebisphosphate aldolase A [Danio rerio]	0.0313	0.0755	up	0.5635	up	1.1169	up	0.4880	up	1.0413	up	0.5533	up
MPF_contig_032867		0.0314	-0.0275	down	0.3260	up	1.1059	up	0.3535	up	1.1334	up	0.7800	up

MPF_LOC101073335.1.1	XM_003978467.1 PREDICTED: Takifugu rubripes tRNA wybutosinesynthesizing protein 3 homolog (LOC101073335), mRNA	0.0314	0.1507	up	0.3237	up	0.6550	up	0.1730	up	0.5043	up	0.3313	up
MPF_ZN569.1.1	ZN569_MOUSE (sp|Q80W31) Zinc finger protein 569 OS=Mus musculus GN=Znf569 PE=2 SV=2	0.0314	0.3624	up	0.3804	up	1.2898	up	0.0180	up	0.9274	up	0.9094	up
MPF_contig_032379		0.0314	0.2589	up	-0.0929	down	-1.1901	down	-0.3518	down	-1.4490	down	-1.0972	down
MPF_COX2.3.4	COX2_DANRE (sp|Q9MIY7) Cytochrome c oxidase subunit 2 OS=Danio rerio GN=mt-co2 PE=3 SV=1	0.0314	0.2545	up	0.0326	up	1.3731	up	-0.2219	down	1.1186	up	1.3405	up
MPF_contig_008402		0.0315	0.0649	up	-0.1307	down	-0.7699	down	-0.1956	down	-0.8348	down	-0.6393	down
MPF_contig_037637		0.0315	-0.3965	down	-0.2927	down	-1.1123	down	0.1038	up	-0.7158	down	-0.8196	down
MPF_LOC100705819.1.1	XP_003438527.1 PREDICTED: hypothetical protein LOC100705819 [Oreochromis niloticus]	0.0315	-0.0730	down	-0.6312	down	-2.1713	down	-0.5582	down	-2.0983	down	-1.5401	down
MPF_ZG57.6.12	ZG57_XENLA (sp|P18729) Gastrula zinc finger protein XlCGF57.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.0315	0.0646	up	0.2586	up	0.4707	up	0.1940	up	0.4062	up	0.2121	up
MPF_LOC101073827.1.1	XP_003967391.1 PREDICTED: actin-related protein 6-like [Takifugu rubripes]	0.0315	-0.0723	down	0.2301	up	1.1738	up	0.3024	up	1.2461	up	0.9437	up

MPF_LOC101169532.31.45	XP_004070110.1 PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Oryzias latipes]	0.0315	-0.0485	down	0.1193	up	0.7168	up	0.1678	up	0.7653	up	0.5974	up

MPF_contig_038087	XM_004542400.1 PREDICTED: Maylandia zebra microtubule-associated serine/threonine-protein kinase 3-like (LOC101482573), transcript variant X5, mRNA	0.0316	0.0080	up	-0.0193	down	0.6972	up	-0.0273	down	0.6891	up	0.7165	up
MPF_contig_003901		0.0316	0.3099	up	0.6223	up	0.7771	up	0.3124	up	0.4672	up	0.1548	up
MPF_contig_034681		0.0316	-0.0533	down	0.2545	up	0.8790	up	0.3078	up	0.9323	up	0.6245	up
MPF_contig_046558	XM_003198881.1 PREDICTED: Danio rerio retrotransposable element Tf2 155 kDa protein type 1like (LOC100535308), mRNA	0.0316	-0.7663	down	-0.1897	down	-1.9225	down	0.5766	up	-1.1562	down	-1.7328	down
MPF_LOC101466696.1.1	XM_004545878.1 PREDICTED: Maylandia zebra uncharacterized LOC101466696 (LOC101466696), mRNA	0.0316	-0.0253	down	0.2709	up	1.1529	up	0.2962	up	1.1782	up	0.8820	up
MPF_contig_037214		0.0316	0.0859	up	-0.0242	down	0.7889	up	-0.1101	down	0.7030	up	0.8132	up
MPF_LOC101476868.2.2	XM_004568867.1 PREDICTED: Maylandia zebra aryl hydrocarbon receptor nuclear translocatorlike protein 2-like (LOC101476868), mRNA	0.0316	-0.1563	down	-0.2756	down	-1.0654	down	-0.1193	down	-0.9090	down	-0.7898	down

MPF_LOC101480539.1.1	XM_004565871.1 PREDICTED: Maylandia zebra autism susceptibility gene 2 protein-like (LOC101480539), transcript variant X5, mRNA	0.0316	-0.0701	down	0.1287	up	0.9445	up	0.1988	up	1.0146	up	0.8158	up
MPF_contig_042609		0.0317	0.0833	up	0.1755	up	0.7583	up	0.0922	up	0.6750	up	0.5829	up
MPF_LOC101486439.1.1	XM_004561632.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 21like (LOC101486439), mRNA	0.0317	-1.0287	down	-0.9150	down	-2.6146	down	0.1136	up	-1.5859	down	-1.6996	down
MPF_LOC100696496.1.2	XM_003458306.1 PREDICTED: Oreochromis niloticus nucleolar protein 11like (LOC100696496), mRNA	0.0317	-0.0634	down	0.1827	up	0.8235	up	0.2461	up	0.8869	up	0.6408	up
MPF_contig_018562		0.0318	0.3452	up	0.4043	up	0.9523	up	0.0591	up	0.6071	up	0.5480	up
MPF_LOC101477400.1.4	XM_004538536.1 PREDICTED: Maylandia zebra cyclin-G2-like (LOC101477400), mRNA	0.0318	0.0863	up	0.2991	up	1.4303	up	0.2128	up	1.3440	up	1.1312	up
MPF_ZG26.1.1	ZG26_XENLA (sp|P18715) Gastrula zinc finger protein XlCGF26.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.0318	0.0401	up	0.2201	up	1.2330	up	0.1800	up	1.1929	up	1.0129	up
MPF_contig_029011		0.0318	0.0903	up	0.0017	up	0.3879	up	-0.0886	down	0.2976	up	0.3862	up

MPF_LOC101482306.1.2	XM_004548843.1 PREDICTED: Maylandia zebra phosphoenolpyruvate carboxykinase, cytosolic [GTP]-like (LOC101482306), mRNA	0.0319	-0.0105	down	0.1288	up	0.8145	up	0.1392	up	0.8250	up	0.6857	up
MPF_PPIF.5.5	PPIF_RAT (sp|P29117) Peptidyl-prolyl cis-trans isomerase F, mitochondrial OS=Rattus norvegicus GN=Ppif PE=1 SV=2	0.0319	0.1454	up	0.3665	up	0.9165	up	0.2211	up	0.7711	up	0.5500	up
MPF_LOC101483661.5.5	XM_004572907.1 PREDICTED: Maylandia zebra traf2 and NCKinteracting protein kinase-like (LOC101483661), transcript variant X1, mRNA	0.0319	-0.1623	down	0.0696	up	0.7966	up	0.2319	up	0.9589	up	0.7270	up
MPF_LOC100708426.1.1	XM_003444752.1 PREDICTED: Oreochromis niloticus integrator complex subunit 10-like, transcript variant 2 (LOC100708426), mRNA	0.0319	0.2551	up	0.3633	up	1.0220	up	0.1082	up	0.7669	up	0.6587	up
MPF_LOC100708169.1.1	XM_003447997.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100708169 (LOC100708169), mRNA	0.0319	-0.1113	down	0.2589	up	0.9658	up	0.3702	up	1.0771	up	0.7069	up
MPF_LOC101472989.2.6	XM_004566934.1 PREDICTED: Maylandia zebra CAP-Gly domaincontaining linker protein 1like (LOC101472989), transcript variant X5, mRNA	0.0319	0.0004	up	-0.1950	down	1.0425	up	-0.1954	down	1.0420	up	1.2374	up
MPF_LOC101078388.2.4	XM_003968304.1 PREDICTED: Takifugu rubripes uncharacterized	0.0319	-0.1443	down	-0.3707	down	-1.2715	down	-0.2264	down	-1.1272	down	-0.9008	down

	LOC101078388 (LOC101078388), mRNA													
MPF_LOC100694852.2.2	XM_003443194.1 PREDICTED: Oreochromis niloticus heme-binding protein 1-like (LOC100694852), mRNA	0.0319	-0.0166	down	0.1306	up	0.6301	up	0.1472	up	0.6467	up	0.4995	up
MPF_LOC101488136.1.2	XM_004558958.1 PREDICTED: Maylandia zebra RNA-binding protein 39like (LOC101488136), mRNA	0.0319	0.0044	up	0.1933	up	0.6860	up	0.1889	up	0.6816	up	0.4927	up

MPF_LOC100696661.1.1	XP_003455356.1 PREDICTED: probable glutathione peroxidase 8-like [Oreochromis niloticus]	0.0319	0.0291	up	0.3097	up	0.9653	up	0.2807	up	0.9362	up	0.6556	up
MPF_LOC101469726.1.2	XM_004572396.1 PREDICTED: Maylandia zebra pre-mRNA 3' end processing protein WDR33like (LOC101469726), transcript variant X2, mRNA	0.0319	0.7623	up	0.5501	up	1.0515	up	-0.2122	down	0.2892	up	0.5014	up
MPF_contig_029231		0.0319	-0.6007	down	-0.7411	down	-2.8796	down	-0.1404	down	-2.2789	down	-2.1385	down
MPF_LOC101483267.2.2	XM_004568893.1 PREDICTED: Maylandia zebra anoctamin-4-like (LOC101483267), transcript variant X2, mRNA	0.0319	0.0517	up	0.1982	up	0.6140	up	0.1465	up	0.5623	up	0.4159	up
MPF_LOC100700824.1.1	XP_003446439.1 PREDICTED: putative ATPdependent Clp protease proteolytic subunit, mitochondrial-like [Oreochromis niloticus]	0.0319	-0.2150	down	0.1947	up	0.9117	up	0.4096	up	1.1267	up	0.7171	up

MPF_CP2K1.1.1	CP2K1_ONCMY (sp|Q92090) Cytochrome P450 2K1 OS=Oncorhynchus mykiss GN=cyp2k1 PE=2 SV=1	0.0319	-0.0379	down	0.1343	up	1.2125	up	0.1722	up	1.2504	up	1.0782	up
MPF_contig_038045		0.0319	-0.1652	down	0.1953	up	0.8944	up	0.3604	up	1.0596	up	0.6991	up
MPF_contig_027390		0.0319	-0.0849	down	0.0596	up	0.9575	up	0.1446	up	1.0425	up	0.8979	up
MPF_LOC101481869.3.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA	0.0319	-0.0089	down	0.1491	up	0.9395	up	0.1580	up	0.9484	up	0.7904	up
MPF_LOC101477513.1.1	XM_004565497.1 PREDICTED: Maylandia zebra syntaphilin-like (LOC101477513), transcript variant X3, mRNA	0.0319	-0.0394	down	0.0027	up	0.7717	up	0.0421	up	0.8110	up	0.7690	up
MPF_LOC100703754.1.1	XM_003456632.1 PREDICTED: Oreochromis niloticus mannosyloligosaccharide 1,2-alphamannosidase IA-like (LOC100703754), mRNA	0.0320	-0.4381	down	-0.4984	down	-2.4804	down	-0.0603	down	-2.0423	down	-1.9820	down
MPF_LOC101476415.1.1	XM_004548724.1 PREDICTED: Maylandia zebra prostacyclin synthaselike (LOC101476415), mRNA	0.0320	-0.1813	down	0.0118	up	-1.3791	down	0.1931	up	-1.1978	down	-1.3910	down
MPF_LOC100693334.1.1	XP_003443821.1 PREDICTED: 39S ribosomal protein L36, mitochondriallike [Oreochromis niloticus]	0.0320	-0.1845	down	0.0082	up	1.3504	up	0.1927	up	1.5349	up	1.3422	up
MPF_contig_029996		0.0321	0.0438	up	0.0631	up	0.7763	up	0.0193	up	0.7325	up	0.7131	up

MPF_contig_006449	XM_004560824.1 PREDICTED: Maylandia zebra striatin-interacting protein 1 homolog (LOC101469586), transcript variant X2, mRNA	0.0321	0.2755	up	0.2167	up	1.2250	up	-0.0588	down	0.9496	up	1.0083	up
MPF_LOC100705343.3.3	XM_003450141.1 PREDICTED: Oreochromis niloticus claudin-8-like (LOC100705343), mRNA	0.0321	-0.4227	down	-2.0663	down	-4.5995	down	-1.6436	down	-4.1767	down	-2.5332	down
MPF_LOC100706657.3.3	XP_003447550.1 PREDICTED: CD48 antigenlike [Oreochromis niloticus]	0.0322	0.1137	up	-1.1837	down	-3.1376	down	-1.2974	down	-3.2513	down	-1.9539	down
MPF_LOC101167735.1.1	XM_004078595.1 PREDICTED: Oryzias latipes heterogeneous nuclear ribonucleoprotein C-like (LOC101167735), mRNA	0.0323	0.1431	up	0.3129	up	1.0349	up	0.1697	up	0.8918	up	0.7221	up
MPF_contig_045551		0.0323	-0.1272	down	-0.6215	down	-1.6476	down	-0.4943	down	-1.5204	down	-1.0261	down
MPF_contig_004345		0.0323	0.1464	up	0.3288	up	0.6513	up	0.1823	up	0.5048	up	0.3225	up
MPF_contig_013080		0.0323	-0.1401	down	0.0477	up	0.8220	up	0.1878	up	0.9621	up	0.7743	up
MPF_LOC100704351.1.1	XM_003448735.1 PREDICTED: Oreochromis niloticus pleckstrin homology domain-containing family M member 1-like (LOC100704351), mRNA	0.0323	0.1610	up	-0.0112	down	0.4859	up	-0.1722	down	0.3248	up	0.4970	up
MPF_LOC101482403.1.1	XM_004548923.1 PREDICTED: Maylandia zebra proteasome subunit beta type-2-like (LOC101482403), transcript variant X2, mRNA	0.0324	0.1066	up	0.0983	up	0.6412	up	-0.0083	down	0.5346	up	0.5429	up

MPF_LOC101464198.1.1	XM_004546987.1 PREDICTED: Maylandia zebra polyadenylate-binding protein-interacting protein 1like (LOC101464198), mRNA	0.0324	-0.2715	down	-0.0217	down	0.6761	up	0.2499	up	0.9476	up	0.6977	up
MPF_LOC101464855.1.1	XM_004546244.1 PREDICTED: Maylandia zebra signal peptide, CUB and EGF-like domaincontaining protein 3-like (LOC101464855), transcript variant X1, mRNA	0.0325	-0.2133	down	-1.7415	down	-4.0917	down	-1.5283	down	-3.8785	down	-2.3502	down
MPF_contig_023741		0.0325	-0.0836	down	0.0306	up	0.6703	up	0.1142	up	0.7540	up	0.6397	up
MPF_contig_013323		0.0325	-0.0327	down	0.1150	up	0.4108	up	0.1477	up	0.4435	up	0.2959	up
MPF_LOC101464081.1.3	XM_004540929.1 PREDICTED: Maylandia zebra gamma-aminobutyric acid receptor subunit beta-2like (LOC101464081), transcript variant X2, mRNA	0.0325	0.0435	up	0.0186	up	0.6036	up	-0.0248	down	0.5601	up	0.5849	up
MPF_AL9A1.2.2	[BBH] AL9A1_ORYLA (sp|Q19A30) Aldehyde dehydrogenase family 9 member A1 OS=Oryzias latipes GN=aldh9A1 PE=2 SV=1	0.0326	0.0249	up	0.2724	up	0.8680	up	0.2475	up	0.8431	up	0.5956	up
MPF_BSL1.1.2	BSL1_TRIVA (sp|Q8MTI2) Putative surface protein bspAlike OS=Trichomonas vaginalis GN=BSPAL1 PE=4 SV=1	0.0326	-0.1467	down	0.0638	up	0.7834	up	0.2105	up	0.9302	up	0.7197	up
MPF_contig_029898		0.0326	-0.1424	down	0.3248	up	1.1752	up	0.4673	up	1.3176	up	0.8503	up

MPF_LOC101485878.1.1	XM_004546034.1 PREDICTED: Maylandia zebra poly(rC)-binding protein 4-like (LOC101485878), transcript variant X2, mRNA	0.0326	-0.1469	down	-0.2300	down	0.8461	up	-0.0830	down	0.9930	up	1.0760	up
MPF_LOC100709088.1.1	XP_003452033.1 PREDICTED: tripartite motifcontaining protein 16-like [Oreochromis niloticus]	0.0326	0.0704	up	0.3815	up	0.8170	up	0.3112	up	0.7466	up	0.4355	up
MPF_LOC101468719.1.2	XM_004559706.1 PREDICTED: Maylandia zebra kinesin light chain 1like (LOC101468719), transcript variant X6, mRNA	0.0326	0.0398	up	0.0439	up	0.6937	up	0.0040	up	0.6539	up	0.6499	up
MPF_LOC101472832.1.1	XM_004552630.1 PREDICTED: Maylandia zebra cysteine and tyrosinerich protein 1-like (LOC101472832), mRNA	0.0326	0.0304	up	0.5057	up	1.1731	up	0.4753	up	1.1427	up	0.6673	up
MPF_contig_018377	XM_004572780.1 PREDICTED: Maylandia zebra unconventional myosinXVIIIa-like (LOC101474105), transcript variant X1, mRNA	0.0326	-0.1170	down	0.1191	up	0.7003	up	0.2361	up	0.8173	up	0.5812	up
MPF_contig_021167	XM_004541554.1 PREDICTED: Maylandia zebra amyloid-like protein 2like (LOC101480044), transcript variant X1, mRNA	0.0326	-0.1791	down	-0.6553	down	-2.2215	down	-0.4762	down	-2.0424	down	-1.5663	down
MPF_LOC100700605.27.27	XM_003458555.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100700605), mRNA	0.0326	0.1232	up	0.5999	up	1.7622	up	0.4767	up	1.6390	up	1.1623	up

MPF_contig_028924		0.0326	0.1202	up	0.2083	up	0.6603	up	0.0882	up	0.5402	up	0.4520	up
MPF_LOC100696796.2.2	XM_003445884.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100696796 (LOC100696796), mRNA	0.0326	0.0286	up	-0.9169	down	-2.5433	down	-0.9456	down	-2.5719	down	-1.6263	down
MPF_LOC101464595.1.1	XM_004550738.1 PREDICTED: Maylandia zebra uncharacterized LOC101464595 (LOC101464595), mRNA	0.0326	0.1336	up	0.2793	up	1.0898	up	0.1457	up	0.9562	up	0.8106	up
MPF_contig_041807		0.0326	-0.0100	down	0.1681	up	0.6442	up	0.1781	up	0.6542	up	0.4760	up
MPF_contig_011981		0.0326	0.0067	up	-1.6122	down	-4.2178	down	-1.6189	down	-4.2244	down	-2.6055	down
MPF_BRAFLDRAFT_96790.1.1	XP_002595816.1 hypothetical protein BRAFLDRAFT_96790 [Branchiostoma floridae]	0.0326	0.0162	up	0.0775	up	0.8334	up	0.0613	up	0.8172	up	0.7559	up
MPF_LOC101488070.1.1	XM_004543546.1 PREDICTED: Maylandia zebra neprilysin-like (LOC101488070), transcript variant X1, mRNA	0.0327	-1.7127	down	-3.7366	down	-6.1583	down	-2.0239	down	-4.4456	down	-2.4217	down
MPF_LOC101464804.1.1	XM_004556769.1 PREDICTED: Maylandia zebra ankyrin-3-like (LOC101464804), transcript variant X1, mRNA	0.0327	-0.2117	down	-0.0201	down	-2.4378	down	0.1916	up	-2.2261	down	-2.4178	down
MPF_LOC101156189.1.1	XM_004076645.1 PREDICTED: Oryzias latipes tetratricopeptide repeat protein 1-like	0.0327	-0.0410	down	0.1364	up	0.5619	up	0.1775	up	0.6029	up	0.4255	up

	(LOC101156189), mRNA													
MPF_LOC101073138.2.2	XP_003966361.1 PREDICTED: tumor necrosis factor receptor superfamily member 5-like [Takifugu rubripes]	0.0327	-0.1843	down	-0.1037	down	0.6191	up	0.0805	up	0.8034	up	0.7228	up
MPF_LOC101169385.2.3	XP_004077303.1 PREDICTED: zinc finger protein 318-like [Oryzias latipes]	0.0327	-0.0648	down	0.1579	up	0.9850	up	0.2227	up	1.0498	up	0.8271	up
MPF_LOC101475582.1.2	XM_004558092.1 PREDICTED: Maylandia zebra mediator of RNA polymerase II transcription subunit 13-like (LOC101475582), mRNA	0.0327	0.1578	up	0.3306	up	1.0538	up	0.1728	up	0.8960	up	0.7232	up
MPF_contig_028027		0.0328	-0.1040	down	0.1087	up	0.6800	up	0.2128	up	0.7841	up	0.5713	up
MPF_LOC100703241.5.9	XM_003440649.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S29-like (LOC100703241), mRNA	0.0328	-0.1433	down	0.2636	up	1.1848	up	0.4069	up	1.3281	up	0.9212	up
MPF_LOC101487598.1.1	XM_004565176.1 PREDICTED: Maylandia zebra transmembrane protein 158-like (LOC101487598), mRNA	0.0328	-0.2486	down	-0.2882	down	0.9827	up	-0.0396	down	1.2313	up	1.2709	up
MPF_contig_041447		0.0329	0.2023	up	0.3901	up	0.7672	up	0.1879	up	0.5649	up	0.3770	up
MPF_contig_037860		0.0329	-0.0370	down	-0.0241	down	0.8136	up	0.0130	up	0.8506	up	0.8376	up
MPF_contig_020093		0.0329	-0.1455	down	0.1689	up	0.8698	up	0.3144	up	1.0153	up	0.7009	up

MPF_LOC101112592.1.4	XP_004015912.1 PREDICTED: 40S ribosomal protein S15a-like [Ovis aries]	0.0329	0.2399	up	-0.2906	down	-1.0389	down	-0.5305	down	-1.2788	down	-0.7483	down
MPF_B2MG.1.10	B2MG_CYPCA (sp|Q03422) Beta-2-microglobulin OS=Cyprinus carpio GN=b2m PE=3 SV=1	0.0329	-0.0030	down	0.1043	up	0.6257	up	0.1073	up	0.6286	up	0.5214	up
MPF_LOC100698998.2.7	XM_003439446.1 PREDICTED: Oreochromis niloticus myosin heavy chain, fast skeletal muscle-like (LOC100698998), mRNA	0.0329	-0.1004	down	-1.2819	down	-3.0861	down	-1.1815	down	-2.9857	down	-1.8043	down
MPF_LOC101470873.3.3	XM_004543575.1 PREDICTED: Maylandia zebra importin subunit alpha- 4-like (LOC101470873), mRNA	0.0329	0.1177	up	0.1490	up	0.7849	up	0.0313	up	0.6673	up	0.6360	up
MPF_LOC101476996.1.1	XM_004575053.1 PREDICTED: Maylandia zebra outer dense fiber protein 2-like (LOC101476996), transcript variant X4, mRNA	0.0329	-0.4120	down	0.0808	up	1.3539	up	0.4928	up	1.7660	up	1.2732	up
MPF_LOC101482450.2.2	XM_004556283.1 PREDICTED: Maylandia zebra putative tRNA (cytidine(32)/guanosine(34)2'-O)-methyltransferase-like (LOC101482450), mRNA	0.0330	0.0006	up	0.2378	up	0.8376	up	0.2372	up	0.8370	up	0.5998	up
MPF_LOC101468323.2.2	XM_004561832.1 PREDICTED: Maylandia zebra exportin-7-like (LOC101468323), mRNA	0.0330	0.0172	up	0.1849	up	0.8740	up	0.1678	up	0.8568	up	0.6890	up

MPF_LOC101476780.4.7	XM_004544243.1 PREDICTED: Maylandia zebra serine/threonineprotein phosphatase 2A 55 kDa regulatory subunit B alpha isoform-like (LOC101476780), mRNA	0.0330	-0.0239	down	0.1191	up	0.5456	up	0.1431	up	0.5696	up	0.4265	up

MPF_LOC101476071.1.1	XM_004541164.1 PREDICTED: Maylandia zebra uncharacterized LOC101476071 (LOC101476071), mRNA	0.0330	-0.7901	down	-1.7977	down	-3.8232	down	-1.0076	down	-3.0331	down	-2.0255	down
MPF_LOC101485038.1.1	XM_004568542.1 PREDICTED: Maylandia zebra uncharacterized LOC101485038 (LOC101485038), transcript variant X2, mRNA	0.0330	0.0475	up	0.1972	up	1.1290	up	0.1497	up	1.0815	up	0.9318	up
MPF_LOC101464439.2.2	XM_004539111.1 PREDICTED: Maylandia zebra CD97 antigen-like (LOC101464439), transcript variant X2, mRNA	0.0330	0.2235	up	-0.7619	down	-1.7515	down	-0.9854	down	-1.9750	down	-0.9896	down
MPF_LOC100694329.2.3	XM_003445703.1 PREDICTED: Oreochromis niloticus proteolipid protein 2like (LOC100694329), mRNA	0.0330	-0.1744	down	-0.9402	down	-2.7488	down	-0.7657	down	-2.5743	down	-1.8086	down
MPF_LOC100696870.1.2	XM_003442549.1 PREDICTED: Oreochromis niloticus WAS/WASL-interacting protein family member 2-like (LOC100696870), mRNA	0.0330	-0.0633	down	-0.0579	down	0.7083	up	0.0054	up	0.7716	up	0.7662	up

MPF_LOC101157745.7.7	XM_004082934.1 PREDICTED: Oryzias latipes uncharacterized LOC101157745 (LOC101157745), mRNA	0.0330	0.0640	up	0.1290	up	1.3841	up	0.0650	up	1.3201	up	1.2550	up
MPF_contig_049010		0.0330	0.3389	up	0.3147	up	0.8674	up	-0.0242	down	0.5285	up	0.5527	up
MPF_LOC101155558.1.1	XM_004082371.1 PREDICTED: Oryzias latipes interferon alpha-inducible protein 27-like protein 2-like (LOC101155558), mRNA	0.0330	-0.5407	down	-0.8960	down	-3.4015	down	-0.3553	down	-2.8608	down	-2.5055	down
MPF_contig_045090		0.0330	-0.0903	down	-0.0498	down	0.8450	up	0.0405	up	0.9353	up	0.8948	up
MPF_contig_031758	XM_004550291.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101467183), transcript variant X2, mRNA	0.0330	-0.0628	down	-0.9450	down	-2.7981	down	-0.8822	down	-2.7353	down	-1.8531	down
MPF_LOC100708308.2.2	XP_003459094.1 PREDICTED: hypothetical protein LOC100708308 [Oreochromis niloticus]	0.0331	0.0576	up	0.0852	up	0.5090	up	0.0276	up	0.4514	up	0.4238	up
MPF_contig_016564		0.0332	-0.0529	down	-0.0201	down	0.5957	up	0.0328	up	0.6486	up	0.6159	up
MPF_LOC101172159.1.1	XP_004070199.1 PREDICTED: L-fucose kinase-like [Oryzias latipes]	0.0332	-0.1832	down	-0.2825	down	0.6146	up	-0.0993	down	0.7978	up	0.8971	up
MPF_contig_044592		0.0332	-0.0872	down	0.0027	up	0.5454	up	0.0899	up	0.6326	up	0.5427	up
MPF_LOC101066181.1.1	XM_003962298.1 PREDICTED: Takifugu rubripes serine dehydrataselike (LOC101066181), mRNA	0.0332	0.3037	up	1.1899	up	1.6137	up	0.8862	up	1.3100	up	0.4238	up

MPF_contig_045308	WP_006987701.1 hypothetical protein [Gillisia limnaea]	0.0332	0.1600	up	0.2415	up	0.8630	up	0.0815	up	0.7030	up	0.6215	up
MPF_LOC101475562.1.1	XM_004576257.1 PREDICTED: Maylandia zebra protein dpy-30 homolog (LOC101475562), transcript variant X2, mRNA	0.0332	0.1729	up	0.1897	up	0.9797	up	0.0168	up	0.8068	up	0.7900	up
MPF_LOC101482427.2.2	XM_004551740.1 PREDICTED: Maylandia zebra arachidonate 5lipoxygenase-like (LOC101482427), mRNA	0.0332	-0.3783	down	-0.3764	down	0.8092	up	0.0019	up	1.1875	up	1.1856	up
MPF_LOC100690746.1.2	XM_003448354.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S23-like (LOC100690746), mRNA	0.0332	-0.0251	down	0.3559	up	1.3025	up	0.3809	up	1.3276	up	0.9466	up
MPF_contig_015878		0.0332	0.1490	up	0.3929	up	0.7920	up	0.2439	up	0.6430	up	0.3991	up
MPF_contig_036782		0.0332	0.0912	up	0.4189	up	0.8517	up	0.3277	up	0.7605	up	0.4328	up
MPF_LOC100701849.2.5	XM_003453196.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100701849 (LOC100701849), mRNA	0.0332	0.1189	up	0.0509	up	0.7867	up	-0.0681	down	0.6678	up	0.7359	up
MPF_LOC101066836.1.1	XP_003975723.1 PREDICTED: pyroglutamylpeptidase 1-like [Takifugu rubripes]	0.0332	-0.0115	down	0.4738	up	0.7595	up	0.4853	up	0.7710	up	0.2858	up
MPF_contig_046862		0.0332	0.0684	up	0.0976	up	0.7101	up	0.0292	up	0.6417	up	0.6126	up
MPF_ACTC.8.8	ACTC_TAKRU (sp|P53480) Actin, alpha cardiac OS=Takifugu rubripes PE=2	0.0332	-0.1367	down	-0.1046	down	0.4366	up	0.0321	up	0.5733	up	0.5412	up

	SV=1													
MPF_LOC101156670.1.1	XP_004076053.1 PREDICTED: POU domain class 2-associating factor 1like [Oryzias latipes]	0.0332	-0.0977	down	-0.0115	down	0.9351	up	0.0862	up	1.0328	up	0.9466	up
MPF_contig_028743		0.0332	-0.0542	down	0.0551	up	0.4372	up	0.1093	up	0.4914	up	0.3821	up
MPF_LOC101475900.1.3	XM_004566477.1 PREDICTED: Maylandia zebra ras-related protein Rab-21-like (LOC101475900), mRNA	0.0332	0.0869	up	0.1850	up	0.7808	up	0.0981	up	0.6938	up	0.5958	up
MPF_contig_028771		0.0332	-0.6541	down	-0.3693	down	-2.5545	down	0.2848	up	-1.9004	down	-2.1852	down
MPF_LOC101483580.1.1	XM_004556746.1 PREDICTED: Maylandia zebra leucine zipper putative tumor suppressor 2 homolog (LOC101483580), mRNA	0.0332	0.2312	up	0.3937	up	1.2516	up	0.1624	up	1.0203	up	0.8579	up
MPF_contig_032225		0.0332	-0.2802	down	-0.3296	down	-1.6266	down	-0.0494	down	-1.3464	down	-1.2970	down
MPF_LOC101162776.1.2	XP_004075996.1 PREDICTED: neurofibrominlike [Oryzias latipes]	0.0332	-0.0151	down	0.1313	up	0.5450	up	0.1464	up	0.5601	up	0.4138	up
MPF_LOC100699792.1.2	XP_003458601.1 PREDICTED: motile sperm domain-containing protein 1like [Oreochromis niloticus]	0.0332	0.3725	up	0.8505	up	1.3930	up	0.4780	up	1.0205	up	0.5425	up
MPF_LOC101466143.1.18	XM_004574840.1 PREDICTED: Maylandia zebra 40S ribosomal protein S18-like (LOC101466143),	0.0332	-0.2346	down	-1.0236	down	-2.4878	down	-0.7890	down	-2.2532	down	-1.4642	down

	mRNA													
MPF_LOC101465998.3.3	XM_004541412.1 PREDICTED: Maylandia zebra serum amyloid Pcomponent-like (LOC101465998), mRNA	0.0332	-0.0603	down	0.1057	up	-0.8636	down	0.1659	up	-0.8033	down	-0.9692	down
MPF_LOC101475513.1.1	XM_004545621.1 PREDICTED: Maylandia zebra EGF-containing fibulinlike extracellular matrix protein 2-like (LOC101475513), mRNA	0.0332	-0.5569	down	-1.8440	down	-3.8950	down	-1.2872	down	-3.3381	down	-2.0509	down
MPF_contig_039869		0.0332	-0.0852	down	0.5875	up	0.5977	up	0.6727	up	0.6829	up	0.0102	up
MPF_LOC100711190.10.17	XM_003443585.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L21-like (LOC100711190), mRNA	0.0332	0.0344	up	0.1653	up	0.5684	up	0.1309	up	0.5340	up	0.4031	up
MPF_contig_004639		0.0332	0.1593	up	0.4296	up	0.9900	up	0.2702	up	0.8306	up	0.5604	up
MPF_LOC101474504.4.5	XM_004557613.1 PREDICTED: Maylandia zebra anthrax toxin receptor 1-like (LOC101474504), mRNA	0.0333	-0.2504	down	-1.0152	down	-3.7435	down	-0.7648	down	-3.4931	down	-2.7283	down
MPF_LOC101480576.2.3	XM_004574067.1 PREDICTED: Maylandia zebra uncharacterized LOC101480576 (LOC101480576), mRNA	0.0333	-0.1421	down	-0.1129	down	-2.4228	down	0.0292	up	-2.2808	down	-2.3099	down
MPF_contig_035573		0.0333	-0.0008	down	0.1391	up	0.3740	up	0.1399	up	0.3748	up	0.2349	up

MPF_MYH10.2.2	MYH10_BOVIN (sp|Q27991) Myosin-10 OS=Bos taurus GN=MYH10 PE=2 SV=2	0.0333	0.0305	up	-0.1802	down	0.8013	up	-0.2106	down	0.7709	up	0.9815	up
MPF_contig_013228		0.0333	-0.2088	down	0.3173	up	1.0987	up	0.5261	up	1.3075	up	0.7814	up
MPF_LOC101465407.2.4	XM_004540009.1 PREDICTED: Maylandia zebra transmembrane protein 87A-like (LOC101465407), mRNA	0.0333	0.1252	up	0.2214	up	0.9605	up	0.0962	up	0.8354	up	0.7391	up
MPF_contig_015244		0.0333	0.0668	up	0.0636	up	0.6760	up	-0.0032	down	0.6092	up	0.6124	up
MPF_LOC101466474.1.1	XM_004562278.1 PREDICTED: Maylandia zebra inactive rhomboid protein 1-like (LOC101466474), transcript variant X3, mRNA	0.0333	-0.0413	down	-0.0500	down	0.5189	up	-0.0087	down	0.5602	up	0.5689	up
MPF_LOC101481987.1.1	XM_004566680.1 PREDICTED: Maylandia zebra sin3 histone deacetylase corepressor complex component SDS3like (LOC101481987), transcript variant X2, mRNA	0.0333	0.3128	up	0.3883	up	0.7175	up	0.0755	up	0.4047	up	0.3292	up
MPF_LOC101475790.3.3	XM_004565656.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101475790), mRNA	0.0333	0.6771	up	1.0111	up	0.6689	up	0.3339	up	-0.0082	down	-0.3422	down
MPF_LOC101473946.3.3	XM_004540042.1 PREDICTED: Maylandia zebra protein salvador homolog 1-like (LOC101473946), mRNA	0.0333	-0.2313	down	-0.2274	down	1.2734	up	0.0039	up	1.5047	up	1.5008	up

MPF_LOC101475797.6.6	XM_004567406.1 PREDICTED: Maylandia zebra RING1 and YY1binding protein B-like (LOC101475797), mRNA	0.0333	0.7723	up	0.6085	up	0.6560	up	-0.1638	down	-0.1162	down	0.0476	up
MPF_LOC100699407.3.3	XM_003451114.1 PREDICTED: Oreochromis niloticus stress-associated endoplasmic reticulum protein 1-like (LOC100699407), mRNA	0.0333	-0.0791	down	-0.3729	down	0.9382	up	-0.2938	down	1.0173	up	1.3111	up
MPF_LOC101154918.1.1	XM_004084703.1 PREDICTED: Oryzias latipes solute carrier family 2, facilitated glucose transporter member 11-like (LOC101154918), mRNA	0.0333	0.1052	up	0.0525	up	0.7881	up	-0.0526	down	0.6829	up	0.7356	up
MPF_contig_019070		0.0333	0.2727	up	0.2921	up	1.2495	up	0.0194	up	0.9768	up	0.9574	up
MPF_LOC101470777.2.7	XM_004568406.1 PREDICTED: Maylandia zebra fatty acid-binding protein, brain-like (LOC101470777), mRNA	0.0333	-0.0151	down	0.1994	up	0.4113	up	0.2145	up	0.4264	up	0.2119	up
MPF_XMRK.1.1	[BBH] XMRK_XIPMA (sp|P13388) Melanoma receptor tyrosine-protein kinase OS=Xiphophorus maculatus GN=xmrk PE=2 SV=2	0.0333	-0.3698	down	-0.4684	down	0.6065	up	-0.0985	down	0.9763	up	1.0749	up
MPF_LOC101482137.1.2	XM_004576146.1 PREDICTED: Maylandia zebra motile sperm domaincontaining protein 1-like (LOC101482137), transcript variant X4, mRNA	0.0333	0.1006	up	0.4379	up	0.7056	up	0.3373	up	0.6050	up	0.2677	up

MPF_contig_000493	XM_004550861.1 PREDICTED: Maylandia zebra INO80 complex subunit E-like (LOC101470596), transcript variant X2, mRNA	0.0333	0.0711	up	-0.1132	down	1.1452	up	-0.1843	down	1.0741	up	1.2585	up
MPF_LOC100706211.1.2	XM_003445662.1 PREDICTED: Oreochromis niloticus piwi-like protein 2-like (LOC100706211), mRNA	0.0333	-0.1208	down	0.0456	up	-1.5208	down	0.1664	up	-1.4001	down	-1.5665	down
MPF_LOC101468417.3.3	XM_004558511.1 PREDICTED: Maylandia zebra aspartate betahydroxylase domaincontaining protein 2-like (LOC101468417), transcript variant X2, mRNA	0.0333	-0.0620	down	0.0328	up	1.4300	up	0.0947	up	1.4920	up	1.3972	up
MPF_LOC101487356.3.4	XM_004573839.1 PREDICTED: Maylandia zebra prostaglandin F2 receptor negative regulatorlike (LOC101487356), mRNA	0.0333	0.0414	up	0.3511	up	0.8594	up	0.3098	up	0.8181	up	0.5083	up
MPF_UBQLN4.2.3	NP_998521.2 ubiquilin-4 [Danio rerio]	0.0333	-0.1257	down	0.1758	up	1.2067	up	0.3014	up	1.3324	up	1.0309	up
MPF_LOC101479984.2.3	XM_004548360.1 PREDICTED: Maylandia zebra G1/S-specific cyclin-D2like (LOC101479984), transcript variant X2, mRNA	0.0333	0.0716	up	0.1572	up	1.6468	up	0.0856	up	1.5752	up	1.4896	up
MPF_LOC101486762.1.1	XM_004570077.1 PREDICTED: Maylandia zebra polyribonucleotide nucleotidyltransferase 1, mitochondrial-like (LOC101486762), mRNA	0.0333	0.1179	up	0.1687	up	0.9596	up	0.0508	up	0.8417	up	0.7908	up
MPF_contig_044689		0.0333	-0.3841	down	-0.0320	down	-0.8165	down	0.3522	up	-0.4324	down	-0.7845	down
MPF_contig_028837		0.0333	0.0427	up	0.2045	up	0.8458	up	0.1618	up	0.8031	up	0.6413	up

MPF_LOC100708246.1.1	XM_003442344.1 PREDICTED: Oreochromis niloticus GPI mannosyltransferase 3-like (LOC100708246), mRNA	0.0333	-0.0172	down	0.0509	up	1.0915	up	0.0680	up	1.1087	up	1.0407	up
MPF_LOC101061900.3.4	XP_003975298.1 PREDICTED: uncharacterized protein LOC101061900 [Takifugu rubripes]	0.0333	-0.1631	down	-0.0945	down	1.2949	up	0.0686	up	1.4581	up	1.3895	up
MPF_UTRN.2.2	XM_003449882.1 PREDICTED: Oreochromis niloticus utrophin (UTRN), mRNA	0.0333	0.0551	up	-0.0928	down	0.9250	up	-0.1478	down	0.8699	up	1.0177	up

MPF_LOC101067778.1.1	XP_003966965.1 PREDICTED: rho guanine nucleotide exchange factor 15-like [Takifugu rubripes]	0.0333	-0.1736	down	-0.0220	down	0.9080	up	0.1515	up	1.0816	up	0.9301	up
MPF_LOC101467621.8.8	XR_190852.1 PREDICTED: Maylandia zebra uncharacterized LOC101467621 (LOC101467621), misc_RNA	0.0334	0.1254	up	-0.1136	down	-1.1163	down	-0.2390	down	-1.2417	down	-1.0027	down
MPF_LOC100696210.1.1	XP_003454199.1 PREDICTED: hypothetical protein LOC100696210 [Oreochromis niloticus]	0.0334	-0.0733	down	0.3509	up	1.0445	up	0.4242	up	1.1178	up	0.6935	up
MPF_LOC100711796.1.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA	0.0334	-0.1353	down	-0.9150	down	-2.8210	down	-0.7797	down	-2.6858	down	-1.9061	down

MPF_LOC101466459.21.29	XM_004554283.1 PREDICTED: Maylandia zebra semaphorin-3G-like (LOC101466459), mRNA	0.0334	0.1402	up	0.2338	up	0.7637	up	0.0936	up	0.6235	up	0.5299	up
MPF_LOC101165259.2.2	XP_004079413.1 PREDICTED: desmoglein-2-like [Oryzias latipes]	0.0334	0.6566	up	-0.0519	down	-1.4983	down	-0.7085	down	-2.1548	down	-1.4464	down
MPF_LOC101163569.1.1	XM_004069621.1 PREDICTED: Oryzias latipes very-long-chain (3R)-3hydroxyacyl-[acyl-carrier protein] dehydratase-like (LOC101163569), mRNA	0.0334	0.0458	up	0.3660	up	0.6622	up	0.3202	up	0.6164	up	0.2962	up
MPF_LOC101468042.2.2	XM_004543565.1 PREDICTED: Maylandia zebra P2Y purinoceptor 13like (LOC101468042), transcript variant X2, mRNA	0.0334	-0.0976	down	-0.0400	down	0.7791	up	0.0577	up	0.8768	up	0.8191	up
MPF_LOC100703265.1.1	XP_003446695.1 PREDICTED: tRNA-specific adenosine deaminase 2-like [Oreochromis niloticus]	0.0335	0.1295	up	0.3912	up	1.0741	up	0.2617	up	0.9446	up	0.6828	up
MPF_LOC100693765.2.2	XM_003440944.1 PREDICTED: Oreochromis niloticus centromere protein Llike (LOC100693765), mRNA	0.0335	0.5242	up	0.7009	up	1.3960	up	0.1767	up	0.8719	up	0.6951	up
MPF_CAM-D.3.4	XM_004082666.1 PREDICTED: Oryzias latipes calmodulin (cam-d), mRNA	0.0335	-0.0499	down	0.2915	up	0.6611	up	0.3415	up	0.7110	up	0.3695	up
MPF_LOC101479799.1.3	XM_004571889.1 PREDICTED: Maylandia zebra protein NDRG3-like (LOC101479799), mRNA	0.0335	-0.2295	down	0.0835	up	-1.0571	down	0.3129	up	-0.8276	down	-1.1406	down

MPF_LOC100709688.1.1	XM_003443167.1 PREDICTED: Oreochromis niloticus solute carrier family 25 member 38-A-like (LOC100709688), mRNA	0.0335	-0.0248	down	0.0865	up	0.3533	up	0.1113	up	0.3781	up	0.2667	up
MPF_ZO6.6.6	ZO6_XENLA (sp|P18749) Oocyte zinc finger protein XlCOF6 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.0335	0.0746	up	0.1821	up	0.9113	up	0.1075	up	0.8368	up	0.7292	up
MPF_LOC101466605.1.2	XM_004571129.1 PREDICTED: Maylandia zebra signal recognition particle subunit SRP72-like (LOC101466605), mRNA	0.0335	-0.3631	down	-0.1421	down	0.9024	up	0.2210	up	1.2656	up	1.0446	up
MPF_LOC100705559.1.1	XM_003439386.1 PREDICTED: Oreochromis niloticus dihydrolipoyl dehydrogenase, mitochondrial-like (LOC100705559), mRNA	0.0335	-0.0263	down	0.2551	up	0.5489	up	0.2813	up	0.5751	up	0.2938	up
MPF_LOC100710096.1.1	XM_003457649.1 PREDICTED: Oreochromis niloticus ufm1-specific protease 1-like (LOC100710096), mRNA	0.0335	-0.1387	down	0.2394	up	0.8313	up	0.3782	up	0.9701	up	0.5919	up
MPF_UBIQP.4.13	UBIQP_XENLA (sp|P62972) Polyubiquitin (Fragment) OS=Xenopus laevis PE=1 SV=2	0.0336	-0.2464	down	-0.1313	down	0.7071	up	0.1151	up	0.9536	up	0.8385	up

MPF_LOC101481351.1.1	XM_004551535.1 PREDICTED: Maylandia zebra transcription factor COE3-like (LOC101481351), transcript variant X2, mRNA	0.0336	0.2718	up	0.1711	up	1.1085	up	-0.1008	down	0.8367	up	0.9375	up
MPF_LOC100709092.1.1	XM_003453780.1 PREDICTED: Oreochromis niloticus solute carrier family 2, facilitated glucose transporter member 9-like (LOC100709092), mRNA	0.0336	-0.0151	down	0.0961	up	1.3147	up	0.1112	up	1.3298	up	1.2186	up
MPF_LOC101483412.1.1	XM_004562773.1 PREDICTED: Maylandia zebra uncharacterized LOC101483412 (LOC101483412), transcript variant X2, mRNA	0.0336	-0.0836	down	0.2574	up	0.9726	up	0.3410	up	1.0562	up	0.7152	up
MPF_NEMVEDRAFT_V1G246137.2.2	XP_001627323.1 predicted protein [Nematostella vectensis]	0.0336	-0.0114	down	0.1812	up	0.8439	up	0.1926	up	0.8553	up	0.6627	up

MPF_LOC100690119.3.18	XP_003448733.1 PREDICTED: zinc finger protein 16-like [Oreochromis niloticus]	0.0337	-0.0354	down	0.1265	up	1.1092	up	0.1619	up	1.1447	up	0.9827	up
MPF_LOC100704265.1.1	XP_003449279.1 PREDICTED: A-kinase anchor protein 13-like [Oreochromis niloticus]	0.0337	-0.2613	down	-0.1533	down	0.4453	up	0.1080	up	0.7066	up	0.5986	up
MPF_LOC100705746.1.3	XP_003443116.1 PREDICTED: trafficking protein particle complex subunit 5-like [Oreochromis niloticus]	0.0337	0.1356	up	0.1998	up	0.7718	up	0.0642	up	0.6362	up	0.5720	up

MPF_LOC101161618.1.1	XM_004067175.1 PREDICTED: Oryzias latipes SAFB-like transcription modulator-like (LOC101161618), mRNA	0.0337	-0.4912	down	-0.1605	down	0.7313	up	0.3307	up	1.2226	up	0.8919	up
MPF_LOC101481937.1.1	XM_004552858.1 PREDICTED: Maylandia zebra allantoinase, mitochondrial-like (LOC101481937), mRNA	0.0337	-0.3945	down	0.1125	up	-1.0286	down	0.5070	up	-0.6341	down	-1.1411	down
MPF_LOC101474552.1.1	XM_004568338.1 PREDICTED: Maylandia zebra BRCA1-associated ATM activator 1-like (LOC101474552), mRNA	0.0337	0.0103	up	-0.1757	down	0.8976	up	-0.1860	down	0.8872	up	1.0732	up
MPF_contig_008897		0.0337	0.2242	up	0.4674	up	1.0562	up	0.2432	up	0.8320	up	0.5888	up
MPF_LOC101072717.2.3	XP_003971444.1 PREDICTED: cytochrome c oxidase subunit 7A2, mitochondrial-like [Takifugu rubripes]	0.0337	0.0792	up	0.2791	up	0.5897	up	0.1999	up	0.5105	up	0.3106	up
MPF_LOC101473855.2.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA	0.0337	-0.0306	down	-1.1831	down	-2.6006	down	-1.1525	down	-2.5700	down	-1.4175	down
MPF_LOC764337.1.1	XP_003726079.1 PREDICTED: uncharacterized protein LOC764337 [Strongylocentrotus purpuratus]	0.0337	-0.6349	down	-0.6993	down	1.2074	up	-0.0644	down	1.8423	up	1.9067	up

MPF_LOC101479910.1.1	XM_004557072.1 PREDICTED: Maylandia zebra sex comb on midleglike protein 2-like (LOC101479910), transcript variant X1, mRNA	0.0338	0.5002	up	-0.0002	down	1.1681	up	-0.5004	down	0.6678	up	1.1683	up
MPF_LOC101469264.1.1	XM_004547946.1 PREDICTED: Maylandia zebra cell division cycleassociated 7-like protein-like (LOC101469264), mRNA	0.0338	0.1357	up	0.3507	up	0.7644	up	0.2151	up	0.6288	up	0.4137	up
MPF_LOC101468989.1.2	XM_004554477.1 PREDICTED: Maylandia zebra fatty acid-binding protein, intestinal-like (LOC101468989), mRNA	0.0338	0.0420	up	-0.0530	down	0.8994	up	-0.0950	down	0.8574	up	0.9524	up
MPF_LECG.21.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.0338	0.4515	up	-2.4782	down	-4.0878	down	-2.9297	down	-4.5393	down	-1.6096	down
MPF_LOC100535679.1.1	XP_003198445.1 PREDICTED: zinc finger protein 721-like [Danio rerio]	0.0338	-0.0750	down	0.0675	up	1.1511	up	0.1424	up	1.2261	up	1.0836	up
MPF_LOC101473158.1.1	XM_004563202.1 PREDICTED: Maylandia zebra bromodomain-containing protein 8-like (LOC101473158), transcript variant X2, mRNA	0.0338	0.1164	up	0.2871	up	0.9747	up	0.1707	up	0.8583	up	0.6875	up
MPF_contig_048033	XM_004563944.1 PREDICTED: Maylandia zebra signal-induced proliferation-associated 1-like protein 2-like (LOC101477688), transcript variant X1, mRNA	0.0338	0.0731	up	0.1326	up	1.6530	up	0.0595	up	1.5800	up	1.5205	up

MPF_CLDNJ.1.1	NM_131769.1 Danio rerio claudin j (cldnj), mRNA gb|AF359430.1|AF359430 Danio rerio claudin j (cldnj) mRNA, complete cds	0.0338	-0.1997	down	-0.6181	down	-1.4142	down	-0.4184	down	-1.2145	down	-0.7961	down
MPF_LOC100700605.16.27	XM_003458555.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100700605), mRNA	0.0338	-0.4731	down	-0.4708	down	-2.1293	down	0.0023	up	-1.6563	down	-1.6586	down
MPF_LOC101484746.1.1	XM_004544275.1 PREDICTED: Maylandia zebra DNA-directed RNA polymerase III subunit RPC4like (LOC101484746), mRNA	0.0338	0.0391	up	0.0024	up	0.7979	up	-0.0367	down	0.7588	up	0.7955	up
MPF_LOC100710715.3.3	XM_003458665.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100710715 (LOC100710715), mRNA	0.0338	0.0454	up	0.2131	up	0.6695	up	0.1677	up	0.6241	up	0.4564	up
MPF_LOC101475075.1.1	XM_004560753.1 PREDICTED: Maylandia zebra mitochondrial dynamic protein MID51-like (LOC101475075), mRNA	0.0338	-0.0407	down	0.3882	up	1.0371	up	0.4288	up	1.0777	up	0.6489	up
MPF_LOC100694557.22.24	XM_003458536.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100694557), mRNA	0.0339	-0.1312	down	0.1578	up	1.2072	up	0.2891	up	1.3384	up	1.0493	up

MPF_LOC100703705.11.14	XM_003444236.1 PREDICTED: Oreochromis niloticus tumor necrosis factor receptor superfamily member 14-like (LOC100703705), mRNA	0.0339	0.0837	up	0.1281	up	1.4903	up	0.0444	up	1.4066	up	1.3622	up
MPF_contig_048185		0.0339	-0.0292	down	0.2456	up	0.6407	up	0.2747	up	0.6699	up	0.3951	up
MPF_LOC101482618.1.1	XM_004555539.1 PREDICTED: Maylandia zebra A-kinase anchor protein 17A-like (LOC101482618), transcript variant X3, mRNA	0.0339	0.0045	up	0.0784	up	0.7683	up	0.0739	up	0.7638	up	0.6899	up
MPF_contig_045514		0.0340	-0.0693	down	0.0699	up	0.9510	up	0.1392	up	1.0203	up	0.8811	up
MPF_LOC101469816.1.1	XM_004571671.1 PREDICTED: Maylandia zebra hamartin-like (LOC101469816), mRNA	0.0340	-0.1106	down	0.1580	up	0.7683	up	0.2686	up	0.8789	up	0.6103	up
MPF_LOC101477159.2.2	XM_004547229.1 PREDICTED: Maylandia zebra mesoderm induction early response protein 3-like (LOC101477159), mRNA	0.0340	0.0566	up	0.1677	up	1.2831	up	0.1111	up	1.2265	up	1.1154	up
MPF_contig_010111		0.0340	-0.0876	down	-0.1303	down	-1.6432	down	-0.0426	down	-1.5556	down	-1.5130	down
MPF_contig_037007		0.0340	-0.9799	down	-1.0820	down	-2.9456	down	-0.1021	down	-1.9657	down	-1.8636	down
MPF_contig_005114		0.0340	-0.2737	down	-0.2473	down	1.1508	up	0.0264	up	1.4245	up	1.3981	up
MPF_contig_035116	XM_004567038.1 PREDICTED: Maylandia zebra transgelin-like (LOC101476292), transcript variant X1, mRNA	0.0341	-0.8475	down	-2.9641	down	-5.5805	down	-2.1166	down	-4.7330	down	-2.6164	down
MPF_contig_045460		0.0341	-0.0524	down	0.0766	up	0.6430	up	0.1290	up	0.6954	up	0.5664	up

MPF_LOC101466833.2.2	XM_004560812.1 PREDICTED: Maylandia zebra sugar phosphate exchanger 3-like (LOC101466833), mRNA	0.0341	0.0171	up	0.3407	up	1.7265	up	0.3236	up	1.7094	up	1.3857	up
MPF_LOC101075367.1.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]	0.0341	-0.0418	down	-1.2000	down	-2.5692	down	-1.1583	down	-2.5274	down	-1.3692	down
MPF_LECE.1.1	LECE_HELCR (sp|P06027) Echinoidin OS=Heliocidaris crassispina PE=1 SV=1	0.0341	0.7992	up	-2.8573	down	-3.8203	down	-3.6565	down	-4.6194	down	-0.9629	down

MPF_LOC101467475.1.1	XM_004551483.1 PREDICTED: Maylandia zebra coiled-coil domaincontaining protein 6-like (LOC101467475), mRNA	0.0341	-0.0821	down	0.0182	up	0.7100	up	0.1003	up	0.7921	up	0.6918	up
MPF_LOC100700438.1.1	XP_003439588.1 PREDICTED: synaptotagmin- 1-like [Oreochromis niloticus]	0.0341	-0.0673	down	0.0681	up	0.7525	up	0.1354	up	0.8198	up	0.6844	up
MPF_LOC100702397.1.1	XM_003456295.1 PREDICTED: Oreochromis niloticus leucine carboxyl methyltransferase 2-like (LOC100702397), mRNA	0.0341	0.0185	up	0.3914	up	0.5102	up	0.3729	up	0.4917	up	0.1188	up
MPF_LOC101485781.3.4	XM_004542132.1 PREDICTED: Maylandia zebra bromo adjacent homology domain-containing 1 protein-like (LOC101485781), mRNA	0.0341	-0.1626	down	-0.0277	down	0.7965	up	0.1349	up	0.9591	up	0.8242	up
MPF_contig_035601		0.0341	0.4712	up	0.1981	up	1.5816	up	-0.2731	down	1.1104	up	1.3834	up

MPF_LOC101469378.1.2	XM_004574378.1 PREDICTED: Maylandia zebra solute carrier family 35 member E1-like (LOC101469378), mRNA	0.0341	0.3248	up	0.0366	up	0.9415	up	-0.2882	down	0.6166	up	0.9049	up
MPF_LOC100695373.1.1	XM_003440950.1 PREDICTED: Oreochromis niloticus junctional adhesion molecule B-like (LOC100695373), mRNA	0.0341	-0.2860	down	-0.2667	down	0.9130	up	0.0193	up	1.1990	up	1.1797	up
MPF_MMP2.1.1	XM_003437534.1 PREDICTED: Oreochromis niloticus matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) (MMP2), mRNA	0.0342	0.5014	up	-0.0723	down	2.0165	up	-0.5737	down	1.5152	up	2.0888	up
MPF_PY00803.1.1	XP_727026.1 hypothetical protein [Plasmodium yoelii yoelii 17XNL]	0.0342	-0.0624	down	0.2020	up	0.6313	up	0.2644	up	0.6937	up	0.4293	up
MPF_LOC100706947.1.1	XP_003452194.1 PREDICTED: proteasomeassociated protein ECM29 homolog [Oreochromis niloticus]	0.0342	-0.0428	down	0.1096	up	0.8673	up	0.1524	up	0.9100	up	0.7577	up
MPF_LOC101479997.1.1	XM_004574065.1 PREDICTED: Maylandia zebra cytochrome b-c1 complex subunit Rieske, mitochondrial-like (LOC101479997), mRNA	0.0342	0.0893	up	0.1616	up	0.6668	up	0.0723	up	0.5774	up	0.5052	up

MPF_AHNK.11.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiationassociated protein AHNAK OS=Homo sapiens	0.0342	0.0121	up	-2.1173	down	-4.4929	down	-2.1294	down	-4.5050	down	-2.3756	down

	GN=AHNAK PE=1 SV=2													
MPF_LOC100702553.1.4	XP_003450101.1 PREDICTED: hypothetical protein LOC100702553 [Oreochromis niloticus]	0.0342	-0.4759	down	0.2167	up	0.5205	up	0.6926	up	0.9964	up	0.3038	up
MPF_contig_017330		0.0342	-0.0833	down	0.0159	up	0.7383	up	0.0992	up	0.8216	up	0.7224	up
MPF_LOC100618396.2.2	XP_003340812.1 PREDICTED: zinc finger protein 420-like [Monodelphis domestica]	0.0343	0.1477	up	0.4288	up	1.0656	up	0.2811	up	0.9179	up	0.6368	up
MPF_LOC101481845.1.1	XM_004555158.1 PREDICTED: Maylandia zebra succinate dehydrogenase cytochrome b560 subunit, mitochondriallike (LOC101481845), mRNA	0.0343	0.1750	up	0.6374	up	0.8113	up	0.4624	up	0.6363	up	0.1739	up
MPF_contig_004047		0.0343	-0.0421	down	0.3027	up	1.1464	up	0.3448	up	1.1885	up	0.8438	up
MPF_contig_029060		0.0343	0.0512	up	0.0337	up	0.3935	up	-0.0175	down	0.3423	up	0.3598	up
MPF_LOC100710045.1.1	XP_003444805.1 PREDICTED: actin-related protein 8-like [Oreochromis niloticus]	0.0343	0.2007	up	-0.6914	down	1.1215	up	-0.8920	down	0.9209	up	1.8129	up
MPF_LOC101485455.1.1	XM_004553256.1 PREDICTED: Maylandia zebra peptidyl-prolyl cis-trans isomerase FKBP4-like (LOC101485455), mRNA	0.0343	-0.0560	down	0.0564	up	0.8857	up	0.1124	up	0.9417	up	0.8293	up
MPF_FZD6.5.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440	0.0343	-0.0468	down	-1.1661	down	-3.0814	down	-1.1192	down	-3.0346	down	-1.9154	down

	IMAGE:6971142), complete cds													
MPF_contig_008344	XM_004545297.1 PREDICTED: Maylandia zebra membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1-like (LOC101479397), transcript variant X7, mRNA	0.0343	-0.0511	down	0.2626	up	1.0228	up	0.3137	up	1.0738	up	0.7602	up
MPF_contig_036703		0.0343	0.0601	up	0.0917	up	0.6630	up	0.0316	up	0.6029	up	0.5713	up
MPF_contig_010766		0.0343	-0.0675	down	-0.3872	down	-1.0166	down	-0.3197	down	-0.9490	down	-0.6294	down
MPF_contig_003630		0.0343	0.0523	up	0.4084	up	0.6532	up	0.3560	up	0.6009	up	0.2449	up
MPF_LOC101478533.1.1	XM_004539963.1 PREDICTED: Maylandia zebra tandem C2 domains nuclear protein-like (LOC101478533), mRNA	0.0343	-0.1814	down	0.0032	up	0.7101	up	0.1845	up	0.8915	up	0.7070	up
MPF_contig_032377		0.0343	-0.0556	down	0.0963	up	0.6337	up	0.1520	up	0.6894	up	0.5374	up
MPF_LOC101487990.1.1	XM_004543644.1 PREDICTED: Maylandia zebra uncharacterized LOC101487990 (LOC101487990), transcript variant X1, mRNA	0.0343	-0.0941	down	0.1912	up	0.7131	up	0.2853	up	0.8072	up	0.5219	up

MPF_LOC101474298.1.1	XM_004551415.1 PREDICTED: Maylandia zebra rhotekin-2-like (LOC101474298), transcript variant X3, mRNA	0.0343	0.0363	up	0.3681	up	1.3901	up	0.3318	up	1.3538	up	1.0220	up
MPF_LOC101474302.1.1	XM_004552075.1 PREDICTED: Maylandia zebra vesicular integralmembrane protein VIP36-like (LOC101474302), transcript variant X1, mRNA	0.0343	-0.0689	down	0.1327	up	0.5698	up	0.2016	up	0.6387	up	0.4370	up
MPF_LOC101470086.1.1	XM_004569475.1 PREDICTED: Maylandia zebra tomoregulin-1-like (LOC101470086), transcript variant X2, mRNA	0.0343	0.0162	up	-0.2678	down	0.8776	up	-0.2840	down	0.8614	up	1.1454	up
MPF_contig_003774		0.0343	-0.1910	down	0.0846	up	0.5700	up	0.2755	up	0.7610	up	0.4855	up
MPF_contig_029062		0.0344	-0.1702	down	-0.0343	down	0.9247	up	0.1359	up	1.0950	up	0.9591	up
MPF_LOC101068078.1.1	XM_003969941.1 PREDICTED: Takifugu rubripes anoctamin-5-like (LOC101068078), mRNA	0.0344	-0.4236	down	-1.3727	down	-3.0617	down	-0.9491	down	-2.6381	down	-1.6890	down
MPF_LOC101471502.1.1	XM_004539386.1 PREDICTED: Maylandia zebra AFG3-like protein 1like (LOC101471502), transcript variant X2, mRNA	0.0344	0.1360	up	0.0095	up	0.5158	up	-0.1265	down	0.3798	up	0.5063	up
MPF_LOC101482448.2.2	XM_004555347.1 PREDICTED: Maylandia zebra protein kinase C iota type-like (LOC101482448), mRNA	0.0344	-0.1841	down	0.0241	up	0.5673	up	0.2082	up	0.7514	up	0.5432	up
MPF_ZNF32.1.1	ZNF32_MOUSE (sp|Q80V23) Zinc finger protein 32 OS=Mus musculus GN=Znf32 PE=2 SV=1	0.0344	-0.0103	down	0.2595	up	1.3990	up	0.2698	up	1.4093	up	1.1395	up

MPF_LOC100699693.1.1	XP_003455536.1 PREDICTED: glutathione Stransferase theta-1-like [Oreochromis niloticus]	0.0344	0.1992	up	0.3338	up	1.3136	up	0.1346	up	1.1143	up	0.9797	up
MPF_LOC101472505.3.3	XM_004567307.1 PREDICTED: Maylandia zebra sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1-like (LOC101472505), transcript variant X4, mRNA	0.0345	0.1239	up	0.5846	up	1.5271	up	0.4607	up	1.4032	up	0.9425	up
MPF_LOC101472031.1.3	XM_004571147.1 PREDICTED: Maylandia zebra exosome complex component RRP40-like (LOC101472031), mRNA	0.0345	-0.0290	down	0.1288	up	0.6227	up	0.1578	up	0.6517	up	0.4939	up
MPF_LOC101478930.2.2	XM_004568966.1 PREDICTED: Maylandia zebra disrupted in renal carcinoma protein 2-like (LOC101478930), mRNA	0.0345	-0.0481	down	0.2543	up	0.8962	up	0.3024	up	0.9443	up	0.6419	up
MPF_LOC101068301.2.3	XM_003966217.1 PREDICTED: Takifugu rubripes protein S100-A11like (LOC101068301), mRNA	0.0345	0.0837	up	-1.3438	down	-4.0392	down	-1.4274	down	-4.1229	down	-2.6955	down
MPF_LOC101480760.3.13	XM_004547526.1 PREDICTED: Maylandia zebra 40S ribosomal protein S10-like (LOC101480760), transcript variant X2, mRNA	0.0345	-0.0146	down	-0.1028	down	0.6232	up	-0.0882	down	0.6378	up	0.7260	up
MPF_LOC101487890.1.1	XM_004542514.1 PREDICTED: Maylandia zebra RING finger protein 126-like (LOC101487890), mRNA	0.0345	0.1118	up	0.2460	up	1.1110	up	0.1342	up	0.9992	up	0.8650	up

MPF_LOC101471219.1.1	XM_004539755.1 PREDICTED: Maylandia zebra A-kinase anchor protein 13-like (LOC101471219), mRNA	0.0345	-0.0054	down	0.0085	up	0.8913	up	0.0139	up	0.8966	up	0.8828	up
MPF_LOC101464701.1.2	XM_004575190.1 PREDICTED: Maylandia zebra angio-associated migratory cell protein-like (LOC101464701), mRNA	0.0346	-0.0108	down	0.2863	up	1.4714	up	0.2972	up	1.4822	up	1.1850	up
MPF_LOC100709667.1.5	XM_003438989.1 PREDICTED: Oreochromis niloticus cellular nucleic acidbinding protein-like (LOC100709667), mRNA	0.0346	-0.1448	down	-0.0936	down	0.5803	up	0.0511	up	0.7251	up	0.6740	up
MPF_LOC101482239.1.1	XM_004553768.1 PREDICTED: Maylandia zebra LIM/homeobox protein Lhx9-like (LOC101482239), transcript variant X1, mRNA	0.0346	0.2207	up	0.1427	up	0.6836	up	-0.0781	down	0.4629	up	0.5409	up
MPF_KCTD9.3.3	KCTD9_HUMAN (sp|Q7L273) BTB/POZ domain-containing protein KCTD9 OS=Homo sapiens GN=KCTD9 PE=2 SV=1	0.0346	0.0216	up	0.1287	up	0.6233	up	0.1071	up	0.6017	up	0.4946	up
MPF_LOC101481619.2.2	XM_004546215.1 PREDICTED: Maylandia zebra RNA-binding protein 38like (LOC101481619), mRNA	0.0346	0.3810	up	-0.3908	down	-1.4415	down	-0.7718	down	-1.8225	down	-1.0507	down
MPF_LOC101487382.2.2	XM_004556477.1 PREDICTED: Maylandia zebra zinc finger protein 358like (LOC101487382), mRNA	0.0346	0.0934	up	0.0116	up	0.7593	up	-0.0818	down	0.6659	up	0.7477	up

MPF_LOC101483308.2.3	XM_004559856.1 PREDICTED: Maylandia zebra lysine-specific demethylase phf2-like (LOC101483308), transcript variant X3, mRNA	0.0346	-0.1148	down	0.1163	up	0.6302	up	0.2311	up	0.7450	up	0.5139	up
MPF_NEMVEDRAFT_V1 G118504.1.1	XP_001628905.1 predicted protein [Nematostella vectensis]	0.0346	0.1418	up	-0.3900	down	-2.6647	down	-0.5319	down	-2.8065	down	-2.2747	down
MPF_LOC101472976.1.1	XM_004540607.1 PREDICTED: Maylandia zebra ataxin-3-like (LOC101472976), transcript variant X2, mRNA	0.0346	-0.1485	down	0.1435	up	0.7454	up	0.2920	up	0.8940	up	0.6020	up
MPF_contig_012347		0.0347	0.0873	up	0.1704	up	0.5150	up	0.0831	up	0.4276	up	0.3445	up
MPF_LOC101484487.1.1	XM_004571996.1 PREDICTED: Maylandia zebra tripartite motifcontaining protein 45-like (LOC101484487), mRNA	0.0347	0.6285	up	0.5036	up	1.3346	up	-0.1249	down	0.7061	up	0.8310	up
MPF_contig_009223		0.0347	0.0649	up	0.2134	up	0.5695	up	0.1484	up	0.5046	up	0.3562	up
MPF_LOC101481920.2.2	XM_004572350.1 PREDICTED: Maylandia zebra zinc finger protein 143like (LOC101481920), mRNA	0.0347	0.0624	up	-0.1732	down	1.2393	up	-0.2356	down	1.1768	up	1.4124	up
MPF_contig_038841		0.0347	-0.3362	down	0.3179	up	-0.5374	down	0.6542	up	-0.2011	down	-0.8553	down
MPF_LOC101477695.1.9	XM_004564867.1 PREDICTED: Maylandia zebra 60S ribosomal protein L18a-like (LOC101477695), transcript variant X2, mRNA	0.0347	-0.1549	down	-0.7550	down	-1.3229	down	-0.6000	down	-1.1680	down	-0.5679	down

MPF_LOC100694194.4.7	XP_003458818.1 PREDICTED: receptorinteracting serine/threonineprotein kinase 3-like [Oreochromis niloticus]	0.0347	0.0022	up	0.4490	up	0.9062	up	0.4467	up	0.9039	up	0.4572	up

MPF_contig_046648	XM_004545215.1 PREDICTED: Maylandia zebra protein FAM219A-like (LOC101484940), transcript variant X2, mRNA	0.0347	0.1649	up	0.0229	up	0.9718	up	-0.1419	down	0.8069	up	0.9488	up
MPF_LOC100709891.1.1	XP_003449549.1 PREDICTED: succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial-like [Oreochromis niloticus]	0.0347	-0.1262	down	-0.1276	down	0.6560	up	-0.0014	down	0.7822	up	0.7836	up
MPF_LOC101161817.1.1	XP_004073964.1 PREDICTED: uncharacterized protein LOC101161817 [Oryzias latipes]	0.0347	0.2875	up	0.3499	up	0.8741	up	0.0624	up	0.5866	up	0.5242	up
MPF_contig_033443		0.0347	0.0985	up	0.2130	up	0.9072	up	0.1146	up	0.8087	up	0.6942	up
MPF_contig_025482	XM_004559970.1 PREDICTED: Maylandia zebra transcription factor HIVEP3-like (LOC101464249), transcript variant X2, mRNA	0.0347	0.5178	up	0.3106	up	-0.9467	down	-0.2072	down	-1.4645	down	-1.2573	down
MPF_LOC101477850.6.10	XM_004575562.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12-like (LOC101477850), mRNA	0.0347	-0.9887	down	-1.3502	down	-3.7837	down	-0.3614	down	-2.7950	down	-2.4336	down

MPF_LOC101158242.1.1	XP_004081874.1 PREDICTED: tRNA-specific adenosine deaminase-like protein 3-like [Oryzias latipes]	0.0347	0.2071	up	0.2916	up	0.6425	up	0.0844	up	0.4353	up	0.3509	up
MPF_LOC101161674.2.2	XM_004079021.1 PREDICTED: Oryzias latipes putative 60S ribosomal protein L37a-like, transcript variant 2 (LOC101161674), mRNA	0.0347	-0.0311	down	-1.3022	down	-3.1262	down	-1.2711	down	-3.0951	down	-1.8240	down
MPF_contig_029207		0.0347	-0.7763	down	-1.3975	down	-2.9011	down	-0.6213	down	-2.1248	down	-1.5035	down
MPF_contig_021242		0.0348	-0.0879	down	0.0593	up	0.6120	up	0.1472	up	0.6999	up	0.5527	up
MPF_contig_044605		0.0348	-0.0729	down	0.2318	up	0.7659	up	0.3047	up	0.8388	up	0.5341	up
MPF_LOC101474475.1.2	XM_004548245.1 PREDICTED: Maylandia zebra kelch domaincontaining protein 10-like (LOC101474475), mRNA	0.0351	0.0325	up	-0.2972	down	0.9913	up	-0.3297	down	0.9588	up	1.2886	up
MPF_LOC100701582.1.9	XP_003455288.1 PREDICTED: zinc finger protein 236-like [Oreochromis niloticus]	0.0351	0.0454	up	0.1323	up	1.1793	up	0.0868	up	1.1339	up	1.0471	up
MPF_LOC101483451.1.1	XM_004547058.1 PREDICTED: Maylandia zebra fumarylacetoacetate hydrolase domain-containing protein 2-like (LOC101483451), transcript variant X2, mRNA	0.0351	-0.2386	down	-0.9292	down	-2.6489	down	-0.6906	down	-2.4103	down	-1.7197	down
MPF_contig_024116		0.0351	-0.0241	down	0.2015	up	1.0510	up	0.2256	up	1.0751	up	0.8495	up
MPF_LOC100929802.1.1	XP_003761948.1 PREDICTED:	0.0351	0.2479	up	-0.9561	down	-2.9685	down	-1.2039	down	-3.2164	down	-2.0124	down

	uncharacterized protein LOC100929802 [Sarcophilus harrisii]													
MPF_LOC101485143.2.2	XM_004569171.1 PREDICTED: Maylandia zebra UDP-GlcNAc:betaGal beta-1,3-Nacetylglucosaminyltransferase 9-like (LOC101485143), transcript variant X3, mRNA	0.0351	0.0980	up	0.3638	up	1.6813	up	0.2658	up	1.5833	up	1.3175	up
MPF_LOC101471056.1.3	XM_004570567.1 PREDICTED: Maylandia zebra guanine nucleotidebinding protein G(I)/G(S)/G(O) subunit gamma-12-like (LOC101471056), mRNA	0.0351	-0.0290	down	0.3557	up	0.6988	up	0.3847	up	0.7278	up	0.3432	up
MPF_contig_045128		0.0351	-0.0900	down	-0.0842	down	0.8267	up	0.0059	up	0.9167	up	0.9108	up
MPF_LOC100707818.1.1	XP_003447961.1 PREDICTED: signal recognition particle 68 kDa protein-like [Oreochromis niloticus]	0.0351	-0.0898	down	0.1029	up	0.6804	up	0.1927	up	0.7702	up	0.5775	up
MPF_LOC101475506.1.2	XM_004544241.1 PREDICTED: Maylandia zebra dihydropyrimidinaserelated protein 2-like (LOC101475506), transcript variant X2, mRNA	0.0351	0.0510	up	0.2601	up	1.1042	up	0.2091	up	1.0532	up	0.8441	up
MPF_LOC101471240.1.1	XM_004544607.1 PREDICTED: Maylandia zebra AP-1 complex subunit beta-1-like (LOC101471240), transcript variant X3, mRNA	0.0351	-0.1310	down	0.1022	up	0.5696	up	0.2332	up	0.7006	up	0.4674	up

MPF_LOC101078876.1.1	XP_003975937.1 PREDICTED: uncharacterized protein LOC101078876 [Takifugu rubripes]	0.0351	0.2258	up	0.0074	up	1.3585	up	-0.2185	down	1.1327	up	1.3511	up

MPF_LOC100712294.2.2	XM_003449092.1 PREDICTED: Oreochromis niloticus suppressor of IKBKE 1-like (LOC100712294), mRNA	0.0351	0.0401	up	0.2773	up	0.7390	up	0.2372	up	0.6989	up	0.4616	up
MPF_contig_037930		0.0351	-0.0264	down	0.0801	up	0.6535	up	0.1065	up	0.6799	up	0.5734	up
MPF_contig_024387		0.0351	0.2675	up	0.2655	up	0.7836	up	-0.0020	down	0.5161	up	0.5181	up
MPF_LOC100703536.1.1	XP_003447455.1 PREDICTED: interferoninduced helicase C domaincontaining protein 1-like [Oreochromis niloticus]	0.0351	0.3777	up	-0.8777	down	-1.7707	down	-1.2554	down	-2.1484	down	-0.8930	down
MPF_LOC100695994.18.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.0351	0.1277	up	0.2150	up	0.8790	up	0.0872	up	0.7513	up	0.6640	up
MPF_LOC101067922.3.6	XM_003966993.1 PREDICTED: Takifugu rubripes metallothionein Alike (LOC101067922), mRNA	0.0351	0.0324	up	0.2698	up	0.6032	up	0.2374	up	0.5708	up	0.3333	up
MPF_LOC101155746.1.1	XM_004065929.1 PREDICTED: Oryzias latipes hedgehog-interacting proteinlike (LOC101155746), mRNA	0.0351	0.1617	up	0.5619	up	1.4556	up	0.4002	up	1.2939	up	0.8936	up
MPF_LOC100710427.3.5	XM_003453537.1 PREDICTED: Oreochromis niloticus complement factor Hlike (LOC100710427), partial mRNA	0.0351	-0.4592	down	-0.3952	down	-0.8867	down	0.0640	up	-0.4274	down	-0.4914	down

MPF_LOC100695994.20.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.0352	0.0262	up	0.0778	up	0.9400	up	0.0516	up	0.9137	up	0.8622	up
MPF_CP250.2.2	CP250_MOUSE (sp|Q60952) Centrosome-associated protein CEP250 OS=Mus musculus GN=Cep250 PE=1 SV=4	0.0352	-0.0115	down	0.0545	up	0.6294	up	0.0661	up	0.6410	up	0.5749	up
MPF_LOC101075367.4.6	XP_003965424.1 PREDICTED: 60S ribosomal protein L17-like [Takifugu rubripes]	0.0352	-0.0063	down	-1.0587	down	-2.4107	down	-1.0524	down	-2.4044	down	-1.3521	down
MPF_ND5.2.8	YP_003127104.1 NADH dehydrogenase subunit 5 [Hyperoglyphe japonica]	0.0352	0.1500	up	0.2305	up	1.3852	up	0.0805	up	1.2352	up	1.1547	up
MPF_LOC101470634.2.2	XM_004559257.1 PREDICTED: Maylandia zebra uncharacterized LOC101470634 (LOC101470634), mRNA	0.0352	-0.3070	down	-0.4959	down	0.7676	up	-0.1889	down	1.0746	up	1.2635	up
MPF_LOC101480468.1.1	XM_004547044.1 PREDICTED: Maylandia zebra ras association domaincontaining protein 2-like (LOC101480468), mRNA	0.0352	-0.0024	down	0.0271	up	1.1057	up	0.0294	up	1.1080	up	1.0786	up
MPF_LOC101472638.1.2	XM_004574297.1 PREDICTED: Maylandia zebra menin-like (LOC101472638), transcript variant X3, mRNA	0.0352	0.0566	up	0.2675	up	1.0557	up	0.2108	up	0.9991	up	0.7883	up
MPF_LOC100711518.1.1	XM_003457965.1 PREDICTED: Oreochromis niloticus sentrin-specific protease 7-like	0.0352	0.0746	up	0.3621	up	1.1294	up	0.2875	up	1.0548	up	0.7673	up

	(LOC100711518), mRNA													
MPF_LOC101157089.1.1	XP_004079208.1 PREDICTED: coatomer subunit beta'-like [Oryzias latipes]	0.0352	-0.2300	down	0.1333	up	1.0649	up	0.3632	up	1.2949	up	0.9316	up
MPF_contig_040702		0.0352	-0.2492	down	-1.6516	down	-4.2602	down	-1.4024	down	-4.0110	down	-2.6086	down
MPF_LOC101475466.1.2	XM_004559920.1 PREDICTED: Maylandia zebra carbohydrate sulfotransferase 11-like (LOC101475466), mRNA	0.0352	0.1220	up	0.2856	up	0.4161	up	0.1636	up	0.2940	up	0.1305	up
MPF_contig_039845		0.0352	0.2949	up	-0.3243	down	1.7838	up	-0.6192	down	1.4889	up	2.1081	up
MPF_LOC101465640.1.1	XM_004573461.1 PREDICTED: Maylandia zebra zinc finger protein 16like (LOC101465640), transcript variant X2, mRNA	0.0352	-0.0915	down	0.2115	up	0.8775	up	0.3030	up	0.9690	up	0.6660	up
MPF_LOC101481869.1.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA	0.0352	-0.1154	down	-0.0184	down	0.7037	up	0.0970	up	0.8191	up	0.7221	up
MPF_LOC100705814.2.2	XM_003437803.1 PREDICTED: Oreochromis niloticus eukaryotic initiation factor 4A-II-like (LOC100705814), mRNA	0.0352	-0.1837	down	-0.3625	down	-1.4997	down	-0.1788	down	-1.3161	down	-1.1372	down

MPF_LOC101465427.3.3	XM_004567927.1 PREDICTED: Maylandia zebra glutamate receptor ionotropic, NMDA 2B-like (LOC101465427), mRNA	0.0352	0.0142	up	0.1594	up	0.5865	up	0.1452	up	0.5723	up	0.4271	up
MPF_LOC101482306.2.2	XM_004548843.1 PREDICTED: Maylandia zebra phosphoenolpyruvate carboxykinase, cytosolic [GTP]-like (LOC101482306), mRNA	0.0352	-0.0374	down	0.3511	up	1.1590	up	0.3885	up	1.1964	up	0.8079	up
MPF_LOC101471048.6.7	XM_004568139.1 PREDICTED: Maylandia zebra cyclin-dependent kinase 16-like (LOC101471048), transcript variant X7, mRNA	0.0352	0.0145	up	0.0724	up	1.2679	up	0.0579	up	1.2535	up	1.1955	up
MPF_LOC101486654.1.1	XM_004542792.1 PREDICTED: Maylandia zebra dystrobrevin alpha-like (LOC101486654), transcript variant X6, mRNA	0.0352	-0.0352	down	-0.0260	down	1.0325	up	0.0092	up	1.0677	up	1.0585	up
MPF_LOC101472090.4.4	XM_004541980.1 PREDICTED: Maylandia zebra vascular endothelial growth factor A-A-like (LOC101472090), mRNA	0.0352	0.1192	up	-0.5750	down	-2.3558	down	-0.6942	down	-2.4750	down	-1.7808	down
MPF_NEMVEDRAFT_V1 G12479.1.1	XP_001625071.1 predicted protein [Nematostella vectensis]	0.0352	0.1447	up	0.2870	up	0.7854	up	0.1423	up	0.6407	up	0.4984	up
MPF_LOC101464848.5.5	XM_004545232.1 PREDICTED: Maylandia zebra bis(5'-nucleosyl)tetraphosphatase [asymmetrical]-like (LOC101464848), transcript variant X2, mRNA	0.0352	-0.6505	down	-0.4054	down	-2.0663	down	0.2451	up	-1.4158	down	-1.6609	down

MPF_LOC101477116.1.2	XM_004558918.1 PREDICTED: Maylandia zebra transcriptional enhancer factor TEF-5-like (LOC101477116), mRNA	0.0352	-0.0501	down	0.1995	up	0.7900	up	0.2496	up	0.8400	up	0.5904	up
MPF_LOC100691043.4.5	XM_003457742.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 12-like (LOC100691043), mRNA	0.0352	-0.4173	down	-0.0906	down	0.7380	up	0.3267	up	1.1553	up	0.8286	up
MPF_contig_040052	XM_004541785.1 PREDICTED: Maylandia zebra NHS-like protein 1-like (LOC101470763), transcript variant X5, mRNA	0.0352	0.1699	up	0.2937	up	0.8749	up	0.1238	up	0.7049	up	0.5812	up
MPF_contig_044329		0.0352	-0.0126	down	0.1486	up	0.5080	up	0.1612	up	0.5205	up	0.3594	up
MPF_LOC101073703.1.1	XP_003974064.1 PREDICTED: DNA-directed RNA polymerases I, II, and III subunit RPABC1-like [Takifugu rubripes]	0.0352	-0.0008	down	0.2537	up	0.6590	up	0.2545	up	0.6598	up	0.4053	up
MPF_LOC101487018.1.1	XM_004564071.1 PREDICTED: Maylandia zebra serine/threonineprotein kinase Chk1-like (LOC101487018), mRNA	0.0352	0.1367	up	0.4300	up	1.3098	up	0.2933	up	1.1731	up	0.8798	up
MPF_LOC101464455.7.13	XM_004542249.1 PREDICTED: Maylandia zebra calmodulin-like (LOC101464455), mRNA	0.0353	0.0518	up	-0.5073	down	-1.6075	down	-0.5591	down	-1.6593	down	-1.1002	down

MPF_contig_008782	XM_004562210.1 PREDICTED: Maylandia zebra WAS/WASL-interacting protein family member 2-like (LOC101472770), transcript variant X1, mRNA	0.0353	-0.1788	down	-0.4405	down	0.7363	up	-0.2617	down	0.9151	up	1.1768	up
MPF_LOC101477689.1.1	XM_004564033.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 18-like (LOC101477689), mRNA	0.0353	0.2770	up	0.3465	up	1.1256	up	0.0695	up	0.8486	up	0.7791	up
MPF_LOC101465583.6.7	XM_004562463.1 PREDICTED: Maylandia zebra histone H3.3-like (LOC101465583), mRNA	0.0353	0.0298	up	0.2776	up	1.0399	up	0.2479	up	1.0101	up	0.7622	up
MPF_contig_016274		0.0353	-0.4395	down	-0.4442	down	-2.2020	down	-0.0047	down	-1.7626	down	-1.7578	down
MPF_LOC101485728.3.8	XM_004574437.1 PREDICTED: Maylandia zebra nucleus accumbensassociated protein 1-like (LOC101485728), transcript variant X3, mRNA	0.0353	0.3909	up	-0.6322	down	-1.0304	down	-1.0231	down	-1.4213	down	-0.3982	down
MPF_LOC101472495.1.1	XM_004541434.1 PREDICTED: Maylandia zebra neurobeachin-like protein 2-like (LOC101472495), transcript variant X2, mRNA	0.0353	-0.0408	down	0.2568	up	0.8337	up	0.2976	up	0.8746	up	0.5770	up
MPF_ZNFX1.2.3	XM_003456110.1 PREDICTED: Oreochromis niloticus zinc finger, NFX1type containing 1 (ZNFX1), mRNA	0.0353	-0.2678	down	-0.3686	down	0.9299	up	-0.1008	down	1.1978	up	1.2986	up
MPF_LOC101477268.1.1	XM_004573228.1 PREDICTED: Maylandia zebra sorting nexin-21-like (LOC101477268), transcript variant X2, mRNA	0.0353	0.0186	up	0.2901	up	0.7407	up	0.2715	up	0.7221	up	0.4506	up

MPF_LOC101477445.3.4	XM_004571089.1 PREDICTED: Maylandia zebra Williams-Beuren syndrome chromosomal region 27 protein-like (LOC101477445), mRNA	0.0354	-0.3616	down	-0.0303	down	-0.8046	down	0.3313	up	-0.4430	down	-0.7744	down
MPF_IARS.1.1	XM_003454548.1 PREDICTED: Oreochromis niloticus isoleucyl-tRNA synthetase (IARS), mRNA	0.0354	0.0571	up	0.3245	up	0.6226	up	0.2674	up	0.5655	up	0.2980	up

MPF_LOC101075231.2.2	XP_003966917.1 PREDICTED: collagen alpha2(IV) chain-like [Takifugu rubripes]	0.0354	0.0239	up	0.2142	up	0.5454	up	0.1902	up	0.5215	up	0.3313	up
MPF_LOC100708328.1.1	XM_003441248.1 PREDICTED: Oreochromis niloticus glutamine-rich protein 1-like (LOC100708328), mRNA	0.0354	-0.0792	down	0.1733	up	0.9435	up	0.2525	up	1.0227	up	0.7702	up
MPF_DKC1.3.3	DKC1_CHICK (sp|Q5ZJH9) H/ACA ribonucleoprotein complex subunit 4 OS=Gallus gallus GN=DKC1 PE=2 SV=1	0.0354	0.0910	up	0.2930	up	0.8799	up	0.2020	up	0.7888	up	0.5869	up
MPF_Z658B.1.1	Z658B_HUMAN (sp|Q4V348) Zinc finger protein 658B OS=Homo sapiens GN=ZNF658B PE=2 SV=1	0.0354	0.0201	up	0.1555	up	1.1861	up	0.1354	up	1.1660	up	1.0306	up
MPF_contig_030785		0.0354	-0.0914	down	0.1539	up	0.7632	up	0.2453	up	0.8546	up	0.6093	up
MPF_LOC101481574.1.1	XM_004538898.1 PREDICTED: Maylandia zebra nuclear factor interleukin-3-regulated protein-like (LOC101481574), mRNA	0.0354	-0.1336	down	0.2996	up	1.3727	up	0.4332	up	1.5063	up	1.0731	up

MPF_LOC101465950.3.3	XM_004573375.1 PREDICTED: Maylandia zebra transcription initiation factor TFIID subunit 1-like (LOC101465950), transcript variant X5, mRNA	0.0354	0.0509	up	0.1180	up	0.9835	up	0.0670	up	0.9326	up	0.8656	up
MPF_contig_018608		0.0354	-0.1390	down	0.1272	up	0.8712	up	0.2662	up	1.0102	up	0.7440	up
MPF_LOC101470901.5.10	XM_004574121.1 PREDICTED: Maylandia zebra 40S ribosomal protein S3-like (LOC101470901), mRNA	0.0354	-0.2210	down	-0.0237	down	0.8613	up	0.1973	up	1.0822	up	0.8849	up
MPF_contig_032370		0.0354	0.1262	up	0.0712	up	0.7450	up	-0.0550	down	0.6188	up	0.6738	up
MPF_contig_030933		0.0354	0.0155	up	0.0779	up	0.5746	up	0.0624	up	0.5591	up	0.4966	up
MPF_LOC101485248.1.2	XM_004546032.1 PREDICTED: Maylandia zebra dystroglycan-like (LOC101485248), transcript variant X3, mRNA	0.0354	0.2136	up	0.3795	up	0.9018	up	0.1660	up	0.6882	up	0.5223	up
MPF_contig_009544		0.0354	0.1130	up	0.3400	up	0.9247	up	0.2270	up	0.8117	up	0.5847	up
MPF_LOC101169047.1.2	XP_004073780.1 PREDICTED: saxitoxin and tetrodotoxin-binding protein 1like [Oryzias latipes]	0.0354	-0.4343	down	-0.0227	down	-0.9428	down	0.4116	up	-0.5085	down	-0.9201	down
MPF_LOC101488123.1.1	XM_004554274.1 PREDICTED: Maylandia zebra ragulator complex protein LAMTOR5-like (LOC101488123), mRNA	0.0354	0.2054	up	0.3644	up	1.0133	up	0.1590	up	0.8079	up	0.6489	up
MPF_contig_000575		0.0354	0.0301	up	0.3853	up	1.1905	up	0.3552	up	1.1604	up	0.8052	up
MPF_contig_037593		0.0354	-0.0746	down	0.1120	up	0.7151	up	0.1867	up	0.7898	up	0.6031	up

MPF_contig_009909		0.0354	-0.4938	down	-0.5298	down	-2.2391	down	-0.0360	down	-1.7453	down	-1.7093	down
MPF_LOC101473182.1.3	XM_004566836.1 PREDICTED: Maylandia zebra sialoadhesin-like (LOC101473182), transcript variant X2, mRNA	0.0354	-0.2568	down	-1.4354	down	-3.8813	down	-1.1787	down	-3.6245	down	-2.4458	down
MPF_contig_025238		0.0354	0.0882	up	0.2144	up	0.8805	up	0.1262	up	0.7923	up	0.6661	up
MPF_LOC101171634.1.1	XP_004084607.1 PREDICTED: complement factor H-like [Oryzias latipes]	0.0354	-0.0023	down	0.3323	up	0.8150	up	0.3347	up	0.8173	up	0.4826	up
MPF_contig_029884	XM_004573730.1 PREDICTED: Maylandia zebra cyclic AMP-responsive element-binding protein 3-like protein 2-like (LOC101480575), transcript variant X1, mRNA	0.0354	-0.0388	down	0.3062	up	0.5649	up	0.3450	up	0.6037	up	0.2587	up
MPF_LOC100693065.5.9	XM_003443772.1 PREDICTED: Oreochromis niloticus NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial-like (LOC100693065), mRNA	0.0354	0.0453	up	0.3603	up	1.3433	up	0.3150	up	1.2980	up	0.9830	up
MPF_LOC101470981.2.2	XM_004547952.1 PREDICTED: Maylandia zebra mitochondrial import receptor subunit TOM7 homolog (LOC101470981), mRNA	0.0354	0.0122	up	0.0727	up	0.9401	up	0.0605	up	0.9280	up	0.8674	up
MPF_contig_012969	XM_004567297.1 PREDICTED: Maylandia zebra mothers against decapentaplegic homolog 2like (LOC101470473), transcript variant X2, mRNA	0.0354	0.3293	up	0.1347	up	0.8046	up	-0.1946	down	0.4752	up	0.6698	up

MPF_LOC101465253.1.1	XM_004548778.1 PREDICTED: Maylandia zebra 2',5'phosphodiesterase 12-like (LOC101465253), transcript variant X1, mRNA	0.0354	0.4062	up	0.3429	up	1.3040	up	-0.0633	down	0.8978	up	0.9611	up
MPF_LOC100685053.1.1	XP_003434657.1 PREDICTED: polyubiquitinlike [Canis lupus familiaris]	0.0354	0.3127	up	0.3499	up	0.4604	up	0.0372	up	0.1477	up	0.1105	up
MPF_contig_034121		0.0354	-0.1076	down	0.0420	up	1.3202	up	0.1496	up	1.4278	up	1.2782	up
MPF_LOC100701582.2.9	XP_003455288.1 PREDICTED: zinc finger protein 236-like [Oreochromis niloticus]	0.0354	0.2240	up	-0.0115	down	1.1682	up	-0.2355	down	0.9442	up	1.1798	up
MPF_LOC101481996.4.6	XM_004569599.1 PREDICTED: Maylandia zebra interferon regulatory factor 2-binding protein 1-like (LOC101481996), mRNA	0.0354	0.0124	up	0.2246	up	0.4663	up	0.2122	up	0.4539	up	0.2417	up
MPF_LOC101478540.1.1	XM_004541456.1 PREDICTED: Maylandia zebra phosphatidylserine synthase 1-like (LOC101478540), mRNA	0.0354	-0.1601	down	0.4191	up	-0.2971	down	0.5792	up	-0.1370	down	-0.7162	down
MPF_LOC100710832.1.1	XM_003441769.1 PREDICTED: Oreochromis niloticus receptor-type tyrosine-protein phosphatase epsilon-like, transcript variant 2 (LOC100710832), mRNA	0.0354	-0.0503	down	-0.3632	down	-1.3189	down	-0.3129	down	-1.2686	down	-0.9557	down
MPF_contig_011891		0.0354	-0.0003	down	-0.1586	down	0.9359	up	-0.1582	down	0.9362	up	1.0944	up
MPF_contig_034000		0.0355	0.1971	up	0.0465	up	1.0044	up	-0.1506	down	0.8073	up	0.9579	up

MPF_contig_021741		0.0355	0.0607	up	0.3595	up	0.5958	up	0.2988	up	0.5352	up	0.2364	up
MPF_LOC101465735.2.9	XM_004548780.1 PREDICTED: Maylandia zebra 40S ribosomal protein S23-like (LOC101465735), mRNA	0.0355	-0.0778	down	0.4015	up	1.4119	up	0.4793	up	1.4897	up	1.0104	up
MPF_ZNF79.1.3	ZNF79_HUMAN (sp|Q15937) Zinc finger protein 79 OS=Homo sapiens GN=ZNF79 PE=1 SV=2	0.0356	0.0407	up	0.1201	up	1.1888	up	0.0793	up	1.1480	up	1.0687	up
MPF_ZG57.5.12	ZG57_XENLA (sp|P18729) Gastrula zinc finger protein XlCGF57.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.0356	0.0222	up	0.1644	up	1.1617	up	0.1423	up	1.1395	up	0.9972	up
MPF_LOC101468598.1.2	XM_004559893.1 PREDICTED: Maylandia zebra cyclin-dependent kinase 18-like (LOC101468598), mRNA	0.0356	-0.1698	down	0.0893	up	1.0258	up	0.2591	up	1.1957	up	0.9366	up
MPF_LOC101471834.1.4	XM_004546921.1 PREDICTED: Maylandia zebra titin-like (LOC101471834), transcript variant X2, mRNA	0.0356	-0.3597	down	-0.7539	down	-2.4042	down	-0.3942	down	-2.0445	down	-1.6503	down
MPF_LOC101468908.1.1	XM_004539040.1 PREDICTED: Maylandia zebra tuberin-like (LOC101468908), transcript variant X5, mRNA	0.0356	0.2492	up	0.5287	up	1.0981	up	0.2795	up	0.8489	up	0.5694	up

MPF_LOC101486005.7.8	XM_004549975.1 PREDICTED: Maylandia zebra 60S ribosomal protein L23a-like (LOC101486005), transcript variant X2, mRNA	0.0356	-0.3173	down	0.2273	up	1.0181	up	0.5446	up	1.3354	up	0.7908	up

MPF_contig_024047		0.0356	-0.7776	down	0.0675	up	-1.7466	down	0.8451	up	-0.9690	down	-1.8141	down
MPF_contig_032559		0.0356	-0.0764	down	0.1892	up	0.8875	up	0.2656	up	0.9638	up	0.6982	up
MPF_contig_044568		0.0356	-0.0063	down	0.3476	up	1.1985	up	0.3539	up	1.2048	up	0.8509	up
MPF_contig_001426	XM_004541604.1 PREDICTED: Maylandia zebra oxidation resistance protein 1-like (LOC101469515), transcript variant X1, mRNA	0.0356	0.2243	up	0.3106	up	0.9117	up	0.0863	up	0.6874	up	0.6011	up
MPF_LOC100699175.2.2	XM_003438110.1 PREDICTED: Oreochromis niloticus serine/arginine-rich splicing factor 11-like (LOC100699175), mRNA	0.0357	0.3405	up	0.1957	up	0.8046	up	-0.1448	down	0.4641	up	0.6089	up
MPF_LOC101066746.1.1	XM_003976864.1 PREDICTED: Takifugu rubripes lysosomal protective protein-like (LOC101066746), mRNA	0.0357	-0.0345	down	0.2407	up	0.3749	up	0.2752	up	0.4094	up	0.1341	up
MPF_LOC101484400.2.5	XM_004572910.1 PREDICTED: Maylandia zebra 60S ribosomal protein L22-like 1-like (LOC101484400), mRNA	0.0357	-0.1746	down	-1.0676	down	-2.6466	down	-0.8930	down	-2.4720	down	-1.5790	down

MPF_LOC101161302.1.1	XP_004068020.1 PREDICTED: very lowdensity lipoprotein receptorlike [Oryzias latipes]	0.0357	0.1019	up	0.0802	up	1.6351	up	-0.0217	down	1.5332	up	1.5549	up
MPF_LOC100690594.1.1	XP_003453678.1 PREDICTED: serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform-like [Oreochromis niloticus]	0.0357	0.0873	up	-0.0523	down	1.0742	up	-0.1396	down	0.9868	up	1.1264	up
MPF_contig_044669		0.0357	-0.0882	down	0.0215	up	0.5722	up	0.1097	up	0.6605	up	0.5507	up
MPF_LOC101169532.3.45	XP_004070110.1 PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Oryzias latipes]	0.0357	-0.3364	down	0.1251	up	-0.8663	down	0.4615	up	-0.5299	down	-0.9914	down
MPF_LOC101466330.1.1	XM_004573549.1 PREDICTED: Maylandia zebra lamin-A-like (LOC101466330), transcript variant X3, mRNA	0.0357	-0.1678	down	0.0927	up	0.6437	up	0.2606	up	0.8116	up	0.5510	up
MPF_IKBKAP.1.1	XM_003443430.1 PREDICTED: Oreochromis niloticus inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein (IKBKAP), mRNA	0.0357	0.1087	up	0.1812	up	0.9462	up	0.0725	up	0.8375	up	0.7650	up
MPF_LOC100371306.1.2	XP_002733578.1 PREDICTED: hypothetical protein [Saccoglossus kowalevskii]	0.0357	-0.0612	down	0.0486	up	1.0041	up	0.1098	up	1.0652	up	0.9554	up
MPF_LOC101472025.2.3	XM_004546739.1 PREDICTED: Maylandia	0.0357	0.1899	up	0.3346	up	1.1524	up	0.1447	up	0.9625	up	0.8177	up

	zebra zinc finger protein 652like (LOC101472025), mRNA													
MPF_LOC100695382.1.1	XM_003443115.1 PREDICTED: Oreochromis niloticus galectin-2-like (LOC100695382), mRNA	0.0357	0.0708	up	-0.3025	down	1.0472	up	-0.3733	down	0.9764	up	1.3497	up
MPF_ZNF22.1.1	ZNF22_PONAB (sp|Q5R4X5) Zinc finger protein 22 OS=Pongo abelii GN=ZNF22 PE=2 SV=1	0.0357	0.1331	up	0.1571	up	0.7484	up	0.0240	up	0.6153	up	0.5913	up
MPF_LOC101464155.1.2	XM_004561739.1 PREDICTED: Maylandia zebra solute carrier family 22 member 5-like (LOC101464155), mRNA	0.0358	0.1765	up	0.5143	up	0.7980	up	0.3378	up	0.6215	up	0.2837	up
MPF_contig_037131		0.0358	-1.0486	down	-0.7687	down	-3.0314	down	0.2799	up	-1.9828	down	-2.2627	down
MPF_LOC100698395.2.2	XM_003442470.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100698395 (LOC100698395), mRNA	0.0358	-0.0703	down	0.0180	up	0.8451	up	0.0883	up	0.9154	up	0.8271	up
MPF_LOC101476946.3.4	XM_004542655.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 5-like (LOC101476946), mRNA	0.0358	-0.3046	down	-0.9671	down	-2.0663	down	-0.6625	down	-1.7617	down	-1.0992	down
MPF_contig_028990		0.0358	-0.4819	down	-0.7958	down	-2.7764	down	-0.3139	down	-2.2945	down	-1.9806	down

MPF_LOC101473852.2.2	XM_004561496.1 PREDICTED: Maylandia zebra cAMP-dependent protein kinase catalytic subunit alpha-like (LOC101473852), transcript variant X3, mRNA	0.0358	-0.0552	down	0.2308	up	0.9592	up	0.2860	up	1.0145	up	0.7284	up
MPF_LOC101463970.1.1	XM_004540289.1 PREDICTED: Maylandia zebra nardilysin-like (LOC101463970), mRNA	0.0358	-0.0407	down	0.2536	up	1.0798	up	0.2943	up	1.1205	up	0.8261	up
MPF_LOC101066134.1.1	XP_003970138.1 PREDICTED: magnesium transporter protein 1-like [Takifugu rubripes]	0.0358	-0.5246	down	-0.6969	down	-2.1802	down	-0.1723	down	-1.6556	down	-1.4834	down
MPF_contig_045642		0.0358	0.1568	up	0.4865	up	1.0156	up	0.3296	up	0.8587	up	0.5291	up
MPF_LOC101173648.1.1	XP_004076912.1 PREDICTED: transmembrane protein C10orf57 homolog [Oryzias latipes]	0.0358	-0.1000	down	0.1449	up	0.7027	up	0.2449	up	0.8028	up	0.5578	up
MPF_LOC100705069.1.1	XP_003447626.1 PREDICTED: shootin-1-like [Oreochromis niloticus]	0.0358	-0.1363	down	-1.3618	down	-3.0088	down	-1.2255	down	-2.8725	down	-1.6470	down
MPF_contig_016872		0.0358	0.0092	up	0.4552	up	0.8536	up	0.4460	up	0.8444	up	0.3984	up
MPF_LOC100700758.2.2	XP_003451835.1 PREDICTED: hypothetical protein LOC100700758 [Oreochromis niloticus]	0.0358	-0.0178	down	0.1110	up	0.9249	up	0.1288	up	0.9427	up	0.8139	up
MPF_contig_029572	XM_004564782.1 PREDICTED: Maylandia zebra arrestin domaincontaining protein 2-like (LOC101479940), transcript variant X3, mRNA	0.0358	0.1831	up	-0.4765	down	-2.3774	down	-0.6596	down	-2.5604	down	-1.9008	down

MPF_LOC101474804.1.1	XM_004565036.1 PREDICTED: Maylandia zebra uncharacterized LOC101474804 (LOC101474804), mRNA	0.0358	-0.1185	down	0.1099	up	0.3671	up	0.2284	up	0.4856	up	0.2572	up
MPF_contig_023467		0.0358	-0.1298	down	0.1716	up	1.2453	up	0.3015	up	1.3751	up	1.0737	up
MPF_LOC101472935.1.1	XM_004576185.1 PREDICTED: Maylandia zebra prestin-like (LOC101472935), mRNA	0.0359	-0.0184	down	0.0107	up	0.9284	up	0.0291	up	0.9467	up	0.9176	up
MPF_contig_004789		0.0359	-0.0013	down	0.0960	up	-0.8045	down	0.0973	up	-0.8032	down	-0.9005	down
MPF_LOC101481807.1.1	XR_191693.1 PREDICTED: Maylandia zebra plectin-like (LOC101481807), transcript variant X11, misc_RNA	0.0359	-0.2684	down	-1.0765	down	-3.2399	down	-0.8081	down	-2.9715	down	-2.1634	down
MPF_contig_020996		0.0359	0.0206	up	0.2021	up	0.7803	up	0.1815	up	0.7597	up	0.5782	up
MPF_contig_044528		0.0359	0.0582	up	0.0055	up	0.7878	up	-0.0527	down	0.7296	up	0.7822	up
MPF_ZN300.3.3	ZN300_HUMAN (sp|Q96RE9) Zinc finger protein 300 OS=Homo sapiens GN=ZNF300 PE=2 SV=1	0.0360	-0.3969	down	-0.0914	down	0.7891	up	0.3055	up	1.1860	up	0.8806	up
MPF_contig_000535		0.0360	-0.0785	down	0.0812	up	0.6093	up	0.1597	up	0.6878	up	0.5281	up
MPF_contig_004162		0.0361	0.0378	up	0.1176	up	0.4970	up	0.0798	up	0.4592	up	0.3794	up
MPF_contig_028069		0.0361	-0.0212	down	0.1759	up	0.6195	up	0.1970	up	0.6407	up	0.4436	up

MPF_LOC101481352.1.3	XM_004574885.1 PREDICTED: Maylandia zebra kinesin-like protein KIF1C-like (LOC101481352), transcript variant X2, mRNA	0.0361	-0.1238	down	0.1803	up	0.8315	up	0.3042	up	0.9553	up	0.6512	up
MPF_RS13.9.9	RS13_GILMI (sp|Q9DFR6) 40S ribosomal protein S13 OS=Gillichthys mirabilis GN=rps13 PE=2 SV=3	0.0361	-0.2874	down	-0.7158	down	-1.5874	down	-0.4285	down	-1.3000	down	-0.8716	down
MPF_LOC101156874.1.1	XM_004066761.1 PREDICTED: Oryzias latipes photoreceptor-specific nuclear receptor-like (LOC101156874), mRNA	0.0361	-0.2718	down	-0.2657	down	0.4696	up	0.0061	up	0.7414	up	0.7353	up
MPF_contig_010460		0.0361	0.0251	up	-0.0552	down	0.5864	up	-0.0802	down	0.5613	up	0.6416	up
MPF_PSMC4.1.1	XM_003451280.1 PREDICTED: Oreochromis niloticus proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4), mRNA	0.0361	0.0951	up	0.3170	up	1.0323	up	0.2219	up	0.9372	up	0.7153	up
MPF_LOC101472393.1.1	XM_004566741.1 PREDICTED: Maylandia zebra calmodulin-regulated spectrin-associated protein 1B-like (LOC101472393), transcript variant X2, mRNA	0.0361	0.4705	up	0.2027	up	1.2534	up	-0.2678	down	0.7829	up	1.0507	up
MPF_LOC100695023.6.6	XM_003443439.1 PREDICTED: Oreochromis niloticus heterogeneous nuclear ribonucleoprotein A0like (LOC100695023), mRNA	0.0362	0.1253	up	0.5032	up	0.9198	up	0.3779	up	0.7945	up	0.4166	up

MPF_LOC100709421.4.10	XM_003444588.1 PREDICTED: Oreochromis niloticus elongation factor 1gamma-like (LOC100709421), mRNA	0.0362	-0.6959	down	-0.5298	down	-1.2553	down	0.1661	up	-0.5595	down	-0.7255	down
MPF_contig_024367		0.0362	-0.0637	down	0.4232	up	1.1171	up	0.4869	up	1.1808	up	0.6939	up
MPF_LOC101464899.1.4	XM_004553991.1 PREDICTED: Maylandia zebra protein bassoon-like (LOC101464899), transcript variant X2, mRNA	0.0362	-0.1626	down	0.0749	up	0.7219	up	0.2375	up	0.8845	up	0.6470	up
MPF_LOC101481532.15.16	XM_004572628.1 PREDICTED: Maylandia zebra REST corepressor 3like (LOC101481532), transcript variant X2, mRNA	0.0362	-1.0553	down	-0.2675	down	-1.3443	down	0.7878	up	-0.2891	down	-1.0768	down
MPF_RL17.5.5	RL17_RAT (sp|P24049) 60S ribosomal protein L17 OS=Rattus norvegicus GN=Rpl17 PE=2 SV=3	0.0362	-0.0007	down	-1.0454	down	-2.3421	down	-1.0447	down	-2.3414	down	-1.2967	down
MPF_contig_032644		0.0362	-0.0789	down	0.1493	up	0.5319	up	0.2282	up	0.6108	up	0.3826	up
MPF_contig_042216		0.0362	-0.1191	down	0.1533	up	0.5436	up	0.2725	up	0.6627	up	0.3902	up
MPF_LOC100691105.1.2	XP_003449231.1 PREDICTED: cytochrome c oxidase subunit 8B, mitochondrial-like [Oreochromis niloticus]	0.0362	0.4687	up	-1.3459	down	-3.2895	down	-1.8147	down	-3.7582	down	-1.9435	down
MPF_LOC101477116.2.2	XM_004558918.1 PREDICTED: Maylandia zebra transcriptional enhancer factor TEF-5-like (LOC101477116), mRNA	0.0362	-0.1960	down	0.1855	up	0.7682	up	0.3815	up	0.9642	up	0.5827	up

MPF_LOC100701544.6.20	XP_003444277.1 PREDICTED: NACHT, LRR and PYD domains-containing protein 3-like [Oreochromis niloticus]	0.0362	0.1907	up	0.5263	up	0.5686	up	0.3356	up	0.3779	up	0.0423	up
MPF_LOC101469409.1.1	XM_004561191.1 PREDICTED: Maylandia zebra phospholysine phosphohistidine inorganic pyrophosphate phosphataselike (LOC101469409), mRNA	0.0362	-0.0180	down	0.1158	up	0.7001	up	0.1338	up	0.7181	up	0.5842	up
MPF_contig_004910		0.0362	-0.0886	down	0.6289	up	-0.1395	down	0.7176	up	-0.0509	down	-0.7684	down
MPF_LOC101484948.1.2	XM_004569795.1 PREDICTED: Maylandia zebra chromodomain-helicase-DNA-binding protein 4-like (LOC101484948), mRNA	0.0362	0.0816	up	-0.1076	down	0.5378	up	-0.1892	down	0.4562	up	0.6454	up
MPF_LOC101476560.1.1	XM_004562225.1 PREDICTED: Maylandia zebra multidrug resistanceassociated protein 7-like (LOC101476560), mRNA	0.0362	0.0175	up	0.2934	up	1.0425	up	0.2758	up	1.0250	up	0.7491	up
MPF_LOC101482548.1.1	XM_004561344.1 PREDICTED: Maylandia zebra protein phosphatase 1 regulatory subunit 1B-like (LOC101482548), mRNA	0.0362	-0.0645	down	0.1976	up	0.7013	up	0.2621	up	0.7658	up	0.5037	up
MPF_contig_031089		0.0362	-0.3782	down	0.0244	up	0.5580	up	0.4026	up	0.9361	up	0.5335	up
MPF_LOC101485100.1.2	XM_004560980.1 PREDICTED: Maylandia zebra chromatin target of PRMT1 protein-like (LOC101485100), mRNA	0.0362	-0.1134	down	0.0666	up	0.6446	up	0.1799	up	0.7579	up	0.5780	up

MPF_LOC101155354.1.5	XP_004071636.1 PREDICTED: uncharacterized protein LOC101155354 [Oryzias latipes]	0.0362	-0.1915	down	-0.2475	down	0.6270	up	-0.0560	down	0.8185	up	0.8745	up
MPF_LOC101487084.1.4	XM_004554809.1 PREDICTED: Maylandia zebra neurofilament light polypeptide-like (LOC101487084), mRNA	0.0362	-0.0797	down	0.0212	up	0.6599	up	0.1009	up	0.7396	up	0.6387	up
MPF_contig_042383		0.0362	0.1909	up	0.3554	up	1.1356	up	0.1645	up	0.9447	up	0.7802	up
MPF_ZO6.1.6	ZO6_XENLA (sp|P18749) Oocyte zinc finger protein XlCOF6 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.0362	-0.2021	down	-0.3769	down	0.8186	up	-0.1749	down	1.0206	up	1.1955	up
MPF_LOC100705680.1.1	XP_003445709.1 PREDICTED: ATPase family AAA domain-containing protein 1-A-like [Oreochromis niloticus]	0.0362	-0.1126	down	0.3472	up	1.0785	up	0.4598	up	1.1911	up	0.7313	up
MPF_RS18.4.8	RS18_ICTPU (sp|Q90YQ5) 40S ribosomal protein S18 OS=Ictalurus punctatus GN=rps18 PE=2 SV=1	0.0362	0.4679	up	-0.5026	down	-1.7448	down	-0.9705	down	-2.2127	down	-1.2422	down
MPF_LOC101484288.1.3	XM_004541479.1 PREDICTED: Maylandia zebra src kinase-associated phosphoprotein 2-like (LOC101484288), mRNA	0.0362	0.1800	up	0.5846	up	-0.0514	down	0.4046	up	-0.2314	down	-0.6360	down

MPF_LOC100696358.1.7	XM_003446291.1 PREDICTED: Oreochromis niloticus heat shock protein HSP 90-beta-like (LOC100696358), mRNA	0.0362	-0.0202	down	0.0926	up	0.5286	up	0.1128	up	0.5488	up	0.4360	up
MPF_LOC101471101.1.1	XM_004557599.1 PREDICTED: Maylandia zebra X-ray repair crosscomplementing protein 5-like (LOC101471101), mRNA	0.0362	0.0962	up	0.2363	up	0.7283	up	0.1401	up	0.6322	up	0.4920	up
MPF_contig_022442		0.0362	0.0759	up	0.3720	up	0.4525	up	0.2961	up	0.3766	up	0.0805	up
MPF_contig_025520		0.0362	-0.0094	down	0.1601	up	0.5710	up	0.1695	up	0.5805	up	0.4109	up
MPF_LOC101162897.2.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]	0.0362	0.3486	up	-1.2201	down	-3.4660	down	-1.5686	down	-3.8146	down	-2.2460	down
MPF_contig_017320	XM_004575932.1 PREDICTED: Maylandia zebra myosin phosphatase Rho-interacting protein-like (LOC101466990), transcript variant X3, mRNA	0.0362	-0.0245	down	0.2150	up	0.9264	up	0.2394	up	0.9508	up	0.7114	up
MPF_LOC100700590.1.1	XP_003454712.1 PREDICTED: hypothetical protein LOC100700590 [Oreochromis niloticus]	0.0362	-0.0896	down	0.2631	up	0.8456	up	0.3527	up	0.9352	up	0.5825	up
MPF_LOC100697996.1.1	XM_003457287.1 PREDICTED: Oreochromis niloticus interferon regulatory factor 4-like (LOC100697996), mRNA	0.0362	0.0035	up	-0.4206	down	0.8330	up	-0.4240	down	0.8296	up	1.2536	up

MPF_LOC101469230.1.2	XM_004541970.1 PREDICTED: Maylandia zebra G patch domaincontaining protein 2-like (LOC101469230), transcript variant X2, mRNA	0.0362	-0.0472	down	0.1341	up	0.7004	up	0.1813	up	0.7476	up	0.5663	up
MPF_LOC101076349.1.1	XP_003966922.1 PREDICTED: LOW QUALITY PROTEIN: dysferlin-like [Takifugu rubripes]	0.0362	0.0259	up	0.2624	up	1.4130	up	0.2365	up	1.3872	up	1.1507	up

MPF_LOC101471166.1.1	XM_004547008.1 PREDICTED: Maylandia zebra clathrin heavy chain 1like (LOC101471166), transcript variant X1, mRNA	0.0363	-0.0209	down	-0.2194	down	-1.2611	down	-0.1985	down	-1.2403	down	-1.0417	down
MPF_LOC100700418.1.1	XM_003457772.1 PREDICTED: Oreochromis niloticus vesicle transport protein SFT2B-like (LOC100700418), mRNA	0.0363	-0.1088	down	0.3981	up	0.9057	up	0.5069	up	1.0145	up	0.5076	up
MPF_contig_048528		0.0363	0.0969	up	0.2579	up	1.0533	up	0.1610	up	0.9564	up	0.7955	up
MPF_LOC101482766.4.4	XM_004543433.1 PREDICTED: Maylandia zebra cyclin-dependent kinase-like 5-like (LOC101482766), mRNA	0.0363	-0.0902	down	0.1586	up	1.0165	up	0.2489	up	1.1067	up	0.8579	up
MPF_contig_020724		0.0364	-0.0229	down	-0.1428	down	0.5141	up	-0.1199	down	0.5370	up	0.6569	up
MPF_LOC101472989.6.6	XM_004566934.1 PREDICTED: Maylandia zebra CAP-Gly domaincontaining linker protein 1like (LOC101472989), transcript variant X5, mRNA	0.0364	-0.0443	down	0.1114	up	0.6843	up	0.1557	up	0.7286	up	0.5729	up

MPF_contig_009982		0.0364	-0.2606	down	-0.1868	down	0.6675	up	0.0739	up	0.9281	up	0.8543	up
MPF_LOC101487908.1.3	XM_004546898.1 PREDICTED: Maylandia zebra rab effector MyRIP-like (LOC101487908), mRNA	0.0364	-0.2499	down	-0.0170	down	1.2634	up	0.2330	up	1.5133	up	1.2803	up
MPF_contig_016715	XM_004543372.1 PREDICTED: Maylandia zebra general transcription factor IIF subunit 2-like (LOC101467240), transcript variant X1, mRNA	0.0364	-0.0967	down	0.3438	up	1.2083	up	0.4405	up	1.3050	up	0.8645	up
MPF_LOC100703329.1.1	XP_003443108.1 PREDICTED: ras-related protein Rab-3D-like [Oreochromis niloticus]	0.0364	-0.0425	down	0.1713	up	0.9233	up	0.2138	up	0.9658	up	0.7520	up
MPF_LOC101165175.3.3	XM_004078345.1 PREDICTED: Oryzias latipes cathepsin S-like (LOC101165175), mRNA	0.0364	0.7037	up	-1.0049	down	-2.5761	down	-1.7086	down	-3.2798	down	-1.5712	down
MPF_LOC101174860.1.1	XP_004078516.1 PREDICTED: protein RRNAD1-like [Oryzias latipes]	0.0364	0.0956	up	0.2817	up	0.5256	up	0.1861	up	0.4300	up	0.2438	up
MPF_LOC100695994.30.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.0364	-0.0241	down	0.1485	up	1.1728	up	0.1726	up	1.1969	up	1.0242	up
MPF_PDZD8.1.1	XM_003454989.1 PREDICTED: Oreochromis niloticus PDZ domain containing 8 (PDZD8), mRNA	0.0364	0.1201	up	0.0332	up	0.9198	up	-0.0869	down	0.7997	up	0.8866	up
MPF_contig_015295		0.0365	-0.0399	down	0.2454	up	0.6841	up	0.2853	up	0.7239	up	0.4386	up

MPF_LOC100712294.1.2	XM_003449092.1 PREDICTED: Oreochromis niloticus suppressor of IKBKE 1-like (LOC100712294), mRNA	0.0365	-0.0383	down	0.1778	up	0.6886	up	0.2161	up	0.7269	up	0.5107	up
MPF_contig_009758		0.0365	-0.0685	down	0.2443	up	0.9120	up	0.3127	up	0.9805	up	0.6678	up
MPF_LOC100709350.2.3	XP_003449297.1 PREDICTED: cryptochrome-2like [Oreochromis niloticus]	0.0365	-0.1980	down	0.1688	up	0.9917	up	0.3668	up	1.1897	up	0.8229	up
MPF_LOC101473792.1.1	XM_004570822.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 5-like (LOC101473792), transcript variant X1, mRNA	0.0365	0.0946	up	0.0383	up	0.6325	up	-0.0563	down	0.5380	up	0.5943	up
MPF_LOC101477305.1.1	XM_004560761.1 PREDICTED: Maylandia zebra uncharacterized LOC101477305 (LOC101477305), mRNA	0.0365	-0.0678	down	0.0392	up	0.6372	up	0.1070	up	0.7050	up	0.5980	up
MPF_LOC100703551.1.2	XM_003450798.1 PREDICTED: Oreochromis niloticus TNF receptorassociated factor 6-like (LOC100703551), mRNA	0.0366	0.2076	up	0.6484	up	1.2907	up	0.4409	up	1.0832	up	0.6423	up
MPF_ATF6B.1.1	XM_004073727.1 PREDICTED: Oryzias latipes cyclic AMP-dependent transcription factor ATF-6 beta-like (LOC101165322), mRNA	0.0366	0.1007	up	0.0889	up	1.0675	up	-0.0118	down	0.9668	up	0.9785	up

MPF_LOC101476442.1.1	XM_004576449.1 PREDICTED: Maylandia zebra uncharacterized LOC101476442 (LOC101476442), mRNA	0.0366	-0.1287	down	-0.1025	down	1.0566	up	0.0262	up	1.1853	up	1.1591	up
MPF_ZNF84.7.14	ZNF84_HUMAN (sp|P51523) Zinc finger protein 84 OS=Homo sapiens GN=ZNF84 PE=1 SV=2	0.0366	-0.0469	down	0.2315	up	1.8329	up	0.2784	up	1.8799	up	1.6014	up
MPF_LOC101479581.3.3	XM_004543518.1 PREDICTED: Maylandia zebra uncharacterized LOC101479581 (LOC101479581), mRNA	0.0366	0.1781	up	0.4040	up	1.1089	up	0.2259	up	0.9308	up	0.7049	up
MPF_LOC101467903.2.2	XM_004554288.1 PREDICTED: Maylandia zebra espin-like (LOC101467903), mRNA	0.0366	0.1528	up	0.6495	up	1.8413	up	0.4968	up	1.6885	up	1.1917	up
MPF_contig_048082		0.0366	-0.1862	down	0.0900	up	0.5816	up	0.2762	up	0.7678	up	0.4916	up
MPF_contig_038777		0.0366	-0.1108	down	0.0840	up	1.2148	up	0.1948	up	1.3256	up	1.1308	up
MPF_LOC101473855.10.12	XM_004561856.1 PREDICTED: Maylandia zebra 60S ribosomal protein L17-like (LOC101473855), transcript variant X2, mRNA	0.0366	-0.0220	down	-1.0589	down	-2.3573	down	-1.0369	down	-2.3352	down	-1.2984	down
MPF_contig_032267		0.0366	-0.2208	down	-1.3808	down	-4.6404	down	-1.1601	down	-4.4197	down	-3.2596	down
MPF_contig_032965		0.0366	-0.1573	down	0.2329	up	0.7050	up	0.3902	up	0.8623	up	0.4721	up

MPF_LECG.27.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.0366	-0.2212	down	-1.9958	down	-4.3451	down	-1.7746	down	-4.1239	down	-2.3493	down
MPF_LOC101170497.1.8	XP_004086004.1 PREDICTED: oocyte zinc finger protein XlCOF6-like [Oryzias latipes]	0.0366	0.1316	up	0.2056	up	0.9482	up	0.0739	up	0.8166	up	0.7427	up
MPF_contig_003862		0.0366	-0.0715	down	-0.0133	down	0.5612	up	0.0582	up	0.6327	up	0.5745	up
MPF_LOC101480205.1.1	XM_004554598.1 PREDICTED: Maylandia zebra exportin-1-like (LOC101480205), transcript variant X4, mRNA	0.0366	0.0759	up	0.2164	up	0.8389	up	0.1405	up	0.7630	up	0.6225	up
MPF_ANK3.5.8	ANK3_MOUSE (sp|G5E8K5) Ankyrin-3 OS=Mus musculus GN=Ank3 PE=1 SV=1	0.0367	-0.0759	down	0.1500	up	-2.2309	down	0.2259	up	-2.1550	down	-2.3809	down
MPF_TCB1.7.8	TCB1_CAEBR (sp|P35072) Transposable element Tcb1 transposase OS=Caenorhabditis briggsae PE=3 SV=1	0.0367	-0.1269	down	0.0510	up	0.7442	up	0.1779	up	0.8712	up	0.6932	up
MPF_LOC101474475.2.2	XM_004548245.1 PREDICTED: Maylandia zebra kelch domaincontaining protein 10-like (LOC101474475), mRNA	0.0367	-0.0712	down	0.1573	up	0.7786	up	0.2285	up	0.8497	up	0.6213	up
MPF_LOC100690233.1.1	XM_003456743.1 PREDICTED: Oreochromis niloticus membrane progestin receptor gamma-B-like, transcript variant 2 (LOC100690233), mRNA	0.0367	0.0303	up	0.0146	up	0.5710	up	-0.0158	down	0.5407	up	0.5564	up
MPF_LOC100707526.1.1	XP_003442552.1 PREDICTED: hypothetical protein LOC100707526 [Oreochromis niloticus]	0.0367	0.3745	up	0.7972	up	1.1424	up	0.4227	up	0.7679	up	0.3452	up

MPF_LOC101467550.1.2	XM_004568834.1 PREDICTED: Maylandia zebra cyclin-dependent kinase 17-like (LOC101467550), transcript variant X2, mRNA	0.0367	0.0523	up	0.0840	up	1.3306	up	0.0316	up	1.2783	up	1.2466	up
MPF_SRRM2.13.15	SRRM2_HUMAN (sp|Q9UQ35) Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	0.0367	-0.0765	down	-1.1787	down	-3.1087	down	-1.1022	down	-3.0322	down	-1.9300	down
MPF_contig_026354		0.0367	-0.0328	down	0.1972	up	0.8558	up	0.2300	up	0.8886	up	0.6586	up
MPF_LOC101475575.2.2	XM_004555508.1 PREDICTED: Maylandia zebra tubulin alpha chain-like (LOC101475575), transcript variant X2, mRNA	0.0367	-0.1509	down	0.1544	up	0.7533	up	0.3053	up	0.9042	up	0.5989	up
MPF_contig_027340		0.0367	-0.1387	down	-0.4931	down	-1.9260	down	-0.3544	down	-1.7873	down	-1.4329	down
MPF_TBA.7.17	TBA_NOTVI (sp|Q91060) Tubulin alpha chain OS=Notophthalmus viridescens PE=2 SV=1	0.0367	-0.1672	down	0.1637	up	0.7537	up	0.3309	up	0.9209	up	0.5900	up
MPF_ALDOC.1.1	ALDOC_CARAU (sp|P53448) Fructose-bisphosphate aldolase C OS=Carassius auratus GN=aldoc PE=2 SV=2	0.0367	-0.0629	down	0.0350	up	0.7874	up	0.0978	up	0.8502	up	0.7524	up
MPF_APBP2.1.1	[BBH] APBP2_HUMAN (sp|Q92624) Amyloid proteinbinding protein 2 OS=Homo sapiens GN=APPBP2 PE=1 SV=2	0.0367	-0.0385	down	0.3982	up	1.2581	up	0.4368	up	1.2966	up	0.8598	up

MPF_LOC101481864.1.1	XM_004561617.1 PREDICTED: Maylandia zebra galactosylgalactosylxylosylprotein 3-beta- glucuronosyltransferase 1like (LOC101481864), transcript variant X3, mRNA	0.0367	-0.0090	down	0.4741	up	1.1767	up	0.4831	up	1.1857	up	0.7026	up
MPF_NEMVEDRAFT_V1 G111168.2.2	XP_001631283.1 predicted protein [Nematostella vectensis]	0.0367	0.1554	up	0.4997	up	0.7270	up	0.3443	up	0.5716	up	0.2273	up
MPF_contig_025542		0.0367	0.0814	up	-0.1867	down	0.7809	up	-0.2681	down	0.6996	up	0.9676	up
MPF_contig_043534		0.0367	0.0595	up	0.3233	up	0.6980	up	0.2639	up	0.6385	up	0.3747	up
MPF_contig_045558		0.0367	-0.1257	down	0.1283	up	0.8720	up	0.2540	up	0.9977	up	0.7436	up
MPF_B2MG.10.10	NM_001198574.1 Salmo salar Beta-2-microglobulin precursor (b2mg), mRNA gb|BT049278.1| Salmo salar clone ssal-rgb2-510-275 Beta2-microglobulin precursor putative mRNA, complete cds	0.0367	0.5543	up	-0.7398	down	-1.7452	down	-1.2941	down	-2.2995	down	-1.0054	down
MPF_contig_009735		0.0367	0.0424	up	0.0377	up	1.1324	up	-0.0047	down	1.0900	up	1.0947	up
MPF_ATP7A.1.1	XM_003455169.1 PREDICTED: Oreochromis niloticus ATPase, Cu++ transporting, alpha polypeptide (ATP7A), mRNA	0.0367	0.1566	up	0.3524	up	0.8911	up	0.1958	up	0.7346	up	0.5388	up
MPF_contig_021115		0.0367	-0.3512	down	-0.1919	down	1.1037	up	0.1593	up	1.4549	up	1.2955	up
MPF_LOC100708377.1.1	XM_003453136.1 PREDICTED: Oreochromis niloticus tubulin	0.0367	0.2432	up	0.6030	up	1.0650	up	0.3598	up	0.8217	up	0.4620	up

	polyglutamylase TTLL5-like (LOC100708377), mRNA													
MPF_LOC100701316.1.1	XP_003456261.1 PREDICTED: U3 small nucleolar RNA-associated protein 14 homolog A-like [Oreochromis niloticus]	0.0367	0.0307	up	0.1536	up	0.8599	up	0.1229	up	0.8292	up	0.7063	up
MPF_LOC101469336.3.3	XM_004566007.1 PREDICTED: Maylandia zebra ras-related protein MRas-like (LOC101469336), mRNA	0.0367	-0.1014	down	-0.2499	down	-1.9397	down	-0.1484	down	-1.8382	down	-1.6898	down
MPF_LOC100710693.1.3	XP_003453586.1 PREDICTED: complement factor H-like [Oreochromis niloticus]	0.0367	-0.1263	down	-1.5459	down	-3.2601	down	-1.4195	down	-3.1337	down	-1.7142	down
MPF_LOC100535956.1.1	XP_003198038.1 PREDICTED: hypothetical protein LOC100535956 [Danio rerio]	0.0367	-0.0355	down	-0.1931	down	-1.5334	down	-0.1576	down	-1.4979	down	-1.3403	down
MPF_CRAMP1L.1.1	XM_003454013.1 PREDICTED: Oreochromis niloticus Crm, cramped-like (Drosophila) (CRAMP1L), mRNA	0.0367	0.1629	up	0.3971	up	1.0268	up	0.2342	up	0.8639	up	0.6297	up
MPF_LOC101073645.1.1	XP_003977503.1 PREDICTED: kunitz-type protease inhibitor 1-like [Takifugu rubripes]	0.0367	-0.4368	down	0.4493	up	0.8100	up	0.8861	up	1.2468	up	0.3607	up
MPF_contig_039266		0.0367	0.0967	up	0.5184	up	0.9565	up	0.4217	up	0.8598	up	0.4381	up
MPF_ZN271.9.19	ZN271_MOUSE (sp|P15620) Zinc finger protein 271 OS=Mus musculus GN=Znf271 PE=2 SV=1	0.0368	0.1664	up	0.3156	up	1.2809	up	0.1492	up	1.1145	up	0.9654	up

MPF_RPB2.1.1	[BBH] RPB2_HUMAN (sp|P30876) DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens GN=POLR2B PE=1 SV=1	0.0368	-0.0571	down	0.2228	up	0.6450	up	0.2799	up	0.7021	up	0.4222	up
MPF_ZG57.12.12	ZG57_XENLA (sp|P18729) Gastrula zinc finger protein XlCGF57.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.0368	-0.0069	down	0.1967	up	1.1589	up	0.2036	up	1.1658	up	0.9622	up
MPF_MTOR.1.2	XP_003449179.1 PREDICTED: serine/threonine-protein kinase mTOR [Oreochromis niloticus]	0.0368	-0.0718	down	0.2004	up	0.8206	up	0.2722	up	0.8924	up	0.6202	up
MPF_contig_023802		0.0369	0.2039	up	0.2339	up	0.9512	up	0.0299	up	0.7473	up	0.7174	up
MPF_LOC100696045.1.1	XP_003458436.1 PREDICTED: general transcription factor II-I repeat domain-containing protein 2Blike [Oreochromis niloticus]	0.0369	-0.2830	down	-0.1595	down	0.5227	up	0.1235	up	0.8057	up	0.6823	up
MPF_LOC101161026.1.1	XP_004084769.1 PREDICTED: oocyte zinc finger protein XlCOF8.4-like [Oryzias latipes]	0.0369	0.0086	up	0.1082	up	1.1248	up	0.0997	up	1.1163	up	1.0166	up
MPF_APC10.1.1	[BBH] APC10_HUMAN (sp|Q9UM13) Anaphasepromoting complex subunit 10 OS=Homo sapiens GN=ANAPC10 PE=1 SV=1	0.0369	-0.0995	down	0.1320	up	1.0269	up	0.2315	up	1.1264	up	0.8949	up
MPF_contig_042300		0.0370	-0.3588	down	0.2451	up	0.8555	up	0.6039	up	1.2144	up	0.6105	up

MPF_LOC101476924.2.2	XM_004539957.1 PREDICTED: Maylandia zebra RNA polymeraseassociated protein RTF1 homolog (LOC101476924), mRNA	0.0370	0.2736	up	0.4137	up	0.7515	up	0.1401	up	0.4780	up	0.3379	up
MPF_LOC100707353.1.5	XM_003445500.1 PREDICTED: Oreochromis niloticus zinc finger MYMtype protein 4-like (LOC100707353), mRNA	0.0370	-0.1191	down	0.0835	up	0.8235	up	0.2026	up	0.9426	up	0.7400	up
MPF_LOC100710590.3.4	XP_003449469.1 PREDICTED: zinc finger protein 836-like, partial [Oreochromis niloticus]	0.0370	0.0520	up	0.1311	up	1.1802	up	0.0791	up	1.1281	up	1.0491	up
MPF_LOC101481641.1.1	XM_004551444.1 PREDICTED: Maylandia zebra mitogen-activated protein kinase kinase kinase MLK4-like (LOC101481641), transcript variant X2, mRNA	0.0370	0.1456	up	0.1555	up	1.1221	up	0.0100	up	0.9765	up	0.9665	up
MPF_LOC100918446.1.1	XP_003762147.1 PREDICTED: uncharacterized protein LOC100918446 [Sarcophilus harrisii]	0.0370	0.0457	up	0.2149	up	0.6990	up	0.1691	up	0.6533	up	0.4842	up
MPF_LOC101158204.2.2	XM_004072523.1 PREDICTED: Oryzias latipes TBC1 domain family member 10A-like (LOC101158204), mRNA	0.0370	-0.0440	down	0.1060	up	0.8744	up	0.1500	up	0.9184	up	0.7684	up
MPF_LOC100753274.1.1	XP_003496316.1 PREDICTED: hypothetical protein LOC100753274 [Cricetulus griseus]	0.0371	0.4090	up	0.0916	up	1.2823	up	-0.3174	down	0.8733	up	1.1907	up

MPF_LOC101481675.1.1	XM_004558563.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase CHFR-like (LOC101481675), transcript variant X4, mRNA	0.0371	-0.1135	down	0.0715	up	0.6476	up	0.1851	up	0.7612	up	0.5761	up
MPF_LOC100691830.1.1	XP_003453451.1 PREDICTED: DPY30 domain-containing protein 1-like [Oreochromis niloticus]	0.0371	0.1463	up	0.1415	up	0.6827	up	-0.0048	down	0.5364	up	0.5412	up
MPF_LOC101487751.2.3	XM_004574697.1 PREDICTED: Maylandia zebra active regulator of SIRT1-like (LOC101487751), transcript variant X1, mRNA	0.0371	0.1180	up	0.0992	up	0.5779	up	-0.0187	down	0.4600	up	0.4787	up
MPF_contig_044487		0.0371	0.0890	up	-0.7477	down	-2.7303	down	-0.8367	down	-2.8193	down	-1.9826	down
MPF_LOC101467736.7.8	XM_004564634.1 PREDICTED: Maylandia zebra peptidyl-prolyl cis-trans isomerase F, mitochondriallike (LOC101467736), mRNA	0.0371	-0.0500	down	0.0652	up	0.6503	up	0.1152	up	0.7003	up	0.5851	up
MPF_LOC100695307.1.3	XM_003448117.1 PREDICTED: Oreochromis niloticus enoyl-CoA hydratase domain-containing protein 3, mitochondrial-like (LOC100695307), mRNA	0.0371	-0.0572	down	0.2525	up	0.9240	up	0.3097	up	0.9812	up	0.6715	up
MPF_LOC101465129.18.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNAbinding protein A-like (LOC101465129), transcript variant X4, mRNA	0.0371	0.0547	up	0.2017	up	0.6145	up	0.1470	up	0.5598	up	0.4128	up

MPF_LOC100695691.2.2	XM_003455952.1 PREDICTED: Oreochromis niloticus actin-related protein 2/3 complex subunit 1B-like (LOC100695691), mRNA	0.0371	-0.0504	down	-1.6922	down	-3.9395	down	-1.6419	down	-3.8891	down	-2.2472	down
MPF_TGFBI.1.1	XM_003443373.1 PREDICTED: Oreochromis niloticus transforming growth factor, beta-induced, 68kDa (TGFBI), mRNA	0.0371	0.0142	up	0.2732	up	0.7539	up	0.2589	up	0.7397	up	0.4807	up

MPF_LOC101469557.1.1	XM_004575292.1 PREDICTED: Maylandia zebra monoacylglycerol lipase ABHD12-like (LOC101469557), transcript variant X3, mRNA	0.0371	0.2307	up	0.7321	up	1.0859	up	0.5014	up	0.8552	up	0.3538	up
MPF_LOC100707427.4.4	XM_003440083.1 PREDICTED: Oreochromis niloticus AN1-type zinc finger protein 5-like, transcript variant 5 (LOC100707427), mRNA	0.0371	-0.1721	down	0.1210	up	1.0351	up	0.2931	up	1.2073	up	0.9142	up
MPF_LOC100693088.1.1	XM_003449441.1 PREDICTED: Oreochromis niloticus neoverrucotoxin subunit alpha-like (LOC100693088), mRNA	0.0371	-0.1569	down	-0.1851	down	0.6089	up	-0.0282	down	0.7658	up	0.7940	up
MPF_LOC101475165.1.1	XM_004557989.1 PREDICTED: Maylandia zebra secretory carrierassociated membrane protein 2-like (LOC101475165), transcript variant X1, mRNA	0.0371	0.0654	up	0.6053	up	0.9353	up	0.5399	up	0.8699	up	0.3300	up

MPF_contig_038936	XM_004550255.1 PREDICTED: Maylandia zebra transcription elongation regulator 1-like (LOC101483186), transcript variant X1, mRNA	0.0371	-0.1430	down	0.0726	up	0.7906	up	0.2156	up	0.9335	up	0.7179	up
MPF_LOC101479407.1.1	XM_004547238.1 PREDICTED: Maylandia zebra macrophage-expressed gene 1 protein-like (LOC101479407), mRNA	0.0371	0.0573	up	-0.8019	down	-2.2350	down	-0.8592	down	-2.2923	down	-1.4331	down
MPF_LOC101481567.1.1	XM_004560226.1 PREDICTED: Maylandia zebra uncharacterized LOC101481567 (LOC101481567), mRNA	0.0371	0.2650	up	-0.6881	down	-1.8270	down	-0.9531	down	-2.0920	down	-1.1389	down
MPF_contig_000565		0.0371	-0.1179	down	0.1445	up	0.6971	up	0.2624	up	0.8150	up	0.5526	up
MPF_LOC101468823.1.1	XM_004561473.1 PREDICTED: Maylandia zebra ankyrin repeat domaincontaining protein 13C-A-like (LOC101468823), mRNA	0.0371	-0.1111	down	0.2859	up	0.7078	up	0.3970	up	0.8188	up	0.4219	up
MPF_LOC100710715.1.3	XP_003458713.1 PREDICTED: hypothetical protein LOC100710715 [Oreochromis niloticus]	0.0371	0.0938	up	0.2453	up	0.6852	up	0.1516	up	0.5914	up	0.4399	up
MPF_LOC100698082.2.2	XR_134880.1 PREDICTED: Oreochromis niloticus keratin, type I cytoskeletal 13-like (LOC100698082), miscRNA	0.0371	-0.8320	down	-3.3984	down	-5.2441	down	-2.5664	down	-4.4121	down	-1.8457	down
MPF_contig_019055		0.0371	-0.0818	down	0.0609	up	0.5235	up	0.1426	up	0.6053	up	0.4626	up

MPF_LOC100692664.1.1	XP_003458729.1 PREDICTED: neutrophil cytosol factor 1-like [Oreochromis niloticus]	0.0371	-0.2544	down	-0.4979	down	-3.0881	down	-0.2435	down	-2.8337	down	-2.5902	down
MPF_contig_025111		0.0371	0.2743	up	0.3254	up	0.5993	up	0.0511	up	0.3250	up	0.2739	up
MPF_contig_015546		0.0371	-0.0051	down	0.1404	up	0.6495	up	0.1455	up	0.6546	up	0.5092	up
MPF_contig_036677	XM_004573888.1 PREDICTED: Maylandia zebra c-Maf-inducing proteinlike (LOC101478585), transcript variant X3, mRNA	0.0371	0.0793	up	0.1120	up	0.6553	up	0.0328	up	0.5760	up	0.5432	up
MPF_LOC100711484.6.8	XM_003448843.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100711484), mRNA	0.0371	0.3646	up	0.4294	up	0.6429	up	0.0648	up	0.2782	up	0.2134	up
MPF_LOC101487548.1.1	XM_004574179.1 PREDICTED: Maylandia zebra prostaglandin reductase 1-like (LOC101487548), mRNA	0.0371	0.0830	up	0.1109	up	0.7213	up	0.0280	up	0.6384	up	0.6104	up
MPF_LOC100711183.1.2	XM_003441343.1 PREDICTED: Oreochromis niloticus protein timeless homolog (LOC100711183), mRNA	0.0371	0.0307	up	0.1428	up	1.1799	up	0.1121	up	1.1492	up	1.0370	up
MPF_LOC101469329.1.2	XM_004564739.1 PREDICTED: Maylandia zebra nogo-B receptor-like (LOC101469329), mRNA	0.0371	-0.0778	down	0.1475	up	0.8413	up	0.2254	up	0.9192	up	0.6938	up
MPF_contig_015319		0.0371	0.0237	up	0.1099	up	0.8318	up	0.0861	up	0.8081	up	0.7219	up

MPF_LOC100702817.1.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.0371	-0.3722	down	-2.0925	down	-4.2242	down	-1.7202	down	-3.8520	down	-2.1318	down
MPF_LOC100711368.2.3	XM_003442435.1 PREDICTED: Oreochromis niloticus keratin, type I cytoskeletal 13-like (LOC100711368), mRNA	0.0371	0.0030	up	0.0267	up	0.7650	up	0.0237	up	0.7620	up	0.7382	up
MPF_LOC101174391.1.1	XP_004084081.1 PREDICTED: microfibrilassociated glycoprotein 4-like [Oryzias latipes]	0.0371	0.4541	up	0.2716	up	0.8581	up	-0.1825	down	0.4040	up	0.5865	up

MPF_AT1A1.1.3	AT1A1_OREMO (sp|Q9YH26) Sodium/potassiumtransporting ATPase subunit alpha-1 OS=Oreochromis mossambicus GN=atp1a1 PE=2 SV=2	0.0371	0.0138	up	-0.0966	down	1.0279	up	-0.1103	down	1.0141	up	1.1245	up
MPF_LOC101465474.1.1	XM_004554819.1 PREDICTED: Maylandia zebra interferon alphainducible protein 27-like protein 2-like (LOC101465474), mRNA	0.0371	0.0691	up	0.1122	up	0.7900	up	0.0432	up	0.7210	up	0.6778	up
MPF_contig_032228		0.0371	0.4188	up	0.4025	up	1.0402	up	-0.0163	down	0.6214	up	0.6377	up
MPF_MUC12.1.1	MUC12_HUMAN (sp|Q9UKN1) Mucin-12 OS=Homo sapiens GN=MUC12 PE=1 SV=2	0.0371	0.0720	up	0.9861	up	-1.6952	down	0.9141	up	-1.7672	down	-2.6813	down

MPF_LOC101471344.2.2	XM_004570568.1 PREDICTED: Maylandia zebra growth arrest and DNA damage-inducible protein GADD45 alpha-like (LOC101471344), transcript variant X1, mRNA	0.0371	-0.0683	down	0.0002	up	0.7840	up	0.0685	up	0.8523	up	0.7838	up
MPF_LOC101079440.1.1	XM_003966182.1 PREDICTED: Takifugu rubripes protein lifeguard 1like (LOC101079440), mRNA	0.0371	0.2431	up	0.2635	up	1.0187	up	0.0205	up	0.7757	up	0.7552	up
MPF_SRRM2.3.15	XP_002926593.1 PREDICTED: serine/arginine repetitive matrix protein 2-like [Ailuropoda melanoleuca]	0.0371	0.0677	up	-0.9484	down	-2.9946	down	-1.0161	down	-3.0623	down	-2.0462	down
MPF_LOC100535356.1.1	XP_003199172.1 PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Danio rerio]	0.0371	-0.3380	down	-0.6857	down	-2.3707	down	-0.3477	down	-2.0327	down	-1.6851	down
MPF_LOC100692576.1.3	XM_003437754.1 PREDICTED: Oreochromis niloticus GPN-loop GTPase 1like (LOC100692576), mRNA	0.0371	0.0172	up	0.1571	up	0.6503	up	0.1399	up	0.6331	up	0.4931	up
MPF_contig_027940		0.0371	-0.1235	down	-0.1369	down	0.6541	up	-0.0135	down	0.7775	up	0.7910	up
MPF_LOC101467350.2.2	XM_004545794.1 PREDICTED: Maylandia zebra 60S ribosomal protein L36a-like (LOC101467350), transcript variant X2, mRNA	0.0371	-0.0967	down	0.1760	up	0.8678	up	0.2727	up	0.9645	up	0.6918	up

MPF_SLC22A4.1.1	NM_001094580.1 Xenopus laevis solute carrier family 22 (organic cation/ergothioneine transporter), member 4 (slc22a4), mRNA gb|BC082839.1| Xenopus laevis hypothetical LOC494743, mRNA (cDNA clone MGC:80800 IMAGE:5513625), complete cds	0.0371	-0.0512	down	0.7180	up	1.1127	up	0.7692	up	1.1639	up	0.3947	up
MPF_LOC100691235.2.2	XP_003438556.1 PREDICTED: integrin beta-4like [Oreochromis niloticus]	0.0371	-0.1649	down	-0.1819	down	0.5934	up	-0.0170	down	0.7583	up	0.7753	up
MPF_contig_036843		0.0371	0.0063	up	0.1863	up	0.6302	up	0.1800	up	0.6239	up	0.4439	up
MPF_LOC101479551.1.1	XM_004555792.1 PREDICTED: Maylandia zebra SEC14-like protein 2like (LOC101479551), mRNA	0.0371	0.1553	up	-0.0598	down	-1.6217	down	-0.2151	down	-1.7770	down	-1.5619	down
MPF_LOC101484034.2.2	XM_004548471.1 PREDICTED: Maylandia zebra protein phosphatase 1 regulatory subunit 12A-like (LOC101484034), mRNA	0.0371	0.0544	up	0.1331	up	0.9215	up	0.0787	up	0.8671	up	0.7884	up
MPF_LOC100708992.1.1	XM_003451899.1 PREDICTED: Oreochromis niloticus COP9 signalosome complex subunit 8-like (LOC100708992), mRNA	0.0371	-0.1896	down	0.1780	up	0.6237	up	0.3676	up	0.8133	up	0.4457	up
MPF_contig_024077		0.0371	-0.0851	down	-0.2158	down	-1.5133	down	-0.1307	down	-1.4282	down	-1.2975	down
MPF_contig_009588		0.0371	-0.0235	down	0.1198	up	0.7031	up	0.1433	up	0.7266	up	0.5833	up
MPF_contig_002810		0.0371	-0.0857	down	0.0353	up	1.1263	up	0.1210	up	1.2120	up	1.0910	up

MPF_LOC100710182.1.2	XM_003456571.1 PREDICTED: Oreochromis niloticus voltage-dependent Ttype calcium channel subunit alpha-1H-like (LOC100710182), mRNA	0.0371	0.1264	up	0.5542	up	1.0758	up	0.4278	up	0.9494	up	0.5216	up
MPF_LOC100705746.3.3	XP_003443116.1 PREDICTED: trafficking protein particle complex subunit 5-like [Oreochromis niloticus]	0.0371	0.0003	up	0.1371	up	1.5541	up	0.1368	up	1.5538	up	1.4170	up
MPF_LOC100705554.1.1	XR_134753.1 PREDICTED: Oreochromis niloticus monocarboxylate transporter 12-B-like (LOC100705554), miscRNA	0.0371	-0.1335	down	-0.0469	down	0.6630	up	0.0866	up	0.7965	up	0.7099	up
MPF_contig_037428		0.0371	-0.8224	down	-1.1733	down	-2.7863	down	-0.3509	down	-1.9639	down	-1.6130	down

MPF_LOC100694719.1.2	XM_003456192.1 PREDICTED: Oreochromis niloticus proteasome subunit alpha type-3-like (LOC100694719), mRNA	0.0371	0.0357	up	0.1803	up	0.6171	up	0.1446	up	0.5815	up	0.4369	up
MPF_contig_034538	XM_004551454.1 PREDICTED: Maylandia zebra pleckstrin homology domain-containing family A member 1-like (LOC101483871), transcript variant X3, mRNA	0.0371	0.0296	up	0.2770	up	0.9349	up	0.2475	up	0.9053	up	0.6579	up
MPF_LOC100699383.6.6	XM_003445310.1 PREDICTED: Oreochromis niloticus translationallycontrolled tumor protein homolog (LOC100699383),	0.0371	0.1714	up	0.4240	up	0.7406	up	0.2526	up	0.5692	up	0.3166	up

	mRNA													
MPF_LOC101066733.1.1	XP_003973635.1 PREDICTED: zinc finger and BTB domain-containing protein 49-like [Takifugu rubripes]	0.0371	0.1314	up	0.3483	up	0.7689	up	0.2169	up	0.6375	up	0.4206	up
MPF_MLL5.2.3	XP_003452082.1 PREDICTED: histone-lysine N-methyltransferase MLL5 [Oreochromis niloticus]	0.0371	-0.1231	down	0.1015	up	0.8835	up	0.2246	up	1.0065	up	0.7819	up
MPF_contig_029034		0.0371	0.0868	up	0.1228	up	0.5357	up	0.0361	up	0.4490	up	0.4129	up
MPF_contig_008249		0.0371	0.1167	up	0.3275	up	0.9080	up	0.2107	up	0.7912	up	0.5805	up
MPF_LOC101464050.1.1	XM_004557944.1 PREDICTED: Maylandia zebra mortality factor 4-like protein 1-like (LOC101464050), transcript variant X1, mRNA	0.0371	0.0624	up	0.4980	up	0.9271	up	0.4356	up	0.8648	up	0.4291	up
MPF_LOC101062099.1.1	XP_003968523.1 PREDICTED: methyltransferase-like protein 16-like [Takifugu rubripes]	0.0371	-0.1446	down	0.2301	up	0.9212	up	0.3748	up	1.0658	up	0.6911	up
MPF_contig_037327		0.0371	0.0479	up	-0.1862	down	1.1317	up	-0.2342	down	1.0838	up	1.3179	up
MPF_LOC100709648.13.13	XM_003457730.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S4-like (LOC100709648), mRNA	0.0371	0.0262	up	0.0106	up	0.7287	up	-0.0156	down	0.7026	up	0.7182	up

MPF_LOC101481882.1.1	XM_004540835.1 PREDICTED: Maylandia zebra major facilitator superfamily domain-containing protein 2A-B-like (LOC101481882), mRNA	0.0371	-0.1753	down	0.2879	up	0.8166	up	0.4631	up	0.9919	up	0.5287	up
MPF_contig_018973		0.0371	0.0173	up	0.1492	up	0.5042	up	0.1319	up	0.4868	up	0.3550	up
MPF_contig_016119		0.0371	-0.1317	down	0.1545	up	0.4184	up	0.2862	up	0.5501	up	0.2640	up

MPF_LOC101485903.1.2	XM_004575263.1 PREDICTED: Maylandia zebra low-density lipoprotein receptor-related protein 10like (LOC101485903), mRNA	0.0371	-0.1497	down	0.0657	up	0.5935	up	0.2154	up	0.7432	up	0.5278	up
MPF_contig_007184		0.0371	-0.0361	down	0.0446	up	0.8599	up	0.0807	up	0.8959	up	0.8152	up
MPF_contig_035016		0.0371	-0.0678	down	0.0509	up	0.6474	up	0.1187	up	0.7152	up	0.5965	up
MPF_LOC101157429.5.5	XM_004086128.1 PREDICTED: Oryzias latipes serine/arginine-rich splicing factor 3-like (LOC101157429), mRNA	0.0371	-0.1606	down	0.1990	up	0.6191	up	0.3596	up	0.7797	up	0.4201	up
MPF_LOC101473755.2.3	XM_004564853.1 PREDICTED: Maylandia zebra CCR4-NOT transcription complex subunit 2-like (LOC101473755), transcript variant X2, mRNA	0.0371	-0.0982	down	-0.0652	down	0.8843	up	0.0331	up	0.9826	up	0.9495	up
MPF_SRRM2.9.15	SRRM2_HUMAN (sp|Q9UQ35) Serine/arginine repetitive matrix protein 2 OS=Homo sapiens	0.0371	-0.0843	down	-1.0691	down	-2.9300	down	-0.9848	down	-2.8457	down	-1.8609	down

	GN=SRRM2 PE=1 SV=2													
MPF_BLCAP.2.2	[BBH] BLCAP_DANRE (sp|Q9IB61) Bladder cancerassociated protein OS=Danio rerio GN=blcap PE=3 SV=1	0.0371	0.0884	up	0.1770	up	0.6146	up	0.0886	up	0.5262	up	0.4376	up
MPF_LOC101464979.2.7	XM_004550563.1 PREDICTED: Maylandia zebra ralBP1-associated Eps domain-containing protein 1like (LOC101464979), transcript variant X4, mRNA	0.0371	-0.0590	down	-0.1751	down	1.1414	up	-0.1161	down	1.2004	up	1.3165	up
MPF_LOC101482130.4.7	XM_004574887.1 PREDICTED: Maylandia zebra low affinity immunoglobulin gamma Fc region receptor II-b-like (LOC101482130), mRNA	0.0371	-0.0468	down	-0.0633	down	0.5607	up	-0.0165	down	0.6075	up	0.6240	up
MPF_LOC101474305.11.20	XM_004575475.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101474305), mRNA	0.0371	-0.0487	down	0.0348	up	-0.9562	down	0.0835	up	-0.9075	down	-0.9910	down
MPF_ZO6.4.6	ZO6_XENLA (sp|P18749) Oocyte zinc finger protein XlCOF6 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.0371	-0.0646	down	0.0417	up	1.0980	up	0.1063	up	1.1626	up	1.0563	up
MPF_LOC100689941.1.1	XM_003449094.1 PREDICTED: Oreochromis niloticus zinc finger CCCHtype with G patch domaincontaining protein-like	0.0372	-0.1204	down	0.3620	up	1.1080	up	0.4824	up	1.2284	up	0.7460	up

	(LOC100689941), mRNA													
MPF_ACTS.6.7	ACTS_ORYLA (sp|Q98972) Actin, alpha skeletal muscle OS=Oryzias latipes GN=acta1 PE=2 SV=1	0.0372	-0.2159	down	-0.5311	down	0.6329	up	-0.3152	down	0.8487	up	1.1639	up
MPF_LOC101478567.1.1	XM_004547038.1 PREDICTED: Maylandia zebra claudin-5-like (LOC101478567), mRNA	0.0372	-0.0401	down	-0.0238	down	0.5106	up	0.0163	up	0.5507	up	0.5343	up
MPF_TBA4A.1.2	TBA4A_RAT (sp|Q5XIF6) Tubulin alpha-4A chain OS=Rattus norvegicus GN=Tuba4a PE=2 SV=1	0.0372	-0.1658	down	0.1609	up	0.7512	up	0.3267	up	0.9171	up	0.5903	up
MPF_LOC101481424.1.2	XM_004546586.1 PREDICTED: Maylandia zebra T-complex protein 1 subunit epsilon-like (LOC101481424), mRNA	0.0372	-0.2132	down	0.2219	up	0.6934	up	0.4351	up	0.9066	up	0.4716	up
MPF_LOC101468190.2.2	XM_004550947.1 PREDICTED: Maylandia zebra cell adhesion molecule 4-like (LOC101468190), transcript variant X4, mRNA	0.0372	0.3676	up	0.5705	up	1.1220	up	0.2029	up	0.7544	up	0.5515	up
MPF_LOC101072211.1.1	XM_003978083.1 PREDICTED: Takifugu rubripes Krueppel-like factor 3-like (LOC101072211), mRNA	0.0373	-0.2373	down	0.1030	up	0.7904	up	0.3403	up	1.0277	up	0.6874	up
MPF_contig_043182		0.0373	-0.2931	down	0.2799	up	0.3560	up	0.5730	up	0.6491	up	0.0761	up

MPF_LOC100691060.1.1	XP_003439383.1 PREDICTED: hypothetical protein LOC100691060 [Oreochromis niloticus]	0.0373	-0.0565	down	-0.2822	down	1.0507	up	-0.2257	down	1.1071	up	1.3328	up
MPF_contig_037024		0.0373	-0.0040	down	0.2077	up	1.1066	up	0.2117	up	1.1106	up	0.8989	up
MPF_LOC101484205.1.2	XM_004546129.1 PREDICTED: Maylandia zebra plexin-D1-like (LOC101484205), mRNA	0.0373	-0.0268	down	0.2862	up	0.7559	up	0.3131	up	0.7827	up	0.4696	up
MPF_LOC101482085.5.5	XM_004544079.1 PREDICTED: Maylandia zebra von Willebrand factor A domain-containing protein 5Alike (LOC101482085), mRNA	0.0373	0.2141	up	0.4958	up	0.5356	up	0.2817	up	0.3215	up	0.0399	up
MPF_contig_040515		0.0373	-0.0232	down	0.0195	up	0.7641	up	0.0427	up	0.7873	up	0.7446	up
MPF_LOC101478467.1.1	XM_004547614.1 PREDICTED: Maylandia zebra pre-miRNA 5'monophosphate methyltransferase-like (LOC101478467), mRNA	0.0373	0.2876	up	0.3937	up	1.0319	up	0.1061	up	0.7444	up	0.6382	up
MPF_LOC101155263.1.1	XM_004086507.1 PREDICTED: Oryzias latipes casein kinase I isoform alphalike (LOC101155263), mRNA	0.0374	0.3116	up	0.9573	up	1.3119	up	0.6457	up	1.0004	up	0.3547	up
MPF_contig_037664		0.0374	-0.3618	down	0.0628	up	0.8756	up	0.4246	up	1.2374	up	0.8128	up
MPF_contig_018948	WP_006047458.1 hypothetical protein [Burkholderia graminis]	0.0374	-0.0367	down	-1.1374	down	-2.4251	down	-1.1007	down	-2.3884	down	-1.2877	down
MPF_LOC101478257.1.2	XM_004562938.1 PREDICTED: Maylandia zebra thioredoxin,	0.0374	0.0244	up	0.2510	up	0.8126	up	0.2266	up	0.7882	up	0.5616	up

	mitochondrial-like (LOC101478257), mRNA													
MPF_LOC101477270.2.2	XM_004551148.1 PREDICTED: Maylandia zebra Krueppel-like factor 8like (LOC101477270), transcript variant X1, mRNA	0.0374	0.5514	up	0.4866	up	0.9943	up	-0.0649	down	0.4428	up	0.5077	up
MPF_contig_031101		0.0374	0.0829	up	0.2598	up	0.7273	up	0.1769	up	0.6444	up	0.4675	up
MPF_LOC101466406.1.1	XM_004568206.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 18-like (LOC101466406), mRNA	0.0374	-0.3153	down	-0.2180	down	0.8198	up	0.0973	up	1.1351	up	1.0378	up
MPF_LOC101474529.1.1	XM_004540517.1 PREDICTED: Maylandia zebra RNA polymerase IIassociated protein 1-like (LOC101474529), transcript variant X2, mRNA	0.0374	-0.0218	down	0.3070	up	1.1274	up	0.3288	up	1.1492	up	0.8204	up
MPF_LOC100699783.1.1	XP_003456177.1 PREDICTED: myosin-XIX-like [Oreochromis niloticus]	0.0374	0.2112	up	0.2536	up	0.9608	up	0.0424	up	0.7496	up	0.7072	up
MPF_LOC101474121.9.17	XM_004575391.1 PREDICTED: Maylandia zebra stonustoxin subunit beta-like (LOC101474121), mRNA	0.0374	-0.1941	down	0.2343	up	-2.0527	down	0.4284	up	-1.8586	down	-2.2870	down
MPF_contig_016136		0.0374	-0.1536	down	-0.4119	down	-1.5686	down	-0.2583	down	-1.4150	down	-1.1567	down
MPF_LOC100696957.1.1	XM_003440207.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100696957	0.0374	0.5057	up	-0.3368	down	-1.7238	down	-0.8426	down	-2.2295	down	-1.3870	down

	(LOC100696957), mRNA													
MPF_contig_014340	XM_004555992.1 PREDICTED: Maylandia zebra protein FAM135A-like (LOC101483692), transcript variant X1, mRNA	0.0374	-0.0628	down	0.1105	up	0.7651	up	0.1734	up	0.8279	up	0.6546	up
MPF_contig_004526		0.0374	0.0149	up	0.2601	up	-0.4908	down	0.2453	up	-0.5057	down	-0.7510	down
MPF_contig_017112		0.0374	0.0165	up	0.2897	up	0.7751	up	0.2732	up	0.7586	up	0.4854	up
MPF_contig_037414		0.0374	-0.3424	down	0.1667	up	-1.4871	down	0.5091	up	-1.1448	down	-1.6539	down
MPF_LOC100703973.1.1	XM_003444318.1 PREDICTED: Oreochromis niloticus protein FAM136Alike (LOC100703973), mRNA	0.0374	-0.1324	down	0.0719	up	0.8656	up	0.2042	up	0.9979	up	0.7937	up
MPF_contig_010789		0.0375	-0.9705	down	-0.1103	down	-1.8636	down	0.8602	up	-0.8931	down	-1.7533	down
MPF_contig_042033		0.0375	-0.1733	down	0.2076	up	0.6544	up	0.3809	up	0.8277	up	0.4468	up
MPF_LOC101471734.1.2	XM_004545073.1 PREDICTED: Maylandia zebra dual specificity tyrosinephosphorylation-regulated kinase 2-like (LOC101471734), transcript variant X3, mRNA	0.0375	0.2058	up	0.0103	up	0.8420	up	-0.1955	down	0.6362	up	0.8317	up
MPF_LOC101480294.1.1	XM_004551160.1 PREDICTED: Maylandia zebra probable E3 ubiquitinprotein ligase DTX2-like (LOC101480294), transcript variant X2, mRNA	0.0375	-0.0641	down	0.0441	up	0.9379	up	0.1082	up	1.0020	up	0.8938	up

MPF_LOC101480587.2.2	XM_004553594.1 PREDICTED: Maylandia zebra fibroblast growth factor receptor-like 1-like (LOC101480587), mRNA	0.0375	-0.0848	down	0.1887	up	1.0997	up	0.2736	up	1.1845	up	0.9110	up
MPF_contig_004045		0.0375	0.0680	up	0.2437	up	0.8017	up	0.1757	up	0.7336	up	0.5579	up
MPF_LOC100690613.1.1	XP_003458492.1 PREDICTED: CWF19-like protein 1-like [Oreochromis niloticus]	0.0376	-0.1899	down	0.1231	up	0.9281	up	0.3130	up	1.1180	up	0.8050	up
MPF_contig_047313	XM_004560032.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF19A-like (LOC101479921), transcript variant X1, mRNA	0.0377	-0.0211	down	-0.0520	down	0.9491	up	-0.0309	down	0.9703	up	1.0012	up
MPF_contig_040419	XM_004539772.1 PREDICTED: Maylandia zebra bifunctional glutamate/proline--tRNA ligase-like (LOC101475483), transcript variant X1, mRNA	0.0378	-0.0317	down	0.1782	up	0.6601	up	0.2099	up	0.6918	up	0.4819	up
MPF_contig_021814	XM_004573589.1 PREDICTED: Maylandia zebra mitogen-activated protein kinase kinase kinase kinase 4-like (LOC101476887), transcript variant X5, mRNA	0.0379	0.0995	up	0.2854	up	0.6529	up	0.1859	up	0.5534	up	0.3675	up

MPF_LOC101465938.1.1	XM_004570981.1 PREDICTED: Maylandia zebra ubiA prenyltransferase domain-containing protein 1like (LOC101465938), transcript variant X3, mRNA	0.0379	-0.1785	down	0.1311	up	1.2335	up	0.3096	up	1.4121	up	1.1024	up
MPF_LOC101475776.1.7	XM_004539154.1 PREDICTED: Maylandia zebra ATP synthase subunit d, mitochondrial-like (LOC101475776), transcript variant X2, mRNA	0.0379	-0.1335	down	-0.0061	down	0.9673	up	0.1274	up	1.1008	up	0.9735	up
MPF_LOC100148223.2.2	XP_003201586.1 PREDICTED: zinc finger protein 729-like [Danio rerio]	0.0379	0.0472	up	0.1294	up	1.1835	up	0.0822	up	1.1363	up	1.0542	up
MPF_LOC100705728.15.17	XM_003459563.1 PREDICTED: Oreochromis niloticus zinc finger protein RFP-like (LOC100705728), mRNA	0.0379	-0.0563	down	0.0981	up	0.7930	up	0.1544	up	0.8494	up	0.6950	up
MPF_LOC101465735.9.9	XM_004548780.1 PREDICTED: Maylandia zebra 40S ribosomal protein S23-like (LOC101465735), mRNA	0.0379	0.0875	up	0.1125	up	0.7357	up	0.0250	up	0.6482	up	0.6232	up
MPF_LOC100705003.1.1	XM_003456797.1 PREDICTED: Oreochromis niloticus charged multivesicular body protein 1b-like (LOC100705003), mRNA	0.0379	-0.2775	down	0.3850	up	0.4812	up	0.6625	up	0.7587	up	0.0962	up
MPF_LOC101479448.4.4	XM_004553132.1 PREDICTED: Maylandia zebra Krueppel-like factor 13like (LOC101479448), mRNA	0.0380	-0.0180	down	0.0007	up	0.8835	up	0.0187	up	0.9015	up	0.8828	up

MPF_LOC101470646.1.1	XM_004562113.1 PREDICTED: Maylandia zebra ephrin type-B receptor 1-like (LOC101470646), mRNA	0.0380	0.0062	up	0.0441	up	0.7809	up	0.0379	up	0.7747	up	0.7368	up
MPF_LOC100706224.1.1	XM_003450725.1 PREDICTED: Oreochromis niloticus transmembrane protein 168-A-like (LOC100706224), mRNA	0.0380	-0.1153	down	0.5205	up	1.0214	up	0.6359	up	1.1367	up	0.5009	up
MPF_LOC100701163.1.1	XP_003439675.1 PREDICTED: Nacetylglucosamine-6sulfatase-like [Oreochromis niloticus]	0.0380	-0.0798	down	0.3229	up	0.8105	up	0.4026	up	0.8903	up	0.4877	up
MPF_LOC101475950.3.3	XM_004553845.1 PREDICTED: Maylandia zebra cAMP-specific 3',5'cyclic phosphodiesterase 4Blike (LOC101475950), transcript variant X3, mRNA	0.0380	-0.9131	down	-2.1465	down	-4.3796	down	-1.2334	down	-3.4666	down	-2.2331	down
MPF_LOC101468171.1.1	XM_004571311.1 PREDICTED: Maylandia zebra aldehyde dehydrogenase, mitochondrial-like (LOC101468171), transcript variant X2, mRNA	0.0380	0.0766	up	-0.2111	down	1.0732	up	-0.2877	down	0.9966	up	1.2843	up
MPF_LOC101486555.1.1	XM_004564613.1 PREDICTED: Maylandia zebra junctophilin-3-like (LOC101486555), mRNA	0.0380	-0.1007	down	-0.2191	down	0.7488	up	-0.1184	down	0.8495	up	0.9678	up
MPF_LOC101482951.1.1	XM_004540645.1 PREDICTED: Maylandia zebra protein FAM161B-like (LOC101482951), mRNA	0.0380	-0.1165	down	0.1627	up	1.1146	up	0.2793	up	1.2312	up	0.9519	up

MPF_RL15.5.6	RL15_PARDA (sp|Q7T3N3) 60S ribosomal protein L15 OS=Paramisgurnus dabryanus GN=rpl15 PE=2 SV=3	0.0380	-0.0560	down	-0.3611	down	0.8610	up	-0.3051	down	0.9170	up	1.2221	up
MPF_LOC101480505.1.1	XM_004557175.1 PREDICTED: Maylandia zebra ankyrin repeat domaincontaining protein 29-like (LOC101480505), transcript variant X3, mRNA	0.0380	0.0032	up	0.3683	up	0.7605	up	0.3652	up	0.7574	up	0.3922	up
MPF_LOC101466459.4.29	XM_004554283.1 PREDICTED: Maylandia zebra semaphorin-3G-like (LOC101466459), mRNA	0.0380	-0.0098	down	0.1337	up	0.6972	up	0.1435	up	0.7071	up	0.5635	up
MPF_VDAC1.1.1	VDAC1_RABIT (sp|Q9TT15) Voltage-dependent anionselective channel protein 1 OS=Oryctolagus cuniculus GN=VDAC1 PE=2 SV=3	0.0380	0.0036	up	0.1100	up	0.7337	up	0.1064	up	0.7301	up	0.6237	up
MPF_LOC101485434.3.3	XM_004549397.1 PREDICTED: Maylandia zebra lens epithelium-derived growth factor-like (LOC101485434), transcript variant X4, mRNA	0.0380	0.5759	up	0.8414	up	1.4952	up	0.2656	up	0.9193	up	0.6538	up
MPF_LOC100371306.2.2	XP_002733578.1 PREDICTED: hypothetical protein [Saccoglossus kowalevskii]	0.0380	-0.0229	down	0.0605	up	1.0185	up	0.0834	up	1.0414	up	0.9581	up
MPF_contig_009396		0.0380	-0.0916	down	-0.0204	down	0.9567	up	0.0712	up	1.0483	up	0.9771	up
MPF_contig_048512		0.0380	0.1572	up	0.4230	up	0.5647	up	0.2658	up	0.4075	up	0.1417	up

MPF_LOC101170497.3.8	XP_004086004.1 PREDICTED: oocyte zinc finger protein XlCOF6-like [Oryzias latipes]	0.0380	-0.0572	down	0.0547	up	1.1883	up	0.1119	up	1.2454	up	1.1335	up
MPF_LOC101484350.2.2	XM_004561892.1 PREDICTED: Maylandia zebra nuclear apoptosisinducing factor 1-like (LOC101484350), mRNA	0.0380	0.0381	up	0.3722	up	1.3332	up	0.3341	up	1.2950	up	0.9610	up
MPF_LOC101467816.1.1	XM_004562471.1 PREDICTED: Maylandia zebra mitochondrial Rho GTPase 2-like (LOC101467816), mRNA	0.0380	0.0947	up	0.1430	up	0.8545	up	0.0483	up	0.7598	up	0.7115	up
MPF_LOC101480012.2.2	XM_004555338.1 PREDICTED: Maylandia zebra hippocampus abundant transcript 1 protein-like (LOC101480012), mRNA	0.0380	-0.2418	down	-0.1920	down	0.7437	up	0.0499	up	0.9856	up	0.9357	up
MPF_LOC100711740.1.1	XM_003444597.1 PREDICTED: Oreochromis niloticus UBX domaincontaining protein 1-like (LOC100711740), mRNA	0.0380	-0.1636	down	-0.0441	down	0.5870	up	0.1194	up	0.7506	up	0.6311	up
MPF_contig_023324		0.0380	-0.1930	down	0.1123	up	0.3845	up	0.3053	up	0.5775	up	0.2722	up
MPF_043R.3.4	043R_FRG3G (sp|Q6GZT3) Uncharacterized protein 043R OS=Frog virus 3 (isolate Goorha) GN=FV3043R PE=4 SV=1	0.0380	-0.0228	down	0.4238	up	0.5994	up	0.4466	up	0.6222	up	0.1756	up
MPF_contig_022785		0.0380	-0.1011	down	0.3156	up	0.7713	up	0.4167	up	0.8724	up	0.4557	up

MPF_COX7R.2.3	COX7R_BOVIN (sp|Q3T061) Cytochrome c oxidase subunit 7A-related protein, mitochondrial OS=Bos taurus GN=COX7A2L PE=3 SV=1	0.0380	-0.0741	down	0.0158	up	0.6100	up	0.0900	up	0.6841	up	0.5942	up
MPF_LOC100696054.1.1	XP_003438731.1 PREDICTED: zinc transporter ZIP11-like [Oreochromis niloticus]	0.0380	0.0251	up	0.2917	up	0.7423	up	0.2666	up	0.7172	up	0.4506	up
MPF_LOC101073558.1.1	XP_003977072.1 PREDICTED: succinate dehydrogenase [ubiquinone] cytochrome b small subunit B, mitochondrial-like [Takifugu rubripes]	0.0381	0.0070	up	0.0616	up	0.5643	up	0.0546	up	0.5573	up	0.5027	up
MPF_LOC100696802.1.1	XP_003447430.1 PREDICTED: Golgi reassembly-stacking protein 2-like [Oreochromis niloticus]	0.0381	-0.5459	down	-0.4588	down	-2.3577	down	0.0871	up	-1.8119	down	-1.8989	down
MPF_LOC101072633.13.15	XM_003970117.1 PREDICTED: Takifugu rubripes non-histone chromosomal protein HMG14A-like (LOC101072633), mRNA	0.0381	0.1307	up	-0.1355	down	1.3840	up	-0.2662	down	1.2534	up	1.5196	up
MPF_LOC100703241.6.9	XM_003440649.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S29-like (LOC100703241), mRNA	0.0381	-0.1344	down	0.2035	up	1.1400	up	0.3379	up	1.2744	up	0.9365	up
		0.0381	-0.4749	down	-0.3214	down	1.1396	up	0.1536	up	1.6146	up	1.4610	up

MPF_LOC101473918.1.1	XM_004552728.1 PREDICTED: Maylandia zebra histone-lysine Nmethyltransferase, H3 lysine-79 specific-like (LOC101473918), transcript variant X1, mRNA	0.0381	0.0912	up	-0.6814	down	-1.0652	down	-0.7726	down	-1.1564	down	-0.3838	down
MPF_LOC101473055.1.4	XM_004560375.1 PREDICTED: Maylandia zebra basement membranespecific heparan sulfate proteoglycan core protein-like (LOC101473055), transcript variant X2, mRNA	0.0381	-0.4305	down	-0.8154	down	-2.5966	down	-0.3849	down	-2.1662	down	-1.7813	down
MPF_CAM-D.2.4	XM_004082666.1 PREDICTED: Oryzias latipes calmodulin (cam-d), mRNA	0.0381	-0.0622	down	0.2927	up	0.6633	up	0.3549	up	0.7255	up	0.3706	up
MPF_LOC101484681.1.1	XM_004573705.1 PREDICTED: Maylandia zebra vesicular glutamate transporter 1-like (LOC101484681), mRNA	0.0382	-0.0150	down	0.2284	up	0.8650	up	0.2434	up	0.8800	up	0.6367	up
MPF_contig_018536		0.0382	-0.0647	down	0.3189	up	1.3051	up	0.3836	up	1.3697	up	0.9861	up
MPF_UBIQH.1.1	UBIQH_DICDI (sp|P0CG81) Polyubiquitin-H OS=Dictyostelium discoideum GN=ubqH PE=1 SV=1	0.0382	-0.0255	down	0.2748	up	0.4748	up	0.3004	up	0.5003	up	0.1999	up
MPF_LOC101478586.2.2	XM_004550792.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 6-like (LOC101478586), transcript variant X2, mRNA	0.0382	0.2286	up	-0.7066	down	-2.7635	down	-0.9352	down	-2.9921	down	-2.0569	down

MPF_LOC101481339.2.2	XM_004547339.1 PREDICTED: Maylandia zebra histone-lysine Nmethyltransferase NSD3-like (LOC101481339), mRNA	0.0382	0.1446	up	0.6039	up	1.2257	up	0.4593	up	1.0811	up	0.6218	up
MPF_LOC100690119.8.18	XP_003448733.1 PREDICTED: zinc finger protein 16-like [Oreochromis niloticus]	0.0382	0.0634	up	0.1419	up	1.1884	up	0.0786	up	1.1250	up	1.0464	up
MPF_contig_044884		0.0382	-0.0015	down	0.0572	up	1.2284	up	0.0586	up	1.2298	up	1.1712	up
MPF_LOC101484616.1.1	XM_004561445.1 PREDICTED: Maylandia zebra anaphase-promoting complex subunit 15-like (LOC101484616), mRNA	0.0383	-0.0946	down	0.1784	up	1.0672	up	0.2730	up	1.1619	up	0.8888	up
MPF_LOC101479456.1.2	XM_004556177.1 PREDICTED: Maylandia zebra phosphatidylserine decarboxylase proenzymelike (LOC101479456), mRNA	0.0383	0.6766	up	0.5512	up	1.4239	up	-0.1254	down	0.7473	up	0.8727	up
MPF_LOC100703335.1.1	XP_003444612.1 PREDICTED: death ligand signal enhancer-like [Oreochromis niloticus]	0.0383	-0.0003	down	0.0388	up	0.9920	up	0.0391	up	0.9923	up	0.9531	up
MPF_contig_023226		0.0383	-0.1159	down	0.3492	up	0.9882	up	0.4652	up	1.1042	up	0.6390	up
MPF_LOC100710259.2.2	XM_003450909.1 PREDICTED: Oreochromis niloticus NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subuni 3like (LOC100710259), mRNA	0.0383	0.1750	up	0.4252	up	0.6303	up	0.2502	up	0.4553	up	0.2050	up
MPF_contig_012534		0.0383	0.0694	up	-0.5987	down	-1.6476	down	-0.6682	down	-1.7170	down	-1.0489	down
MPF_LOC100707655.19.19	XM_003454192.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S6-like	0.0383	0.0636	up	-0.2832	down	-0.7900	down	-0.3468	down	-0.8537	down	-0.5068	down

	(LOC100707655), mRNA													
MPF_LOC101475522.1.1	XM_004546567.1 PREDICTED: Maylandia zebra 5-oxoprolinase-like (LOC101475522), transcript variant X3, mRNA	0.0383	0.2780	up	0.2364	up	1.1661	up	-0.0416	down	0.8881	up	0.9297	up
MPF_ZNF84.11.14	ZNF84_HUMAN (sp|P51523) Zinc finger protein 84 OS=Homo sapiens GN=ZNF84 PE=1 SV=2	0.0383	0.1528	up	0.2430	up	1.9350	up	0.0903	up	1.7822	up	1.6919	up
MPF_LOC101470109.1.2	XM_004573660.1 PREDICTED: Maylandia zebra pogo transposable element with ZNF domain-like (LOC101470109), transcript variant X3, mRNA	0.0383	0.1491	up	0.5701	up	1.0038	up	0.4211	up	0.8548	up	0.4337	up
MPF_LOC101464344.1.2	XM_004561642.1 PREDICTED: Maylandia zebra autism susceptibility gene 2 protein-like (LOC101464344), mRNA	0.0383	-0.7327	down	-0.2774	down	0.9087	up	0.4554	up	1.6414	up	1.1860	up
MPF_LOC101482508.1.1	XM_004547905.1 PREDICTED: Maylandia zebra calcium-binding mitochondrial carrier protein Aralar2-like (LOC101482508), transcript variant X1, mRNA	0.0384	-0.0919	down	-0.0059	down	1.1451	up	0.0861	up	1.2370	up	1.1510	up
MPF_contig_003091		0.0385	-0.0085	down	0.1264	up	0.8756	up	0.1349	up	0.8841	up	0.7492	up

MPF_LOC100705338.1.2	XM_003448982.1 PREDICTED: Oreochromis niloticus delta-like protein C-like (LOC100705338), mRNA	0.0385	-0.1641	down	0.0572	up	-0.7170	down	0.2214	up	-0.5529	down	-0.7742	down
MPF_LOC101169139.1.1	XP_004077685.1 PREDICTED: rRNA 2'-O-methyltransferase fibrillarinlike isoform 1 [Oryzias latipes]	0.0385	-0.0495	down	0.3248	up	0.5406	up	0.3743	up	0.5902	up	0.2159	up
MPF_LOC101070379.1.1	XP_003974368.1 PREDICTED: uncharacterized protein LOC101070379 [Takifugu rubripes]	0.0385	0.0507	up	-1.3352	down	-2.4540	down	-1.3859	down	-2.5047	down	-1.1188	down
MPF_contig_020594		0.0386	0.0721	up	0.1138	up	0.5510	up	0.0417	up	0.4789	up	0.4372	up
MPF_LOC101475538.1.1	XM_004572884.1 PREDICTED: Maylandia zebra uncharacterized LOC101475538 (LOC101475538), transcript variant X7, mRNA	0.0386	-0.1657	down	0.3453	up	1.0563	up	0.5110	up	1.2219	up	0.7109	up
MPF_LOC101170688.1.2	XP_004073787.1 PREDICTED: protein AF1q-like [Oryzias latipes]	0.0386	0.1500	up	0.2165	up	1.0106	up	0.0666	up	0.8606	up	0.7940	up
MPF_LOC101472018.1.3	XM_004545608.1 PREDICTED: Maylandia zebra ubiquitin-like protein 3like (LOC101472018), mRNA	0.0386	-0.1311	down	0.3969	up	0.9438	up	0.5281	up	1.0749	up	0.5469	up
MPF_LOC100699974.1.1	XM_003437619.1 PREDICTED: Oreochromis niloticus retinol dehydrogenase 13-like (LOC100699974), mRNA	0.0386	-0.0950	down	0.8779	up	1.6106	up	0.9729	up	1.7056	up	0.7327	up

MPF_LOC100703734.1.1	XM_003451798.1 PREDICTED: Oreochromis niloticus sorting nexin-25-like (LOC100703734), mRNA	0.0386	0.4117	up	0.1907	up	1.1651	up	-0.2210	down	0.7534	up	0.9744	up
MPF_LOC101158441.1.1	XP_004069906.1 PREDICTED: thromboxane-A synthase-like [Oryzias latipes]	0.0387	-0.0674	down	0.2885	up	1.1769	up	0.3558	up	1.2443	up	0.8885	up
MPF_LOC101466905.1.3	XM_004554823.1 PREDICTED: Maylandia zebra tripartite motifcontaining protein 35-like (LOC101466905), mRNA	0.0387	-0.4178	down	0.0464	up	-0.9873	down	0.4642	up	-0.5695	down	-1.0337	down

MPF_SGS4.3.10	SGS4_DROME (sp|Q00725) Salivary glue protein Sgs-4 OS=Drosophila melanogaster GN=Sgs4 PE=2 SV=1	0.0387	-0.0968	down	-0.0297	down	0.8865	up	0.0671	up	0.9834	up	0.9163	up
MPF_LOC101158204.1.2	XM_004072523.1 PREDICTED: Oryzias latipes TBC1 domain family member 10A-like (LOC101158204), mRNA	0.0387	-0.0768	down	0.0925	up	0.8354	up	0.1693	up	0.9122	up	0.7429	up
MPF_contig_047695		0.0387	0.0575	up	0.3090	up	2.1158	up	0.2515	up	2.0584	up	1.8069	up
MPF_contig_026550		0.0387	-0.1267	down	-0.3137	down	-1.1641	down	-0.1870	down	-1.0374	down	-0.8504	down
MPF_LOC101478959.2.6	XM_004574587.1 PREDICTED: Maylandia zebra zinc finger MYND domain-containing protein 11like (LOC101478959), transcript variant X4, mRNA	0.0387	-0.0261	down	0.1068	up	0.3808	up	0.1330	up	0.4069	up	0.2739	up

MPF_LOC101480445.3.3	XM_004543133.1 PREDICTED: Maylandia zebra nuclear factor of activated T-cells 5-like (LOC101480445), transcript variant X2, mRNA	0.0387	-0.1215	down	0.0073	up	1.3939	up	0.1288	up	1.5153	up	1.3866	up
MPF_LOC100699805.1.1	XP_003439497.1 PREDICTED: lon protease homolog 2, peroxisomal-like [Oreochromis niloticus]	0.0387	-0.0275	down	0.3087	up	0.8552	up	0.3362	up	0.8827	up	0.5465	up
MPF_LOC101477365.1.1	XM_004574579.1 PREDICTED: Maylandia zebra WD repeat-containing protein 37-like (LOC101477365), transcript variant X2, mRNA	0.0387	-0.0586	down	0.2127	up	0.7038	up	0.2713	up	0.7624	up	0.4911	up
MPF_LOC100690707.1.1	XP_003439051.1 PREDICTED: glutaminyltRNA synthetase-like [Oreochromis niloticus]	0.0387	0.3619	up	0.4179	up	1.2073	up	0.0559	up	0.8453	up	0.7894	up
MPF_RL18A.5.14	RL18A_DANRE (sp|Q7ZWJ4) 60S ribosomal protein L18a OS=Danio rerio GN=rpl18a PE=2 SV=1	0.0387	0.0265	up	-0.8452	down	-1.1370	down	-0.8717	down	-1.1635	down	-0.2918	down
MPF_LOC101481069.1.1	XM_004556635.1 PREDICTED: Maylandia zebra sideroflexin-2-like (LOC101481069), mRNA	0.0387	0.1071	up	0.2191	up	1.0600	up	0.1120	up	0.9528	up	0.8409	up
MPF_LOC100693203.3.4	XM_003457748.1 PREDICTED: Oreochromis niloticus tetraspanin-5-like (LOC100693203), mRNA	0.0387	-0.1623	down	-0.4886	down	-1.7711	down	-0.3263	down	-1.6088	down	-1.2825	down
MPF_LOC100695417.1.1	XP_003451815.1 PREDICTED: caspase-3-like [Oreochromis niloticus]	0.0387	-0.1891	down	-0.2474	down	0.8250	up	-0.0583	down	1.0142	up	1.0724	up

MPF_LOC100710590.1.4	XP_003449469.1 PREDICTED: zinc finger protein 836-like, partial [Oreochromis niloticus]	0.0387	0.0306	up	0.1171	up	1.1917	up	0.0865	up	1.1611	up	1.0746	up
MPF_LOC101483362.1.1	XM_004574078.1 PREDICTED: Maylandia zebra UPF0547 protein C16orf87 homolog (LOC101483362), mRNA	0.0388	-0.1425	down	0.3014	up	0.7395	up	0.4439	up	0.8820	up	0.4380	up
MPF_LOC101479263.1.1	XM_004559378.1 PREDICTED: Maylandia zebra coronin-7-like (LOC101479263), mRNA	0.0388	-0.0529	down	0.2256	up	1.2456	up	0.2784	up	1.2985	up	1.0200	up
MPF_CD68.2.2	NP_001158857.1 Macrosialin precursor [Salmo salar]	0.0388	0.3657	up	-0.4383	down	-2.7316	down	-0.8039	down	-3.0973	down	-2.2933	down
MPF_LOC101173041.1.1	XP_004066354.1 PREDICTED: protein Wizlike [Oryzias latipes]	0.0388	-0.3815	down	0.0229	up	0.7391	up	0.4044	up	1.1207	up	0.7162	up
MPF_contig_002337	XM_004562453.1 PREDICTED: Maylandia zebra SUMO-conjugating enzyme UBC9-like (LOC101487009), transcript variant X3, mRNA	0.0388	-0.1132	down	0.2526	up	0.6332	up	0.3658	up	0.7464	up	0.3806	up
MPF_LOC100692490.2.4	XM_003457423.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L37a-like (LOC100692490), mRNA	0.0388	-0.0963	down	-1.2498	down	-3.0840	down	-1.1534	down	-2.9876	down	-1.8342	down
MPF_LOC101465192.1.6	XM_004554818.1 PREDICTED: Maylandia zebra interferon alphainducible protein 27-like protein 2B-like (LOC101465192), mRNA	0.0388	-0.3743	down	-0.8825	down	-2.7939	down	-0.5082	down	-2.4195	down	-1.9114	down

MPF_LOC101488089.1.1	XM_004570084.1 PREDICTED: Maylandia zebra uncharacterized LOC101488089 (LOC101488089), transcript variant X3, mRNA	0.0388	0.0501	up	-1.0434	down	-3.2171	down	-1.0935	down	-3.2672	down	-2.1737	down
MPF_LOC101464254.1.1	XM_004537921.1 PREDICTED: Maylandia zebra upstream stimulatory factor 1-like (LOC101464254), transcript variant X1, mRNA	0.0388	-0.0710	down	0.2468	up	1.0450	up	0.3177	up	1.1159	up	0.7982	up
MPF_contig_048529		0.0388	-0.0905	down	0.0636	up	0.6196	up	0.1541	up	0.7101	up	0.5560	up
MPF_contig_044724		0.0388	0.0266	up	0.2929	up	1.1956	up	0.2662	up	1.1690	up	0.9028	up
MPF_contig_037002		0.0388	-0.4639	down	0.3469	up	0.6119	up	0.8108	up	1.0758	up	0.2650	up
MPF_LOC101487307.5.5	XM_004564717.1 PREDICTED: Maylandia zebra ankyrin repeat domaincontaining protein 6-like (LOC101487307), transcript variant X4, mRNA	0.0388	-0.0837	down	-0.2393	down	-1.1350	down	-0.1556	down	-1.0513	down	-0.8957	down
MPF_contig_032481		0.0388	-0.9371	down	-0.4619	down	-2.3259	down	0.4752	up	-1.3888	down	-1.8640	down
MPF_LOC100699307.1.1	XM_003449296.1 PREDICTED: Oreochromis niloticus serine/threonineprotein kinase SIK3 homolog (LOC100699307), mRNA	0.0388	-0.0371	down	0.1587	up	0.8306	up	0.1958	up	0.8677	up	0.6719	up

MPF_LOC101476968.1.2	XM_004546759.1 PREDICTED: Maylandia zebra solute carrier family 22 member 13-like (LOC101476968), transcript variant X2, mRNA	0.0388	-0.0227	down	0.4061	up	1.3629	up	0.4288	up	1.3856	up	0.9568	up
MPF_contig_039619		0.0388	-0.1917	down	0.2682	up	1.1230	up	0.4599	up	1.3147	up	0.8548	up
MPF_LOC101479939.1.1	XM_004563953.1 PREDICTED: Maylandia zebra zinc finger protein 260like (LOC101479939), mRNA	0.0388	-0.0924	down	0.0539	up	0.8851	up	0.1463	up	0.9775	up	0.8312	up
MPF_LOC101469201.1.1	XM_004557967.1 PREDICTED: Maylandia zebra acidic leucine-rich nuclear phosphoprotein 32 family member A-like (LOC101469201), transcript variant X3, mRNA	0.0388	0.0173	up	0.0194	up	0.6321	up	0.0022	up	0.6149	up	0.6127	up
MPF_contig_011890		0.0388	-0.1746	down	-0.0043	down	0.9110	up	0.1704	up	1.0857	up	0.9153	up
MPF_contig_025289	XM_004549968.1 PREDICTED: Maylandia zebra baculoviral IAP repeatcontaining protein 2-like (LOC101484124), transcript variant X3, mRNA	0.0389	0.0835	up	0.0930	up	0.8977	up	0.0095	up	0.8143	up	0.8048	up
MPF_LOC101484216.2.2	XM_004571457.1 PREDICTED: Maylandia zebra ubiquitin-conjugating enzyme E2 D4-like (LOC101484216), mRNA	0.0389	-0.1996	down	0.7293	up	0.5744	up	0.9289	up	0.7741	up	-0.1548	down
MPF_contig_035410	XM_004556101.1 PREDICTED: Maylandia zebra transforming acidic coiled-coil-containing protein 2-like (LOC101481661), transcript variant X15, mRNA	0.0389	-0.1245	down	0.0008	up	0.9468	up	0.1254	up	1.0713	up	0.9460	up

MPF_contig_026645		0.0389	0.0299	up	0.1468	up	0.3194	up	0.1170	up	0.2895	up	0.1725	up
MPF_LOC100698896.12.16	XM_003456695.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 9-like (LOC100698896), mRNA	0.0390	-0.0048	down	0.4225	up	1.0767	up	0.4273	up	1.0815	up	0.6542	up
MPF_contig_032409		0.0390	-0.1599	down	0.1784	up	0.2669	up	0.3384	up	0.4269	up	0.0885	up
MPF_LOC101068645.2.2	XM_003975361.1 PREDICTED: Takifugu rubripes guanine nucleotidebinding protein G(I)/G(S)/G(O) subunit gamma-5-like (LOC101068645), mRNA	0.0390	-0.0361	down	-0.0399	down	0.3506	up	-0.0038	down	0.3868	up	0.3906	up
MPF_contig_023125		0.0390	0.0051	up	0.2114	up	0.5071	up	0.2062	up	0.5020	up	0.2957	up
MPF_contig_047060	XM_004544973.1 PREDICTED: Maylandia zebra zinc finger protein Xfinlike (LOC101469799), transcript variant X13, mRNA	0.0390	-0.0605	down	0.2351	up	0.8587	up	0.2956	up	0.9192	up	0.6236	up
MPF_LOC101467668.1.1	XM_004546256.1 PREDICTED: Maylandia zebra UHRF1-binding protein 1-like (LOC101467668), mRNA	0.0390	-0.0142	down	0.4064	up	0.9516	up	0.4206	up	0.9657	up	0.5451	up
MPF_LOC100703813.1.2	XM_003448149.1 PREDICTED: Oreochromis niloticus sodium channel protein type 8 subunit alphalike (LOC100703813), mRNA	0.0390	0.2187	up	1.6865	up	0.1897	up	1.4678	up	-0.0290	down	-1.4968	down

MPF_LOC101487338.2.2	XM_004546896.1 PREDICTED: Maylandia zebra protein AF-10-like (LOC101487338), mRNA	0.0390	0.2321	up	0.4472	up	1.2243	up	0.2152	up	0.9923	up	0.7771	up
MPF_LOC101160141.1.1	XR_177319.1 PREDICTED: Oryzias latipes keratin, type I cytoskeletal 13-like (LOC101160141), misc_RNA	0.0390	-0.6757	down	-2.9708	down	-4.4209	down	-2.2951	down	-3.7453	down	-1.4501	down
MPF_contig_031114		0.0390	-0.0345	down	0.1909	up	0.6510	up	0.2255	up	0.6855	up	0.4601	up
MPF_RL23.2.9	RL23_RAT (sp|P62832) 60S ribosomal protein L23 OS=Rattus norvegicus GN=Rpl23 PE=2 SV=1	0.0391	-0.0458	down	-0.9649	down	-2.4135	down	-0.9190	down	-2.3676	down	-1.4486	down
MPF_LOC100698625.19.22	XM_003456694.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100698625), mRNA	0.0392	0.0680	up	0.1361	up	1.0553	up	0.0681	up	0.9873	up	0.9192	up
MPF_LOC100690853.1.1	XP_003450715.1 PREDICTED: zinc finger protein 574-like [Oreochromis niloticus]	0.0392	0.1051	up	0.1132	up	1.0099	up	0.0081	up	0.9048	up	0.8967	up
MPF_LOC100690917.1.1	XM_003446189.1 PREDICTED: Oreochromis niloticus transmembrane protein 50A-like (LOC100690917), mRNA	0.0392	0.1507	up	0.2390	up	0.4977	up	0.0882	up	0.3469	up	0.2587	up
MPF_contig_019661		0.0392	0.0548	up	0.1282	up	0.5298	up	0.0735	up	0.4751	up	0.4016	up
MPF_LOC100690250.1.2	XM_003438915.1 PREDICTED: Oreochromis niloticus ras-related protein Rap-1b-like (LOC100690250), mRNA	0.0392	-0.1429	down	0.4442	up	0.7366	up	0.5871	up	0.8795	up	0.2924	up

MPF_RSSA.9.9	RSSA_SPAAU (sp|Q4QY71) 40S ribosomal protein SA OS=Sparus aurata GN=rpsa PE=2 SV=2	0.0392	-0.2062	down	-0.9076	down	-2.0582	down	-0.7014	down	-1.8520	down	-1.1506	down
MPF_contig_032688		0.0393	-0.0079	down	0.1874	up	0.5972	up	0.1953	up	0.6051	up	0.4098	up
MPF_SETB2.1.1	SETB2_DANRE (sp|Q06ZW3) Histone-lysine N-methyltransferase SETDB2 OS=Danio rerio GN=setdb2 PE=2 SV=2	0.0393	-0.1680	down	0.3924	up	0.5222	up	0.5604	up	0.6902	up	0.1298	up
MPF_LOC101173244.5.8	XM_004076629.1 PREDICTED: Oryzias latipes ATP synthase subunit g, mitochondrial-like (LOC101173244), mRNA	0.0394	0.3524	up	0.5454	up	1.0180	up	0.1929	up	0.6656	up	0.4726	up
MPF_contig_037980		0.0394	-0.3880	down	-1.6334	down	-3.3974	down	-1.2453	down	-3.0094	down	-1.7640	down
MPF_LOC101063630.1.1	XM_003979835.1 PREDICTED: Takifugu rubripes high mobility group-T protein-like (LOC101063630), mRNA	0.0394	-0.0989	down	-0.1689	down	0.9151	up	-0.0701	down	1.0140	up	1.0841	up
MPF_LOC101169833.1.2	XP_004065652.1 PREDICTED: atlastin-2-like [Oryzias latipes]	0.0394	-0.0476	down	0.2100	up	0.7501	up	0.2576	up	0.7978	up	0.5402	up
MPF_LOC101473359.1.1	XM_004538782.1 PREDICTED: Maylandia zebra endonuclease V-like (LOC101473359), transcript variant X4, mRNA	0.0394	-0.0015	down	0.2485	up	0.6895	up	0.2500	up	0.6911	up	0.4410	up
MPF_LOC100695231.1.1	XM_003450602.1 PREDICTED: Oreochromis niloticus josephin-2-like (LOC100695231), mRNA	0.0394	-0.0837	down	0.2333	up	0.9617	up	0.3170	up	1.0454	up	0.7284	up

MPF_LOC100709295.1.1	XM_003458274.1 PREDICTED: Oreochromis niloticus protein furry homolog (LOC100709295), mRNA	0.0394	0.4815	up	0.4566	up	1.2807	up	-0.0249	down	0.7992	up	0.8240	up
MPF_LOC101477256.2.2	XM_004570210.1 PREDICTED: Maylandia zebra TGF-beta-activated kinase 1 and MAP3K7binding protein 3-like (LOC101477256), mRNA	0.0394	-0.0817	down	-0.0693	down	0.8405	up	0.0123	up	0.9221	up	0.9098	up

MPF_LOC100698606.1.1	XM_003451611.1 PREDICTED: Oreochromis niloticus ceroid-lipofuscinosis neuronal protein 5-like (LOC100698606), mRNA	0.0394	-0.1042	down	0.0166	up	-0.5253	down	0.1208	up	-0.4211	down	-0.5419	down
MPF_LOC100148223.1.2	XP_003201586.1 PREDICTED: zinc finger protein 729-like [Danio rerio]	0.0394	-0.0807	down	-0.4593	down	1.4576	up	-0.3787	down	1.5383	up	1.9170	up
MPF_LOC101467697.1.1	XM_004575205.1 PREDICTED: Maylandia zebra gem-associated protein 8-like (LOC101467697), transcript variant X4, mRNA	0.0394	-0.2388	down	0.1423	up	0.7975	up	0.3811	up	1.0362	up	0.6551	up
MPF_KLHL7.1.1	XP_003444163.1 PREDICTED: kelch-like protein 7 [Oreochromis niloticus]	0.0394	-0.1005	down	-0.0539	down	0.7176	up	0.0466	up	0.8180	up	0.7714	up
MPF_LOC101168889.1.1	XM_004077080.1 PREDICTED: Oryzias latipes methylated-DNA--proteincysteine methyltransferaselike (LOC101168889), mRNA	0.0394	-0.3047	down	0.3204	up	0.3222	up	0.6251	up	0.6270	up	0.0019	up
MPF_contig_039966		0.0394	0.1019	up	0.4372	up	0.9564	up	0.3353	up	0.8544	up	0.5192	up

MPF_LOC101484122.5.9	XM_004572909.1 PREDICTED: Maylandia zebra eukaryotic translation initiation factor 5A-1-like (LOC101484122), mRNA	0.0394	0.0188	up	0.1731	up	1.0158	up	0.1543	up	0.9970	up	0.8427	up
MPF_LOC101477737.4.5	XM_004550788.1 PREDICTED: Maylandia zebra complement C1r subcomponent-like (LOC101477737), mRNA	0.0394	-0.0301	down	0.1158	up	0.5648	up	0.1459	up	0.5949	up	0.4490	up
MPF_contig_022579		0.0394	-0.2216	down	0.0944	up	0.6487	up	0.3160	up	0.8703	up	0.5543	up
MPF_contig_033262		0.0395	0.3076	up	0.3976	up	1.2816	up	0.0900	up	0.9740	up	0.8839	up
MPF_contig_044692		0.0395	0.1040	up	0.2215	up	0.6226	up	0.1175	up	0.5185	up	0.4010	up
MPF_contig_032689		0.0395	-0.1575	down	0.2696	up	-0.8944	down	0.4271	up	-0.7369	down	-1.1640	down
MPF_contig_019349		0.0395	-0.1783	down	-0.0996	down	0.3784	up	0.0787	up	0.5567	up	0.4780	up
MPF_LOC100708713.1.2	XP_003448467.1 PREDICTED: coiled-coil domain-containing protein 66like [Oreochromis niloticus]	0.0395	-0.0807	down	0.4416	up	1.2514	up	0.5222	up	1.3321	up	0.8099	up
MPF_LOC101473154.1.1	XM_004539054.1 PREDICTED: Maylandia zebra zinc finger and SCAN domain-containing protein 25like (LOC101473154), transcript variant X3, mRNA	0.0395	-0.0527	down	0.3970	up	0.7606	up	0.4497	up	0.8133	up	0.3635	up
MPF_contig_009915		0.0395	-0.9612	down	-0.5149	down	-2.7029	down	0.4463	up	-1.7417	down	-2.1880	down
MPF_LOC100693362.6.13	XP_003450310.1 PREDICTED: fucolectin-1like [Oreochromis niloticus]	0.0395	-0.2202	down	0.0704	up	0.8818	up	0.2905	up	1.1020	up	0.8114	up

MPF_LOC101464474.1.1	XM_004570085.1 PREDICTED: Maylandia zebra S1 RNA-binding domain-containing protein 1like (LOC101464474), mRNA	0.0395	-0.0935	down	0.2219	up	0.7815	up	0.3154	up	0.8750	up	0.5596	up
MPF_LOC101469146.1.1	XM_004567105.1 PREDICTED: Maylandia zebra dedicator of cytokinesis protein 11-like (LOC101469146), transcript variant X3, mRNA	0.0395	-0.0521	down	-0.0642	down	1.0297	up	-0.0121	down	1.0819	up	1.0940	up
MPF_contig_023460		0.0395	-0.0532	down	0.2176	up	0.6201	up	0.2708	up	0.6733	up	0.4025	up
MPF_contig_018897		0.0396	-0.0007	down	0.2723	up	0.7370	up	0.2729	up	0.7377	up	0.4648	up
MPF_LOC101477130.1.1	XM_004564031.1 PREDICTED: Maylandia zebra nuclear factor related to kappa-B-binding proteinlike (LOC101477130), mRNA	0.0396	-0.1666	down	0.0086	up	1.6551	up	0.1751	up	1.8217	up	1.6465	up
MPF_contig_032229		0.0397	0.2925	up	0.4453	up	1.2718	up	0.1528	up	0.9793	up	0.8265	up
MPF_LOC100703126.6.7	XM_003459102.1 PREDICTED: Oreochromis niloticus tripartite motifcontaining protein 16-like (LOC100703126), mRNA	0.0397	-0.0578	down	0.2359	up	0.8237	up	0.2937	up	0.8815	up	0.5878	up
MPF_contig_027611		0.0397	0.0267	up	0.2922	up	0.9282	up	0.2656	up	0.9015	up	0.6360	up
MPF_contig_013367		0.0397	0.4265	up	0.2312	up	1.3624	up	-0.1953	down	0.9360	up	1.1312	up
MPF_CD63.2.2	NM_001124496.1 Oncorhynchus mykiss Cd63 antigen (cd63), mRNA gb|AY593998.1| Oncorhynchus mykiss CD63 (CD63) mRNA, complete cds	0.0397	-0.1774	down	-0.0188	down	0.7785	up	0.1585	up	0.9559	up	0.7973	up

MPF_contig_043871		0.0397	-0.3385	down	-0.5291	down	-0.7327	down	-0.1906	down	-0.3942	down	-0.2036	down
MPF_LOC101168923.4.7	XP_004085899.1 PREDICTED: oocyte zinc finger protein XlCOF22-like, partial [Oryzias latipes]	0.0397	0.0158	up	0.2203	up	1.1264	up	0.2045	up	1.1106	up	0.9061	up
MPF_contig_015309		0.0397	0.0231	up	0.2642	up	1.4937	up	0.2411	up	1.4706	up	1.2295	up
MPF_contig_021461		0.0398	-0.1562	down	0.1679	up	0.5848	up	0.3241	up	0.7410	up	0.4169	up
MPF_NEMVEDRAFT_V1G111168.1.2	XP_001631283.1 predicted protein [Nematostella vectensis]	0.0398	0.2111	up	0.5485	up	0.7755	up	0.3374	up	0.5643	up	0.2270	up
MPF_contig_002577		0.0398	0.1208	up	0.0698	up	0.9493	up	-0.0510	down	0.8284	up	0.8794	up
MPF_LOC100012601.1.1	XP_001366940.2 PREDICTED: zinc finger protein 135-like, partial [Monodelphis domestica]	0.0398	0.1004	up	0.3429	up	1.1997	up	0.2425	up	1.0993	up	0.8568	up
MPF_LOC100712063.3.7	XM_003438416.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100712063 (LOC100712063), mRNA	0.0398	-0.1351	down	0.1716	up	0.5069	up	0.3067	up	0.6420	up	0.3353	up
MPF_LOC100701472.1.1	XP_003449934.1 PREDICTED: F-box only protein 30-like [Oreochromis niloticus]	0.0399	-0.0605	down	0.1976	up	0.9419	up	0.2581	up	1.0024	up	0.7443	up
MPF_LOC100700762.1.1	XP_003453240.1 PREDICTED: serine/threonine-protein kinase 11-interacting proteinlike [Oreochromis niloticus]	0.0399	-0.0171	down	0.2420	up	0.9647	up	0.2591	up	0.9818	up	0.7227	up

MPF_ZNF84.8.14	ZNF84_HUMAN (sp|P51523) Zinc finger protein 84 OS=Homo sapiens GN=ZNF84 PE=1 SV=2	0.0399	-0.1252	down	0.2856	up	1.4177	up	0.4108	up	1.5429	up	1.1321	up
MPF_LOC101467980.1.1	XM_004571487.1 PREDICTED: Maylandia zebra protein fem-1 homolog B-like (LOC101467980), transcript variant X2, mRNA	0.0399	0.3338	up	0.4718	up	1.3873	up	0.1381	up	1.0535	up	0.9154	up
MPF_LOC101485267.1.1	XM_004573747.1 PREDICTED: Maylandia zebra kelch-like protein 42like (LOC101485267), mRNA	0.0399	-0.0639	down	0.2280	up	0.7814	up	0.2919	up	0.8453	up	0.5534	up
MPF_LOC101470436.2.2	XM_004558518.1 PREDICTED: Maylandia zebra cytochrome c oxidase subunit 6A1, mitochondriallike (LOC101470436), mRNA	0.0399	-0.0443	down	0.1799	up	0.6071	up	0.2242	up	0.6514	up	0.4272	up
MPF_contig_039977		0.0399	0.2351	up	-0.2360	down	-1.1276	down	-0.4711	down	-1.3627	down	-0.8915	down
MPF_LOC101485347.1.2	XM_004549213.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 10like (LOC101485347), transcript variant X2, mRNA	0.0400	-0.2746	down	0.0291	up	0.4897	up	0.3037	up	0.7643	up	0.4606	up
MPF_LOC100702019.1.1	XP_003449936.1 PREDICTED: calpain-7-like protein-like [Oreochromis niloticus]	0.0400	0.0761	up	0.2359	up	0.8528	up	0.1598	up	0.7767	up	0.6169	up
MPF_LOC101473906.1.3	XM_004549447.1 PREDICTED: Maylandia zebra max dimerization protein 4-like (LOC101473906), mRNA	0.0400	0.1283	up	0.1895	up	0.9825	up	0.0612	up	0.8542	up	0.7930	up

MPF_LOC101487555.1.1	XM_004575183.1 PREDICTED: Maylandia zebra actin-related protein 2/3 complex subunit 2-like (LOC101487555), mRNA	0.0400	-0.0656	down	-0.1324	down	0.5246	up	-0.0667	down	0.5902	up	0.6569	up
MPF_SYJ2B.1.1	[BBH] SYJ2B_BOVIN (sp|Q3T0C9) Synaptojanin-2binding protein OS=Bos taurus GN=SYNJ2BP PE=2 SV=1	0.0400	-0.1945	down	0.0943	up	0.9515	up	0.2889	up	1.1460	up	0.8571	up
MPF_contig_034872		0.0400	-0.1474	down	-0.1347	down	0.5606	up	0.0127	up	0.7080	up	0.6952	up
MPF_contig_008278		0.0400	0.1381	up	0.4671	up	0.7446	up	0.3291	up	0.6066	up	0.2775	up
MPF_LOC100693055.1.1	XM_003440029.1 PREDICTED: Oreochromis niloticus cyclic AMPdependent transcription factor ATF-6 alpha-like (LOC100693055), mRNA	0.0400	0.0747	up	-0.0599	down	1.3122	up	-0.1347	down	1.2375	up	1.3722	up
MPF_LOC100706696.4.16	XM_003457393.1 PREDICTED: Oreochromis niloticus tripartite motifcontaining protein 39-like (LOC100706696), mRNA	0.0400	0.2942	up	-0.1633	down	-0.8616	down	-0.4575	down	-1.1558	down	-0.6983	down
MPF_LOC101484359.1.1	XM_004540271.1 PREDICTED: Maylandia zebra programmed cell death protein 10-like (LOC101484359), mRNA	0.0400	-0.0774	down	0.1861	up	0.7300	up	0.2635	up	0.8074	up	0.5439	up
MPF_LOC100693622.1.1	XP_003448661.1 PREDICTED: hypothetical protein LOC100693622 [Oreochromis niloticus]	0.0400	-0.0324	down	0.1984	up	0.6621	up	0.2309	up	0.6945	up	0.4637	up
MPF_LOC100695915.1.1	XP_003443746.1 PREDICTED: zinc finger protein ZFAT-like [Oreochromis niloticus]	0.0400	0.1353	up	0.3145	up	0.9112	up	0.1792	up	0.7760	up	0.5967	up

MPF_contig_027704		0.0400	0.0174	up	0.1661	up	0.7465	up	0.1487	up	0.7290	up	0.5804	up
MPF_contig_005338	XM_004566691.1 PREDICTED: Maylandia zebra kinase suppressor of Ras 2-like (LOC101484837), transcript variant X1, mRNA	0.0400	0.1973	up	0.4982	up	0.7888	up	0.3009	up	0.5915	up	0.2906	up
MPF_LOC101463873.2.2	XM_004541312.1 PREDICTED: Maylandia zebra zinc finger protein 592like (LOC101463873), transcript variant X3, mRNA	0.0400	-0.2252	down	0.1748	up	0.8541	up	0.4000	up	1.0793	up	0.6793	up
MPF_LOC101466459.15.29	XM_004554283.1 PREDICTED: Maylandia zebra semaphorin-3G-like (LOC101466459), mRNA	0.0400	-0.0501	down	0.2715	up	0.5621	up	0.3216	up	0.6122	up	0.2906	up
MPF_ZNF84.13.14	ZNF84_HUMAN (sp|P51523) Zinc finger protein 84 OS=Homo sapiens GN=ZNF84 PE=1 SV=2	0.0401	0.1698	up	0.3399	up	1.2488	up	0.1701	up	1.0790	up	0.9089	up
MPF_LOC101476160.2.2	XM_004557247.1 PREDICTED: Maylandia zebra unconventional myosinX-like (LOC101476160), mRNA	0.0401	-0.1184	down	0.1287	up	0.7851	up	0.2471	up	0.9034	up	0.6564	up
MPF_LOC101162274.1.1	XR_177692.1 PREDICTED: Oryzias latipes uncharacterized LOC101162274 (LOC101162274), misc_RNA	0.0401	-0.0656	down	-0.0037	down	0.5790	up	0.0618	up	0.6446	up	0.5827	up

MPF_LOC101484672.2.6	XM_004548379.1 PREDICTED: Maylandia zebra lysine-specific demethylase 7A-like (LOC101484672), transcript variant X2, mRNA	0.0401	-0.0202	down	-0.0379	down	0.6326	up	-0.0177	down	0.6528	up	0.6705	up
MPF_LOC101468796.3.3	XM_004575287.1 PREDICTED: Maylandia zebra barrier-toautointegration factor-like protein-like (LOC101468796), mRNA	0.0401	-0.0466	down	0.0406	up	0.6013	up	0.0872	up	0.6478	up	0.5606	up
MPF_LOC101468845.1.1	XM_004567562.1 PREDICTED: Maylandia zebra melanoma-associated antigen G1-like (LOC101468845), mRNA	0.0401	-0.1324	down	0.0284	up	0.5003	up	0.1608	up	0.6327	up	0.4718	up
MPF_ZN271.5.19	ZN271_MOUSE (sp|P15620) Zinc finger protein 271 OS=Mus musculus GN=Znf271 PE=2 SV=1	0.0401	0.0637	up	0.2123	up	0.9105	up	0.1486	up	0.8468	up	0.6982	up
MPF_LOC101168815.1.2	XP_004079344.1 PREDICTED: fractalkine-like [Oryzias latipes]	0.0401	0.6153	up	0.1889	up	0.9477	up	-0.4265	down	0.3324	up	0.7589	up
MPF_LOC101061379.1.2	XP_003976891.1 PREDICTED: sushi, von Willebrand factor type A, EGF and pentraxin domaincontaining protein 1-like, partial [Takifugu rubripes]	0.0401	-0.5814	down	-0.5923	down	-2.6981	down	-0.0108	down	-2.1167	down	-2.1059	down
MPF_contig_044705		0.0401	-0.2449	down	-0.1660	down	-0.8732	down	0.0789	up	-0.6282	down	-0.7071	down
MPF_LOC100701273.13.44	XM_003444228.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 12-like (LOC100701273), mRNA	0.0401	0.0700	up	0.5277	up	0.6926	up	0.4577	up	0.6226	up	0.1648	up

MPF_LOC100690077.1.1	XP_003458490.1 PREDICTED: CCR4-NOT transcription complex subunit 2-like [Oreochromis niloticus]	0.0401	-0.0972	down	-0.0402	down	0.8860	up	0.0570	up	0.9832	up	0.9262	up

MPF_LOC101463842.1.1	XM_004554815.1 PREDICTED: Maylandia zebra rab3 GTPaseactivating protein noncatalytic subunit-like (LOC101463842), transcript variant X3, mRNA	0.0401	-0.0397	down	0.0778	up	0.6931	up	0.1175	up	0.7328	up	0.6153	up
MPF_contig_000215		0.0402	-0.1532	down	0.1462	up	1.0023	up	0.2993	up	1.1554	up	0.8561	up
MPF_LOC101473738.1.2	XM_004538235.1 PREDICTED: Maylandia zebra matrix metalloproteinase-17-like (LOC101473738), mRNA	0.0402	-0.1484	down	-0.2702	down	0.9130	up	-0.1218	down	1.0613	up	1.1832	up
MPF_contig_038643		0.0402	-0.0131	down	0.1284	up	0.7742	up	0.1415	up	0.7873	up	0.6458	up
MPF_LOC101470011.1.1	XM_004572767.1 PREDICTED: Maylandia zebra agrin-like (LOC101470011), transcript variant X5, mRNA	0.0402	0.2136	up	-0.6638	down	-2.7345	down	-0.8774	down	-2.9481	down	-2.0707	down
MPF_LOC101063443.1.1	XM_003969518.1 PREDICTED: Takifugu rubripes F-box only protein 22-like (LOC101063443), mRNA	0.0402	-0.2141	down	0.1897	up	0.6035	up	0.4039	up	0.8176	up	0.4138	up
MPF_LOC100703911.1.1	XM_003452308.1 PREDICTED: Oreochromis niloticus proto-oncogene cRel-like (LOC100703911), mRNA	0.0402	-0.0577	down	0.1920	up	0.8684	up	0.2497	up	0.9262	up	0.6765	up

MPF_LOC101486640.4.4	XM_004538564.1 PREDICTED: Maylandia zebra ubiquitin carboxylterminal hydrolase 32-like (LOC101486640), mRNA	0.0402	0.0929	up	0.1969	up	0.8750	up	0.1040	up	0.7821	up	0.6781	up
MPF_contig_028601		0.0402	-0.7178	down	-0.8391	down	-2.7477	down	-0.1212	down	-2.0299	down	-1.9087	down
MPF_RPS27.3.3	XP_003817383.1 PREDICTED: 40S ribosomal protein S27 [Pan paniscus]	0.0402	-0.0307	down	0.2475	up	0.5039	up	0.2782	up	0.5346	up	0.2564	up
MPF_LOC100696180.1.1	XR_134816.1 PREDICTED: Oreochromis niloticus fibronectin-like (LOC100696180), miscRNA	0.0402	0.3649	up	-1.9472	down	-4.4956	down	-2.3121	down	-4.8605	down	-2.5484	down
MPF_LOC101467815.1.1	XM_004538582.1 PREDICTED: Maylandia zebra iporin-like (LOC101467815), mRNA	0.0403	0.4803	up	0.0345	up	1.3291	up	-0.4458	down	0.8488	up	1.2947	up
MPF_contig_016434	XM_004569703.1 PREDICTED: Maylandia zebra caskin-2-like (LOC101484206), transcript variant X2, mRNA	0.0403	0.1204	up	0.4089	up	1.0337	up	0.2885	up	0.9133	up	0.6248	up
MPF_contig_044548		0.0403	-0.7288	down	-0.6957	down	-2.7596	down	0.0332	up	-2.0308	down	-2.0640	down
MPF_contig_019366		0.0403	-0.1021	down	0.0647	up	0.6537	up	0.1668	up	0.7558	up	0.5890	up
MPF_contig_001265	XM_004544289.1 PREDICTED: Maylandia zebra rab11 family-interacting protein 1-like (LOC101463597), transcript variant X1, mRNA	0.0403	0.3682	up	0.5628	up	0.9877	up	0.1946	up	0.6195	up	0.4249	up

MPF_LOC101158287.1.1	XP_004073601.1 PREDICTED: iduronate 2sulfatase-like [Oryzias latipes]	0.0403	0.0243	up	0.1839	up	0.5601	up	0.1596	up	0.5357	up	0.3762	up
MPF_LOC100706818.9.9	XR_134822.1 PREDICTED: Oreochromis niloticus selenoprotein Pa-like (LOC100706818), miscRNA	0.0403	-0.0767	down	0.2886	up	0.6743	up	0.3653	up	0.7509	up	0.3857	up
MPF_contig_007515		0.0403	-0.0539	down	-0.0691	down	0.8148	up	-0.0152	down	0.8687	up	0.8838	up
MPF_contig_048334		0.0403	-0.1306	down	0.0843	up	0.7755	up	0.2150	up	0.9061	up	0.6911	up
MPF_LOC101478927.1.1	XM_004545195.1 PREDICTED: Maylandia zebra transforming acidic coiled-coil-containing protein 1-like (LOC101478927), transcript variant X4, mRNA	0.0403	-0.4808	down	-0.1262	down	-1.8755	down	0.3546	up	-1.3946	down	-1.7492	down
MPF_contig_004602		0.0403	-0.1258	down	0.0604	up	0.4755	up	0.1862	up	0.6013	up	0.4151	up
MPF_LOC100699374.1.1	XP_003443010.1 PREDICTED: hypothetical protein LOC100699374 [Oreochromis niloticus]	0.0403	-0.0367	down	0.1859	up	0.9661	up	0.2226	up	1.0027	up	0.7801	up
MPF_SRRM2.5.15	SRRM2_HUMAN (sp|Q9UQ35) Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	0.0403	-0.1382	down	-0.8452	down	-3.0800	down	-0.7070	down	-2.9418	down	-2.2348	down
MPF_contig_031648		0.0403	-0.0601	down	0.1303	up	0.8203	up	0.1904	up	0.8804	up	0.6900	up
MPF_LOC101466320.1.2	XM_004547664.1 PREDICTED: Maylandia zebra mitochondrial import inner membrane translocase subunit Tim17-A-like (LOC101466320), mRNA	0.0403	-0.1156	down	0.3401	up	0.9425	up	0.4557	up	1.0581	up	0.6024	up

MPF_contig_020041		0.0403	-0.1601	down	-0.1503	down	0.7511	up	0.0098	up	0.9112	up	0.9014	up
MPF_LOC101474065.2.3	XM_004565481.1 PREDICTED: Maylandia zebra partitioning defective 6 homolog beta-like (LOC101474065), mRNA	0.0403	-0.2765	down	0.2664	up	0.5523	up	0.5429	up	0.8288	up	0.2859	up
MPF_RL13.2.5	RL13_DANRE (sp|Q90Z10) 60S ribosomal protein L13 OS=Danio rerio GN=rpl13 PE=2 SV=3	0.0403	-0.0166	down	-0.7901	down	-2.0334	down	-0.7735	down	-2.0167	down	-1.2433	down
MPF_LOC101477265.1.1	XM_004549266.1 PREDICTED: Maylandia zebra pericentriolar material 1 protein-like (LOC101477265), transcript variant X2, mRNA	0.0403	-0.0948	down	0.2123	up	0.8616	up	0.3071	up	0.9564	up	0.6494	up
MPF_contig_015694		0.0403	-0.0234	down	0.1300	up	0.5333	up	0.1534	up	0.5567	up	0.4033	up
MPF_LOC100710544.1.1	XP_003458875.1 PREDICTED: zinc finger CCHC domain-containing protein 4-like [Oreochromis niloticus]	0.0403	0.0180	up	0.3610	up	0.9706	up	0.3431	up	0.9526	up	0.6096	up
MPF_LOC100692382.1.1	XM_003455542.1 PREDICTED: Oreochromis niloticus lecithin retinol acyltransferase-like (LOC100692382), mRNA	0.0403	-0.0420	down	0.3374	up	0.8244	up	0.3794	up	0.8664	up	0.4870	up
MPF_contig_010078		0.0403	-0.1392	down	-0.0117	down	0.5124	up	0.1275	up	0.6516	up	0.5241	up

MPF_LOC101483250.1.1	XM_004543044.1 PREDICTED: Maylandia zebra guanine nucleotidebinding protein G(o) subunit alpha-like (LOC101483250), mRNA	0.0403	0.0112	up	0.0962	up	0.9452	up	0.0850	up	0.9340	up	0.8490	up
MPF_contig_015992		0.0403	0.1548	up	0.3334	up	0.8122	up	0.1786	up	0.6575	up	0.4789	up
MPF_LOC101474595.1.2	XM_004556427.1 PREDICTED: Maylandia zebra ADP-ribosylation factorlike protein 6-interacting protein 1-like (LOC101474595), mRNA	0.0403	0.1980	up	0.3071	up	0.7816	up	0.1090	up	0.5836	up	0.4745	up
MPF_LOC101470665.1.1	XM_004566549.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 8Alike (LOC101470665), transcript variant X3, mRNA	0.0403	0.0448	up	0.3307	up	0.9730	up	0.2859	up	0.9282	up	0.6423	up
MPF_LOC101487497.1.1	XM_004563160.1 PREDICTED: Maylandia zebra integral membrane protein GPR137-like (LOC101487497), mRNA	0.0403	-0.0613	down	0.1645	up	0.6148	up	0.2258	up	0.6761	up	0.4503	up
MPF_LOC101486578.1.2	XM_004546432.1 PREDICTED: Maylandia zebra solute carrier family 52, riboflavin transporter, member 3-A-like (LOC101486578), mRNA	0.0403	-0.2173	down	-0.0403	down	1.0328	up	0.1770	up	1.2501	up	1.0731	up
MPF_LOC100699618.1.3	XM_003458706.1 PREDICTED: Oreochromis niloticus macrophagecapping protein-like (LOC100699618), mRNA	0.0403	0.1325	up	-1.3970	down	-3.2296	down	-1.5295	down	-3.3621	down	-1.8325	down

MPF_PTT_12042.2.2	XP_003300709.1 hypothetical protein PTT_12042 [Pyrenophora teres f. teres 0-1]	0.0403	0.0267	up	0.1788	up	0.6884	up	0.1521	up	0.6616	up	0.5096	up
MPF_LOC101483496.1.1	XM_004556827.1 PREDICTED: Maylandia zebra CCR4-NOT transcription complex subunit 8-like (LOC101483496), transcript variant X2, mRNA	0.0403	0.1394	up	0.3588	up	1.0170	up	0.2194	up	0.8777	up	0.6583	up
MPF_LOC100690203.1.1	XP_003448147.1 PREDICTED: 3'-5' exoribonuclease 1-like [Oreochromis niloticus]	0.0403	-0.0623	down	0.2911	up	0.7840	up	0.3534	up	0.8463	up	0.4929	up
MPF_PDPR.1.1	XP_003437743.1 PREDICTED: pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial [Oreochromis niloticus]	0.0403	-0.1513	down	-0.4391	down	-1.7358	down	-0.2878	down	-1.5845	down	-1.2968	down
MPF_LOC101166248.1.1	XP_004077993.1 PREDICTED: c-Jun-aminoterminal kinase-interacting protein 3-like [Oryzias latipes]	0.0403	-0.0454	down	0.2067	up	0.8746	up	0.2521	up	0.9199	up	0.6678	up
MPF_CTU1.1.1	[BBH] CTU1_DANRE (sp|Q803X1) Cytoplasmic tRNA 2-thiolation protein 1 OS=Danio rerio GN=ctu1 PE=2 SV=1	0.0403	0.0437	up	0.1985	up	0.7936	up	0.1549	up	0.7499	up	0.5950	up
MPF_LOC101467115.1.1	XM_004560257.1 PREDICTED: Maylandia zebra tetraspanin-31-like (LOC101467115), mRNA	0.0404	-0.2264	down	0.2341	up	0.7461	up	0.4605	up	0.9725	up	0.5120	up

MPF_LOC101472703.2.2	XM_004569035.1 PREDICTED: Maylandia zebra axin-1-like (LOC101472703), transcript variant X3, mRNA	0.0404	-0.1397	down	0.1029	up	0.7770	up	0.2426	up	0.9167	up	0.6741	up
MPF_contig_020978		0.0404	-0.0017	down	0.4334	up	1.5309	up	0.4351	up	1.5326	up	1.0975	up
MPF_LOC101473493.1.3	XM_004569487.1 PREDICTED: Maylandia zebra deubiquitinating protein VCIP135-like (LOC101473493), mRNA	0.0404	0.2531	up	0.5179	up	0.8515	up	0.2648	up	0.5985	up	0.3337	up
MPF_LOC101475366.1.1	XM_004557617.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 22-like (LOC101475366), transcript variant X2, mRNA	0.0404	-0.1150	down	-0.0196	down	0.7387	up	0.0954	up	0.8538	up	0.7584	up
MPF_LOC100705964.1.1	XM_003453127.1 PREDICTED: Oreochromis niloticus iron-sulfur cluster assembly 2 homolog, mitochondrial-like (LOC100705964), mRNA	0.0404	-0.3126	down	0.2663	up	0.4927	up	0.5788	up	0.8053	up	0.2265	up
MPF_LOC101477249.1.1	XM_004569229.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 22like (LOC101477249), transcript variant X3, mRNA	0.0404	-0.0346	down	0.1933	up	0.8611	up	0.2279	up	0.8957	up	0.6679	up
MPF_LOC101154812.1.1	XM_004080807.1 PREDICTED: Oryzias latipes eukaryotic translation initiation factor 5A-1-like, transcript variant 2	0.0404	0.0265	up	0.1704	up	1.0418	up	0.1440	up	1.0154	up	0.8714	up

	(LOC101154812), mRNA													
MPF_FCGBP.1.3	FCGBP_HUMAN (sp|Q9Y6R7) IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3	0.0404	-0.1137	down	0.0933	up	0.5431	up	0.2070	up	0.6568	up	0.4498	up
MPF_LOC101475678.1.1	XM_004559730.1 PREDICTED: Maylandia zebra translin-associated protein X-like (LOC101475678), transcript variant X2, mRNA	0.0404	-0.1946	down	0.1565	up	0.7358	up	0.3511	up	0.9304	up	0.5793	up
MPF_LOC101470419.1.3	XM_004576108.1 PREDICTED: Maylandia zebra histone acetyltransferase KAT7-like (LOC101470419), transcript variant X3, mRNA	0.0405	0.2995	up	0.1720	up	1.0325	up	-0.1275	down	0.7330	up	0.8606	up
MPF_LOC101475675.1.1	XM_004558632.1 PREDICTED: Maylandia zebra Golgi phosphoprotein 3like (LOC101475675), mRNA	0.0405	-0.1328	down	0.1323	up	1.0163	up	0.2651	up	1.1491	up	0.8841	up
MPF_COX1.6.7	COX1_PETMA (sp|Q35536) Cytochrome c oxidase subunit 1 OS=Petromyzon marinus GN=MT-CO1 PE=3 SV=1	0.0405	0.0737	up	0.0342	up	1.2756	up	-0.0396	down	1.2018	up	1.2414	up
MPF_LOC100701795.2.5	XM_003460324.1 PREDICTED: Oreochromis niloticus tripartite motifcontaining protein 16-like (LOC100701795), mRNA	0.0405	0.8369	up	0.9646	up	0.8009	up	0.1276	up	-0.0360	down	-0.1637	down

MPF_LOC101481461.1.1	XM_004554503.1 PREDICTED: Maylandia zebra partner of Y14 and mago A-like (LOC101481461), mRNA	0.0405	0.1378	up	0.3100	up	1.1018	up	0.1722	up	0.9640	up	0.7918	up
MPF_contig_002256		0.0406	0.0125	up	0.0648	up	0.5307	up	0.0523	up	0.5182	up	0.4659	up
MPF_DHX57.1.1	XP_003450769.1 PREDICTED: putative ATPdependent RNA helicase DHX57 [Oreochromis niloticus]	0.0406	-0.2139	down	0.1314	up	0.8924	up	0.3453	up	1.1063	up	0.7610	up
MPF_LOC101478179.1.1	XM_004546668.1 PREDICTED: Maylandia zebra transgelin-3-like (LOC101478179), mRNA	0.0406	0.0028	up	0.0846	up	1.1323	up	0.0818	up	1.1295	up	1.0477	up
MPF_LOC101471216.1.1	XM_004539479.1 PREDICTED: Maylandia zebra ras-related protein Rab-4A-like (LOC101471216), mRNA	0.0406	-0.1470	down	0.2208	up	0.9025	up	0.3678	up	1.0495	up	0.6817	up
MPF_contig_038340		0.0406	-0.0423	down	0.1993	up	0.7822	up	0.2416	up	0.8245	up	0.5830	up
MPF_LOC101064916.1.1	XP_003968610.1 PREDICTED: integrin-linked protein kinase-like [Takifugu rubripes]	0.0406	-0.1535	down	0.2298	up	0.8020	up	0.3834	up	0.9555	up	0.5722	up
MPF_contig_005519		0.0406	-0.4540	down	-0.5548	down	-2.7642	down	-0.1009	down	-2.3102	down	-2.2094	down
MPF_LOC100692032.2.6	XP_003458104.1 PREDICTED: E3 ubiquitin/ISG15 ligase TRIM25-like [Oreochromis niloticus]	0.0406	0.0332	up	0.4126	up	0.8961	up	0.3794	up	0.8628	up	0.4835	up

MPF_contig_004625	XM_004542709.1 PREDICTED: Maylandia zebra histone-lysine Nmethyltransferase MLL3-like (LOC101465418), transcript variant X4, mRNA	0.0406	-0.0545	down	-0.2215	down	0.6495	up	-0.1670	down	0.7040	up	0.8710	up
MPF_LOC101066966.3.3	XP_003974674.1 PREDICTED: zinc finger protein 287-like [Takifugu rubripes]	0.0406	-0.2802	down	0.0170	up	-0.9460	down	0.2972	up	-0.6658	down	-0.9630	down
MPF_LOC101466738.2.3	XM_004556678.1 PREDICTED: Maylandia zebra guanine nucleotidebinding protein subunit alpha- 13-like (LOC101466738), mRNA	0.0406	-0.0090	down	0.3092	up	1.3966	up	0.3182	up	1.4056	up	1.0874	up
MPF_LOC100709019.1.2	XM_003458034.1 PREDICTED: Oreochromis niloticus ATP synthase subunit g, mitochondrial-like (LOC100709019), mRNA	0.0406	0.0324	up	0.1421	up	0.7050	up	0.1097	up	0.6726	up	0.5629	up
MPF_LOC100689711.4.6	XP_003459483.1 PREDICTED: h-2 class I histocompatibility antigen, LD alpha chain-like [Oreochromis niloticus]	0.0406	-0.5041	down	-0.6929	down	-2.2929	down	-0.1888	down	-1.7888	down	-1.6000	down
MPF_LOC101467664.1.2	XM_004569013.1 PREDICTED: Maylandia zebra serine/threonineprotein kinase PLK1-like (LOC101467664), mRNA	0.0406	0.0118	up	0.0448	up	0.8729	up	0.0330	up	0.8612	up	0.8282	up
MPF_LOC100705458.1.1	XP_003457013.1 PREDICTED: syntenin-1-like [Oreochromis niloticus]	0.0407	-0.1241	down	-0.0222	down	0.8423	up	0.1019	up	0.9664	up	0.8645	up

MPF_LOC101466459.1.29	XM_004554283.1 PREDICTED: Maylandia zebra semaphorin-3G-like (LOC101466459), mRNA	0.0407	-0.0765	down	0.1140	up	0.8685	up	0.1905	up	0.9450	up	0.7545	up
MPF_LOC100689854.16.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0.0407	0.0464	up	0.2341	up	0.6487	up	0.1876	up	0.6023	up	0.4147	up
MPF_LOC101480151.1.1	XM_004542860.1 PREDICTED: Maylandia zebra abhydrolase domaincontaining protein 3-like (LOC101480151), mRNA	0.0407	-0.1624	down	0.0176	up	1.3584	up	0.1801	up	1.5208	up	1.3408	up
MPF_contig_041295		0.0407	0.0040	up	0.4904	up	1.0130	up	0.4864	up	1.0090	up	0.5226	up
MPF_LOC100700860.1.1	XP_003455201.1 PREDICTED: placenta-specific gene 8 protein-like [Oreochromis niloticus]	0.0407	0.0678	up	0.2446	up	0.8004	up	0.1768	up	0.7327	up	0.5558	up
MPF_LOC101471048.3.7	XM_004568139.1 PREDICTED: Maylandia zebra cyclin-dependent kinase 16-like (LOC101471048), transcript variant X7, mRNA	0.0407	-0.0800	down	0.2199	up	0.6918	up	0.2999	up	0.7718	up	0.4720	up
MPF_LOC100709275.1.1	XM_003454278.1 PREDICTED: Oreochromis niloticus regulator of telomere elongation helicase 1-like (LOC100709275), mRNA	0.0407	-0.0654	down	0.0976	up	0.8110	up	0.1631	up	0.8765	up	0.7134	up
MPF_LOC100706980.1.1	XP_003459830.1 PREDICTED: hypothetical protein LOC100706980 [Oreochromis niloticus]	0.0408	0.1248	up	0.1320	up	0.5673	up	0.0072	up	0.4425	up	0.4353	up

MPF_LOC101062903.1.1	XP_003965204.1 PREDICTED: protein phosphatase 1 regulatory subunit 3B-like [Takifugu rubripes]	0.0408	-0.0785	down	0.0850	up	0.5694	up	0.1636	up	0.6479	up	0.4844	up
MPF_KIT.1.1	[BBH] KIT_TAKRU (sp|Q8AXC6) Mast/stem cell growth factor receptor Kit OS=Takifugu rubripes GN=kit PE=3 SV=1	0.0409	0.0226	up	0.2327	up	1.3549	up	0.2101	up	1.3323	up	1.1222	up
MPF_LOC101478118.1.3	XM_004575056.1 PREDICTED: Maylandia zebra probable palmitoyltransferase ZDHHC12-like (LOC101478118), transcript variant X2, mRNA	0.0409	0.0682	up	0.2194	up	0.5078	up	0.1512	up	0.4396	up	0.2884	up
MPF_LOC101479710.1.1	XM_004573330.1 PREDICTED: Maylandia zebra poliovirus receptorrelated protein 3-like (LOC101479710), transcript variant X2, mRNA	0.0410	0.0403	up	0.0985	up	0.7842	up	0.0582	up	0.7439	up	0.6856	up
MPF_LOC100710876.1.1	XP_003454498.1 PREDICTED: pachytene checkpoint protein 2 homolog [Oreochromis niloticus]	0.0410	0.0096	up	0.3715	up	0.9208	up	0.3619	up	0.9112	up	0.5493	up
MPF_LOC101480617.2.3	XM_004564970.1 PREDICTED: Maylandia zebra mucin-2-like (LOC101480617), mRNA	0.0410	-0.0080	down	0.0962	up	0.6918	up	0.1042	up	0.6998	up	0.5956	up
MPF_LOC100707328.1.3	XP_003459760.1 PREDICTED: splicing factor 1-like isoform 2 [Oreochromis niloticus]	0.0410	-0.0921	down	0.2566	up	0.5308	up	0.3487	up	0.6229	up	0.2742	up

MPF_LOC101484672.1.6	XM_004548379.1 PREDICTED: Maylandia zebra lysine-specific demethylase 7A-like (LOC101484672), transcript variant X2, mRNA	0.0410	0.1231	up	0.1513	up	0.8758	up	0.0282	up	0.7527	up	0.7245	up
MPF_contig_044394		0.0410	0.0196	up	0.0413	up	0.7143	up	0.0217	up	0.6947	up	0.6730	up
MPF_LOC100696859.1.1	XM_003439611.1 PREDICTED: Oreochromis niloticus UDP-Nacetylhexosamine pyrophosphorylase-like protein 1-like (LOC100696859), mRNA	0.0410	-0.2387	down	0.5452	up	0.3945	up	0.7839	up	0.6332	up	-0.1507	down
MPF_LOC101464093.1.1	XM_004543931.1 PREDICTED: Maylandia zebra signal recognition particle receptor subunit alpha-like (LOC101464093), mRNA	0.0410	0.3006	up	0.3770	up	1.2384	up	0.0764	up	0.9378	up	0.8614	up
MPF_LOC100702817.3.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like (LOC100702817), mRNA	0.0410	-0.5096	down	-2.5982	down	-4.7294	down	-2.0887	down	-4.2198	down	-2.1311	down
MPF_LOC101471828.1.2	XM_004545262.1 PREDICTED: Maylandia zebra receptor-type tyrosineprotein phosphatase alphalike (LOC101471828), transcript variant X2, mRNA	0.0410	0.0857	up	-0.0855	down	1.2255	up	-0.1711	down	1.1398	up	1.3110	up

MPF_LOC101470444.1.1	XM_004560365.1 PREDICTED: Maylandia zebra ATP-dependent RNA helicase DDX19A-like (LOC101470444), mRNA	0.0410	-0.2023	down	0.3866	up	1.0051	up	0.5890	up	1.2075	up	0.6185	up
MPF_contig_000291		0.0410	0.0371	up	0.0853	up	1.2938	up	0.0482	up	1.2567	up	1.2085	up
MPF_LOC101172154.1.1	XP_004068682.1 PREDICTED: epithelial membrane protein 3-like [Oryzias latipes]	0.0411	0.0783	up	-0.9349	down	-3.3326	down	-1.0132	down	-3.4108	down	-2.3976	down
MPF_LOC101477080.1.1	XM_004549745.1 PREDICTED: Maylandia zebra uncharacterized LOC101477080 (LOC101477080), transcript variant X4, mRNA	0.0411	0.1658	up	-0.0665	down	0.9476	up	-0.2323	down	0.7818	up	1.0141	up
MPF_LOC101476056.1.2	XM_004559923.1 PREDICTED: Maylandia zebra phosphatase and actin regulator 3-like (LOC101476056), transcript variant X2, mRNA	0.0411	-0.0998	down	0.1155	up	0.9392	up	0.2154	up	1.0391	up	0.8237	up
MPF_LOC101473099.1.1	XM_004547018.1 PREDICTED: Maylandia zebra voltage-dependent anion-selective channel protein 2-like (LOC101473099), transcript variant X3, mRNA	0.0411	-0.1472	down	0.1908	up	0.7744	up	0.3379	up	0.9215	up	0.5836	up
MPF_LOC101486559.1.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA	0.0411	-0.8715	down	-2.6127	down	-4.7191	down	-1.7412	down	-3.8475	down	-2.1063	down
MPF_contig_037711		0.0411	-0.0142	down	0.1084	up	0.5587	up	0.1226	up	0.5730	up	0.4503	up

MPF_LOC100697286.1.1	XP_003455106.1 PREDICTED: phosphatidylinositol-binding clathrin assembly protein-like [Oreochromis niloticus]	0.0411	0.0544	up	-0.0273	down	0.6903	up	-0.0817	down	0.6358	up	0.7175	up
MPF_LOC101480380.1.2	XM_004573988.1 PREDICTED: Maylandia zebra ras-related protein Rab-2A-like (LOC101480380), mRNA	0.0411	-0.1921	down	-0.4307	down	-1.4679	down	-0.2386	down	-1.2758	down	-1.0372	down
MPF_contig_003623		0.0411	-0.0504	down	0.2557	up	1.0605	up	0.3061	up	1.1108	up	0.8047	up
MPF_LOC101073876.1.2	XM_003978783.1 PREDICTED: Takifugu rubripes uncharacterized LOC101073876 (LOC101073876), mRNA	0.0411	-0.0463	down	0.0113	up	0.6549	up	0.0576	up	0.7013	up	0.6436	up
MPF_contig_048812		0.0411	-0.1031	down	0.1178	up	0.7358	up	0.2209	up	0.8389	up	0.6180	up
MPF_contig_015625		0.0411	0.1495	up	0.2436	up	0.6944	up	0.0940	up	0.5449	up	0.4508	up
MPF_contig_019195	XM_004556094.1 PREDICTED: Maylandia zebra transforming acidic coiled-coil-containing protein 2-like (LOC101481661), transcript variant X8, mRNA	0.0411	-0.1297	down	-0.4039	down	0.8994	up	-0.2741	down	1.0291	up	1.3032	up
MPF_contig_003956		0.0411	-0.0444	down	0.1429	up	0.6926	up	0.1873	up	0.7370	up	0.5497	up

MPF_LOC101485466.1.3	XM_004557559.1 PREDICTED: Maylandia zebra trinucleotide repeatcontaining gene 6B proteinlike (LOC101485466), transcript variant X4, mRNA	0.0411	-0.0226	down	0.0690	up	0.8310	up	0.0916	up	0.8537	up	0.7620	up
MPF_LOC100689854.8.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0.0411	-0.0781	down	0.0080	up	0.8288	up	0.0861	up	0.9068	up	0.8207	up
MPF_FCGBP.2.3	FCGBP_HUMAN (sp|Q9Y6R7) IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3	0.0411	-0.2420	down	0.9850	up	2.3084	up	1.2270	up	2.5505	up	1.3234	up
MPF_LOC100695994.29.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.0411	0.0932	up	0.0832	up	1.3105	up	-0.0100	down	1.2172	up	1.2273	up
MPF_LOC101480733.1.1	XM_004541182.1 PREDICTED: Maylandia zebra TCF3 fusion partner homolog (LOC101480733), transcript variant X1, mRNA	0.0411	-0.2298	down	-0.3076	down	0.9716	up	-0.0778	down	1.2014	up	1.2791	up
MPF_TOR1A.1.1	TOR1A_MOUSE (sp|Q9ER39) Torsin-1A OS=Mus musculus GN=Tor1a PE=1 SV=1	0.0411	-0.1155	down	-0.3864	down	-2.5166	down	-0.2709	down	-2.4010	down	-2.1301	down
MPF_contig_040359		0.0411	-0.0448	down	0.4096	up	0.8008	up	0.4544	up	0.8456	up	0.3912	up
MPF_contig_042687		0.0411	0.0538	up	-1.0327	down	-2.5678	down	-1.0864	down	-2.6216	down	-1.5352	down
MPF_RPB1.4.5	RPB1_ASHGO (sp|Q75A34) DNA-directed RNA polymerase II subunit RPB1 OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) GN=RPB1 PE=3 SV=2	0.0411	-0.3490	down	0.0801	up	-0.9153	down	0.4292	up	-0.5662	down	-0.9954	down

MPF_CELF2.8.8	CELF2_DANRE (sp|Q6P0B1) CUGBP Elav-like family member 2 OS=Danio rerio GN=celf2 PE=2 SV=1	0.0411	-0.3646	down	-0.0397	down	0.6669	up	0.3249	up	1.0315	up	0.7066	up

MPF_LOC101070225.1.1	XM_003971715.1 PREDICTED: Takifugu rubripes histidine triad nucleotide-binding protein 3like (LOC101070225), mRNA	0.0411	0.0641	up	0.0020	up	1.2269	up	-0.0621	down	1.1628	up	1.2249	up
MPF_LOC101467782.1.3	XM_004575774.1 PREDICTED: Maylandia zebra bone morphogenetic protein receptor type-1A-like (LOC101467782), transcript variant X6, mRNA	0.0411	-0.0012	down	0.3332	up	0.7749	up	0.3344	up	0.7762	up	0.4417	up
MPF_contig_046607	XM_004570275.1 PREDICTED: Maylandia zebra paired amphipathic helix protein Sin3a-like (LOC101468364), transcript variant X2, mRNA	0.0412	-0.2055	down	-0.0639	down	0.8791	up	0.1416	up	1.0847	up	0.9431	up
MPF_NRXN2B.1.1	NP_001073453.1 neurexin 2b precursor [Danio rerio]	0.0412	0.0123	up	-0.0920	down	0.5900	up	-0.1043	down	0.5777	up	0.6819	up
MPF_LOC100703672.1.1	XM_003437959.1 PREDICTED: Oreochromis niloticus pre-mRNA-splicing factor 38B-like (LOC100703672), mRNA	0.0412	-0.2603	down	0.0553	up	0.6352	up	0.3156	up	0.8956	up	0.5800	up
MPF_LOC101477793.2.2	XM_004540981.1 PREDICTED: Maylandia zebra zinc finger protein 711like (LOC101477793), mRNA	0.0412	-0.0610	down	0.4387	up	0.7573	up	0.4997	up	0.8183	up	0.3186	up

MPF_LOC100695409.2.2	XM_003449611.1 PREDICTED: Oreochromis niloticus microtubuleassociated serine/threonineprotein kinase 4-like (LOC100695409), mRNA	0.0413	0.5748	up	0.2224	up	0.9807	up	-0.3525	down	0.4059	up	0.7584	up
MPF_LOC101474510.1.1	XM_004561211.1 PREDICTED: Maylandia zebra probable vesicular acetylcholine transporter-Alike (LOC101474510), mRNA	0.0413	-0.2109	down	-0.4639	down	1.0896	up	-0.2529	down	1.3005	up	1.5534	up
MPF_LOC100696737.1.2	XM_003451435.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100696737 (LOC100696737), mRNA	0.0413	-0.0634	down	0.1502	up	0.8385	up	0.2135	up	0.9018	up	0.6883	up
MPF_LOC101482932.1.1	XM_004557736.1 PREDICTED: Maylandia zebra neurabin-1-like (LOC101482932), transcript variant X3, mRNA	0.0413	-0.1949	down	0.1782	up	1.2045	up	0.3731	up	1.3995	up	1.0263	up
MPF_LOC101465279.1.1	XR_191264.1 PREDICTED: Maylandia zebra TAR DNAbinding protein 43-like (LOC101465279), transcript variant X2, misc_RNA	0.0413	0.2173	up	0.3646	up	0.7527	up	0.1473	up	0.5355	up	0.3882	up
MPF_LOC101469020.1.2	XM_004563187.1 PREDICTED: Maylandia zebra ancient ubiquitous protein 1-like (LOC101469020), transcript variant X2, mRNA	0.0413	0.2438	up	0.4387	up	0.9108	up	0.1949	up	0.6670	up	0.4721	up

MPF_SHPRH.1.1	XP_003443042.1 PREDICTED: E3 ubiquitinprotein ligase SHPRH [Oreochromis niloticus]	0.0414	0.1498	up	0.2440	up	0.8047	up	0.0943	up	0.6549	up	0.5607	up
MPF_contig_032773		0.0414	0.1058	up	0.3278	up	0.9319	up	0.2220	up	0.8261	up	0.6041	up
MPF_LOC101468054.1.1	XM_004569557.1 PREDICTED: Maylandia zebra phosphoenolpyruvate carboxykinase [GTP], mitochondrial-like (LOC101468054), mRNA	0.0414	-0.1007	down	0.0273	up	0.9374	up	0.1280	up	1.0381	up	0.9101	up
MPF_LOC777971.1.1	NM_001078595.1 Takifugu rubripes macoilin-2 (LOC777971), mRNA gb|AY845028.1| Takifugu rubripes macoilin-2 mRNA, complete cds	0.0414	0.2049	up	-0.0669	down	0.9243	up	-0.2718	down	0.7194	up	0.9912	up
MPF_LOC101487878.1.1	XM_004539725.1 PREDICTED: Maylandia zebra serine/threonineprotein kinase ULK3-like (LOC101487878), mRNA	0.0414	-0.1012	down	0.2263	up	0.8935	up	0.3275	up	0.9947	up	0.6672	up
MPF_CFAH.14.15	CFAH_MOUSE (sp|P06909) Complement factor H OS=Mus musculus GN=Cfh PE=1 SV=2	0.0414	0.5548	up	-1.0375	down	-2.9919	down	-1.5923	down	-3.5467	down	-1.9544	down
MPF_LOC101470972.1.1	XM_004569116.1 PREDICTED: Maylandia zebra protein QN1 homolog (LOC101470972), mRNA	0.0414	0.0037	up	0.1011	up	0.7724	up	0.0974	up	0.7687	up	0.6713	up
MPF_LOC101480472.2.2	XM_004547721.1 PREDICTED: Maylandia zebra splicing factor 3A subunit 2-like (LOC101480472), mRNA	0.0414	0.0881	up	0.5450	up	0.7847	up	0.4569	up	0.6966	up	0.2397	up

MPF_LOC100697283.1.3	XM_003454317.1 PREDICTED: Oreochromis niloticus short coiled-coil protein A-like (LOC100697283), mRNA	0.0414	-0.1331	down	0.0015	up	0.8217	up	0.1347	up	0.9548	up	0.8201	up
MPF_LOC100692770.1.1	XM_003459224.1 PREDICTED: Oreochromis niloticus PHD finger protein 12-like (LOC100692770), mRNA	0.0415	-0.0802	down	0.1298	up	0.9427	up	0.2099	up	1.0228	up	0.8129	up
MPF_contig_032594		0.0415	-0.0641	down	0.0803	up	0.6322	up	0.1445	up	0.6963	up	0.5518	up
MPF_LOC100706502.11.17	XP_003454732.1 PREDICTED: protein NLRC3like [Oreochromis niloticus]	0.0415	-0.0267	down	0.1451	up	0.3804	up	0.1718	up	0.4071	up	0.2353	up
MPF_LOC101470873.1.3	XM_004543575.1 PREDICTED: Maylandia zebra importin subunit alpha-4-like (LOC101470873), mRNA	0.0415	0.4363	up	0.9264	up	0.4569	up	0.4901	up	0.0205	up	-0.4695	down
MPF_LOC101475621.1.1	XM_004568862.1 PREDICTED: Maylandia zebra cytochrome c oxidase assembly factor 6 homolog (LOC101475621), mRNA	0.0415	0.1083	up	0.2430	up	0.6690	up	0.1346	up	0.5606	up	0.4260	up
MPF_LOC101479028.1.1	XM_004545839.1 PREDICTED: Maylandia zebra DNA replication licensing factor mcm7-like (LOC101479028), transcript variant X2, mRNA	0.0415	-0.0299	down	0.1742	up	0.8208	up	0.2041	up	0.8507	up	0.6466	up
MPF_contig_028702		0.0416	0.2512	up	0.3734	up	0.9461	up	0.1222	up	0.6949	up	0.5727	up

MPF_LOC100710548.3.4	XP_003459320.1 PREDICTED: major histocompatibility complex class I-related gene proteinlike [Oreochromis niloticus]	0.0416	0.4353	up	-1.0936	down	-3.2350	down	-1.5289	down	-3.6703	down	-2.1415	down
MPF_LOC101486403.1.2	XM_004551184.1 PREDICTED: Maylandia zebra vacuolar protein sorting-associated protein 37D-like (LOC101486403), mRNA	0.0416	0.3422	up	-0.0089	down	1.0660	up	-0.3510	down	0.7239	up	1.0749	up
MPF_LOC101471705.1.1	XM_004538956.1 PREDICTED: Maylandia zebra transcription initiation factor TFIID subunit 5-like (LOC101471705), mRNA	0.0417	0.0046	up	0.1762	up	0.7507	up	0.1716	up	0.7461	up	0.5744	up
MPF_contig_022160		0.0417	-0.1605	down	0.4782	up	0.4374	up	0.6387	up	0.5979	up	-0.0407	down
MPF_LOC101160082.1.1	XM_004073912.1 PREDICTED: Oryzias latipes zinc finger protein 8-like (LOC101160082), mRNA	0.0417	0.1123	up	0.3594	up	1.0351	up	0.2471	up	0.9228	up	0.6757	up
MPF_RACK1.15.22	XM_003455178.1 PREDICTED: Oreochromis niloticus receptor for activated protein kinase C (RACK1), mRNA	0.0417	0.2715	up	0.4201	up	0.8112	up	0.1486	up	0.5397	up	0.3911	up
MPF_LOC101480954.1.2	XM_004572806.1 PREDICTED: Maylandia zebra versican core proteinlike (LOC101480954), mRNA	0.0418	-0.0240	down	-0.0005	down	0.7152	up	0.0235	up	0.7392	up	0.7157	up

MPF_LOC101471689.1.2	XM_004555845.1 PREDICTED: Maylandia zebra peroxisome proliferatoractivated receptor gamma coactivator-related protein 1like (LOC101471689), transcript variant X2, mRNA	0.0418	0.1488	up	-0.0026	down	0.8391	up	-0.1514	down	0.6903	up	0.8417	up
MPF_LOC100709144.1.1	XM_003441930.1 PREDICTED: Oreochromis niloticus DNA cross-link repair 1A protein-like (LOC100709144), mRNA	0.0418	0.0463	up	0.0674	up	0.9998	up	0.0211	up	0.9535	up	0.9323	up
MPF_LOC101483728.1.1	XM_004565065.1 PREDICTED: Maylandia zebra myosin-7-like (LOC101483728), mRNA	0.0418	0.1070	up	0.5031	up	1.1776	up	0.3961	up	1.0705	up	0.6745	up
MPF_contig_032698		0.0418	0.1525	up	0.1832	up	0.7091	up	0.0307	up	0.5565	up	0.5258	up
MPF_contig_045177		0.0418	0.0313	up	0.3170	up	0.7408	up	0.2857	up	0.7095	up	0.4238	up
MPF_LOC101468196.2.2	XM_004575285.1 PREDICTED: Maylandia zebra caspase-12-like (LOC101468196), mRNA	0.0418	-0.8076	down	-1.4319	down	-3.6091	down	-0.6243	down	-2.8015	down	-2.1772	down
MPF_LOC100692844.2.8	XM_003458212.1 PREDICTED: Oreochromis niloticus tripartite motifcontaining protein 16-like (LOC100692844), mRNA	0.0418	0.0000	down	-0.1575	down	0.7462	up	-0.1575	down	0.7462	up	0.9038	up
MPF_LOC100705802.1.1	XM_003457313.1 PREDICTED: Oreochromis niloticus transloconassociated protein subunit alpha-like, transcript variant 1 (LOC100705802), mRNA	0.0418	-0.0012	down	0.3191	up	0.5417	up	0.3203	up	0.5428	up	0.2226	up

MPF_LOC101478303.1.1	XM_004573593.1 PREDICTED: Maylandia zebra probable ribonuclease ZC3H12C-like (LOC101478303), transcript variant X2, mRNA	0.0418	-0.0883	down	0.1553	up	0.8436	up	0.2436	up	0.9319	up	0.6883	up
MPF_LOC100496164.7.12	XM_002937054.1 PREDICTED: Xenopus (Silurana) tropicalis hypothetical protein LOC100496164 (LOC100496164), mRNA	0.0418	-0.1777	down	0.1214	up	0.9010	up	0.2991	up	1.0787	up	0.7795	up
MPF_LOC101475578.1.1	XM_004555860.1 PREDICTED: Maylandia zebra RRP12-like protein-like (LOC101475578), transcript variant X1, mRNA	0.0418	0.0118	up	0.0406	up	1.0917	up	0.0287	up	1.0799	up	1.0511	up
MPF_LOC101465950.2.3	XM_004573375.1 PREDICTED: Maylandia zebra transcription initiation factor TFIID subunit 1-like (LOC101465950), transcript variant X5, mRNA	0.0418	0.1307	up	0.0945	up	0.9306	up	-0.0361	down	0.7999	up	0.8361	up
MPF_LOC101475397.1.1	XM_004541258.1 PREDICTED: Maylandia zebra double-stranded RNAspecific adenosine deaminase-like (LOC101475397), transcript variant X3, mRNA	0.0418	-0.3428	down	0.1037	up	0.6510	up	0.4465	up	0.9938	up	0.5473	up
MPF_contig_038119		0.0419	-0.1164	down	0.3172	up	0.8647	up	0.4336	up	0.9811	up	0.5475	up
MPF_LOC101470969.1.1	XM_004544876.1 PREDICTED: Maylandia zebra selenocysteine-specific elongation factor-like	0.0419	-0.1065	down	0.2886	up	0.8090	up	0.3951	up	0.9155	up	0.5203	up

	(LOC101470969), mRNA													
MPF_LOC101481605.1.1	XM_004544263.1 PREDICTED: Maylandia zebra transcription factor 7like 1-A-like (LOC101481605), transcript variant X2, mRNA	0.0419	0.0087	up	-0.0039	down	0.8404	up	-0.0126	down	0.8317	up	0.8443	up
MPF_MYCTH_2312519.1.1	XM_003667052.1 Myceliophthora thermophila ATCC 42464 hypothetical protein (MYCTH_2312519) mRNA, complete cds	0.0419	0.1475	up	-0.2531	down	0.9248	up	-0.4006	down	0.7772	up	1.1779	up
MPF_LOC100690858.1.1	XM_003451414.1 PREDICTED: Oreochromis niloticus uncharacterized protein C5orf4 homolog (LOC100690858), mRNA	0.0419	0.0993	up	0.3212	up	0.8393	up	0.2219	up	0.7400	up	0.5181	up
MPF_LOC100709414.1.1	XM_003442768.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100709414 (LOC100709414), mRNA	0.0419	-0.0918	down	0.2590	up	0.8652	up	0.3508	up	0.9570	up	0.6062	up
MPF_LOC101487373.24.24	XM_004576282.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101487373), mRNA	0.0419	-0.4746	down	-0.7233	down	-2.6183	down	-0.2487	down	-2.1436	down	-1.8949	down
MPF_LOC101469870.4.4	XM_004537942.1 PREDICTED: Maylandia zebra A disintegrin and metalloproteinase with thrombospondin motifs 8-like (LOC101469870), mRNA	0.0419	0.1777	up	0.0254	up	-0.4491	down	-0.1524	down	-0.6268	down	-0.4744	down

MPF_contig_020829		0.0419	-0.1543	down	-0.0054	down	0.5015	up	0.1489	up	0.6558	up	0.5069	up
MPF_LOC100698256.2.2	XM_003454320.1 PREDICTED: Oreochromis niloticus tubulin beta-6 chainlike (LOC100698256), mRNA	0.0419	0.1690	up	-0.5420	down	-2.0973	down	-0.7110	down	-2.2662	down	-1.5553	down
MPF_LOC101474595.2.2	XM_004556427.1 PREDICTED: Maylandia zebra ADP-ribosylation factorlike protein 6-interacting protein 1-like (LOC101474595), mRNA	0.0419	0.2115	up	0.3133	up	0.7813	up	0.1018	up	0.5698	up	0.4680	up
MPF_LOC101467851.1.5	XM_004568656.1 PREDICTED: Maylandia zebra chromobox protein homolog 1-like (LOC101467851), mRNA	0.0419	0.1708	up	0.2424	up	0.6950	up	0.0716	up	0.5242	up	0.4526	up
MPF_LOC101155904.1.1	XM_004065552.1 PREDICTED: Oryzias latipes uncharacterized LOC101155904 (LOC101155904), mRNA	0.0419	0.1305	up	0.1429	up	0.8993	up	0.0124	up	0.7689	up	0.7565	up
MPF_contig_007828	XM_004540693.1 PREDICTED: Maylandia zebra intraflagellar transport protein 43 homolog A-like (LOC101469972), transcript variant X2, mRNA	0.0419	0.0272	up	0.5284	up	0.8125	up	0.5012	up	0.7853	up	0.2842	up
MPF_LOC101477317.1.1	XM_004539502.1 PREDICTED: Maylandia zebra dimethyladenosine transferase 2, mitochondriallike (LOC101477317), mRNA	0.0419	-0.1175	down	0.1196	up	0.6965	up	0.2371	up	0.8140	up	0.5769	up

MPF_LOC101487812.1.3	XM_004569359.1 PREDICTED: Maylandia zebra microtubule-associated serine/threonine-protein kinase 2-like (LOC101487812), transcript variant X6, mRNA	0.0419	0.2363	up	0.3510	up	0.8034	up	0.1147	up	0.5671	up	0.4524	up
MPF_contig_033833		0.0419	-0.3180	down	0.0090	up	-1.1077	down	0.3270	up	-0.7897	down	-1.1167	down
MPF_LOC101483732.1.1	XM_004541934.1 PREDICTED: Maylandia zebra TATA box-binding protein-like protein 1-like (LOC101483732), transcript variant X3, mRNA	0.0419	-0.0215	down	0.2351	up	0.8882	up	0.2566	up	0.9097	up	0.6530	up
MPF_LOC101475667.1.1	XM_004555321.1 PREDICTED: Maylandia zebra AP-1 complex subunit mu-1-like (LOC101475667), mRNA	0.0419	0.1862	up	0.2133	up	0.6783	up	0.0271	up	0.4921	up	0.4649	up
MPF_LOC100703589.1.1	XM_003460117.1 PREDICTED: Oreochromis niloticus plasminogen activator inhibitor 1-like (LOC100703589), mRNA	0.0419	-1.3006	down	-3.0857	down	-5.0992	down	-1.7851	down	-3.7986	down	-2.0135	down
MPF_LOC100706560.2.2	XM_003449154.1 PREDICTED: Oreochromis niloticus mitogen-activated protein kinase 13-like (LOC100706560), mRNA	0.0419	0.2989	up	0.2986	up	0.9722	up	-0.0003	down	0.6732	up	0.6735	up
MPF_COX3.3.3	[BBH] COX3_GADMO (sp|P55777) Cytochrome c oxidase subunit 3 OS=Gadus morhua GN=mt-co3 PE=3 SV=1	0.0419	0.0250	up	0.2473	up	1.2009	up	0.2223	up	1.1759	up	0.9536	up

MPF_LOC101465200.2.2	XM_004558426.1 PREDICTED: Maylandia zebra trinucleotide repeatcontaining gene 6C proteinlike (LOC101465200), transcript variant X4, mRNA	0.0419	0.0936	up	0.3039	up	1.0356	up	0.2104	up	0.9420	up	0.7317	up
MPF_LOC101465613.1.1	XM_004544760.1 PREDICTED: Maylandia zebra SUZ domain-containing protein 1-like (LOC101465613), mRNA	0.0419	-0.3550	down	0.3447	up	-0.7303	down	0.6997	up	-0.3753	down	-1.0750	down
MPF_LOC100698625.18.22	XM_003456694.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100698625), mRNA	0.0419	0.1016	up	0.1733	up	0.9952	up	0.0717	up	0.8935	up	0.8219	up
MPF_SRRM2.14.15	SRRM2_MOUSE (sp|Q8BTI8) Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3	0.0419	0.2112	up	-0.7456	down	-2.7922	down	-0.9568	down	-3.0034	down	-2.0466	down
MPF_LOC101487908.2.3	XM_004546898.1 PREDICTED: Maylandia zebra rab effector MyRIP-like (LOC101487908), mRNA	0.0419	-0.2914	down	0.0116	up	1.2292	up	0.3030	up	1.5206	up	1.2176	up
MPF_LOC101479518.3.5	XM_004570668.1 PREDICTED: Maylandia zebra alpha-actinin-3-like (LOC101479518), mRNA	0.0419	-0.5100	down	-1.3556	down	-2.7286	down	-0.8456	down	-2.2186	down	-1.3730	down
MPF_LOC100711758.1.1	XP_003448892.1 PREDICTED: TRMT1-like protein-like [Oreochromis niloticus]	0.0419	0.1266	up	0.6295	up	0.9126	up	0.5029	up	0.7860	up	0.2831	up
MPF_contig_003866		0.0419	-0.0148	down	0.1922	up	0.6089	up	0.2070	up	0.6237	up	0.4167	up

MPF_LOC100695054.1.1	XM_003452186.1 PREDICTED: Oreochromis niloticus condensin complex subunit 3-like (LOC100695054), mRNA	0.0419	-0.0314	down	0.2796	up	0.8997	up	0.3111	up	0.9312	up	0.6201	up
MPF_LOC101474461.1.1	XM_004546190.1 PREDICTED: Maylandia zebra ataxin-1-like (LOC101474461), transcript variant X2, mRNA	0.0419	-0.6619	down	-1.2096	down	-2.7453	down	-0.5477	down	-2.0834	down	-1.5357	down
MPF_contig_000006		0.0419	0.6929	up	0.7324	up	-1.2915	down	0.0395	up	-1.9844	down	-2.0239	down
MPF_LOC100700653.1.1	XP_003448440.1 PREDICTED: REM2- and Rab-like small GTPase 1-like [Oreochromis niloticus]	0.0419	-0.0046	down	0.1775	up	0.9303	up	0.1822	up	0.9350	up	0.7528	up
MPF_contig_018953		0.0419	0.0116	up	0.3445	up	0.7572	up	0.3328	up	0.7456	up	0.4128	up
MPF_contig_037441		0.0419	-0.0017	down	0.1970	up	0.7694	up	0.1987	up	0.7711	up	0.5724	up
MPF_contig_037377		0.0419	-0.1369	down	-0.0913	down	0.7760	up	0.0456	up	0.9130	up	0.8674	up
MPF_LOC101072513.1.1	XP_003977218.1 PREDICTED: transmembrane protein 223-like [Takifugu rubripes]	0.0419	0.1579	up	0.4570	up	1.0404	up	0.2991	up	0.8825	up	0.5833	up
MPF_LOC101469611.1.3	XM_004544219.1 PREDICTED: Maylandia zebra nuclear receptor RORbeta-like (LOC101469611), transcript variant X3, mRNA	0.0419	0.0827	up	0.1581	up	0.8084	up	0.0754	up	0.7257	up	0.6503	up

MPF_contig_025001	XM_004551159.1 PREDICTED: Maylandia zebra probable E3 ubiquitinprotein ligase DTX2-like (LOC101480294), transcript variant X1, mRNA	0.0419	-0.3030	down	-0.3861	down	0.6505	up	-0.0831	down	0.9535	up	1.0366	up
MPF_LOC100705400.2.2	XP_003441709.1 PREDICTED: hypothetical protein LOC100705400 [Oreochromis niloticus]	0.0419	-0.0200	down	-0.4332	down	-1.2076	down	-0.4132	down	-1.1876	down	-0.7744	down
MPF_contig_027842		0.0419	-0.0928	down	0.1330	up	0.5383	up	0.2257	up	0.6311	up	0.4054	up
MPF_LOC101477393.1.1	XM_004559371.1 PREDICTED: Maylandia zebra sarcalumenin-like (LOC101477393), transcript variant X2, mRNA	0.0419	-0.1027	down	0.3497	up	0.8297	up	0.4525	up	0.9325	up	0.4800	up
MPF_LOC101466535.2.3	XM_004574367.1 PREDICTED: Maylandia zebra R3H domain-containing protein 4-like (LOC101466535), mRNA	0.0419	0.0340	up	0.1227	up	0.6423	up	0.0888	up	0.6083	up	0.5196	up
MPF_LOC100701400.1.1	XM_003453836.1 PREDICTED: Oreochromis niloticus 5formyltetrahydrofolate cycloligase-like (LOC100701400), mRNA	0.0419	-0.0386	down	0.6005	up	0.9183	up	0.6391	up	0.9569	up	0.3179	up
MPF_LOC100712461.1.1	XM_003446184.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100712461 (LOC100712461), mRNA	0.0419	-0.1589	down	-0.0952	down	1.0162	up	0.0638	up	1.1751	up	1.1113	up

MPF_LOC101477952.1.2	XM_004553681.1 PREDICTED: Maylandia zebra transmembrane protein 33-like (LOC101477952), mRNA	0.0419	-0.2542	down	-0.0434	down	0.7481	up	0.2108	up	1.0023	up	0.7915	up
MPF_LOC101483967.1.1	XM_004553054.1 PREDICTED: Maylandia zebra E3 SUMO-protein ligase PIAS1-like (LOC101483967), mRNA	0.0419	-0.1033	down	0.0673	up	0.7668	up	0.1706	up	0.8700	up	0.6995	up
MPF_LOC101484239.1.1	XM_004551175.1 PREDICTED: Maylandia zebra protein EMSY-like (LOC101484239), transcript variant X1, mRNA	0.0419	-0.0460	down	0.1550	up	0.8410	up	0.2011	up	0.8870	up	0.6859	up
MPF_LOC100696990.1.1	XM_003447956.1 PREDICTED: Oreochromis niloticus protein CYR61-like (LOC100696990), mRNA	0.0419	-0.0656	down	0.4072	up	0.8086	up	0.4728	up	0.8742	up	0.4014	up
MPF_LOC100711070.2.2	XM_003455767.1 PREDICTED: Oreochromis niloticus prefoldin subunit 6like (LOC100711070), mRNA	0.0420	0.3010	up	0.6165	up	0.9785	up	0.3154	up	0.6774	up	0.3620	up
MPF_LOC101487315.1.1	XM_004543356.1 PREDICTED: Maylandia zebra protocadherin-17-like (LOC101487315), transcript variant X1, mRNA	0.0420	0.0315	up	-0.1767	down	1.1921	up	-0.2082	down	1.1606	up	1.3687	up
MPF_LOC101463592.1.3	XM_004543454.1 PREDICTED: Maylandia zebra high affinity cAMPspecific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A-like (LOC101463592), mRNA	0.0421	-0.1754	down	-0.1510	down	0.5962	up	0.0244	up	0.7716	up	0.7472	up

MPF_LOC100709523.2.2	XP_003448801.1 PREDICTED: UPF0539 protein C7orf59 homolog isoform 1 [Oreochromis niloticus] ref|XP_003448802.1| PREDICTED: UPF0539 protein C7orf59 homolog isoform 2 [Oreochromis niloticus]	0.0421	-0.1158	down	0.2200	up	0.5304	up	0.3358	up	0.6462	up	0.3104	up
MPF_LOC101475088.1.1	XM_004563653.1 PREDICTED: Maylandia zebra DNA polymerase sigmalike (LOC101475088), transcrip variant X2, mRNA	0.0421	-0.2006	down	0.0722	up	0.8480	up	0.2728	up	1.0486	up	0.7758	up
MPF_contig_005232		0.0421	-0.1088	down	0.0336	up	0.9299	up	0.1425	up	1.0387	up	0.8963	up
MPF_contig_026412		0.0421	-0.0879	down	-0.1186	down	0.5638	up	-0.0307	down	0.6517	up	0.6824	up
MPF_ZG20.1.1	ZG20_XENLA (sp|P18714) Gastrula zinc finger protein xFG20-1 OS=Xenopus laevis PE=3 SV=2	0.0421	0.1398	up	0.2889	up	1.2479	up	0.1490	up	1.1081	up	0.9591	up
MPF_ZN214.7.8	ZN214_HUMAN (sp|Q9UL59) Zinc finger protein 214 OS=Homo sapiens GN=ZNF214 PE=2 SV=2	0.0421	0.0490	up	0.2257	up	0.8097	up	0.1767	up	0.7608	up	0.5840	up
MPF_LOC101483414.2.3	XM_004562959.1 PREDICTED: Maylandia zebra microtubule-associated serine/threonine-protein kinase 1-like (LOC101483414), mRNA	0.0421	0.0229	up	0.1008	up	0.6680	up	0.0779	up	0.6451	up	0.5672	up

MPF_LOC100698107.1.1	XM_003459012.1 PREDICTED: Oreochromis niloticus U3 small nucleolar ribonucleoprotein protein IMP4-like (LOC100698107), mRNA	0.0421	0.0142	up	0.2441	up	0.7406	up	0.2299	up	0.7264	up	0.4965	up
MPF_LOC100702208.1.7	XM_003452776.1 PREDICTED: Oreochromis niloticus zinc-binding protein A33-like (LOC100702208), mRNA	0.0421	-0.0184	down	0.3170	up	0.6610	up	0.3355	up	0.6795	up	0.3440	up
MPF_LOC100709883.1.1	XP_003447642.1 PREDICTED: nitrilase homolog 1-like [Oreochromis niloticus]	0.0421	0.1091	up	0.2151	up	0.6527	up	0.1060	up	0.5436	up	0.4376	up
MPF_LOC101476169.2.2	XM_004561593.1 PREDICTED: Maylandia zebra EF-hand domaincontaining family member A1like (LOC101476169), mRNA	0.0421	-0.1964	down	0.2082	up	0.4552	up	0.4046	up	0.6516	up	0.2470	up
MPF_LOC101464732.3.3	XM_004538651.1 PREDICTED: Maylandia zebra F-box only protein 48like (LOC101464732), mRNA	0.0421	-0.3554	down	0.2314	up	0.6763	up	0.5868	up	1.0317	up	0.4449	up
MPF_LECG.4.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.0421	1.0346	up	-3.0536	down	-4.0868	down	-4.0881	down	-5.1214	down	-1.0333	down
MPF_LOC101483176.1.1	XM_004548925.1 PREDICTED: Maylandia zebra claspin-like (LOC101483176), transcript variant X1, mRNA	0.0421	-0.1235	down	0.0838	up	0.9712	up	0.2073	up	1.0947	up	0.8875	up

MPF_LOC100705728.6.17	XM_003459563.1 PREDICTED: Oreochromis niloticus zinc finger protein RFP-like (LOC100705728), mRNA	0.0421	0.2616	up	0.5019	up	0.6928	up	0.2403	up	0.4312	up	0.1908	up
MPF_SNR40.1.1	SNR40_MOUSE (sp|Q6PE01) U5 small nuclear ribonucleoprotein 40 kDa protein OS=Mus musculus GN=Snrnp40 PE=2 SV=1	0.0421	-0.1453	down	0.1999	up	0.8538	up	0.3451	up	0.9990	up	0.6539	up
MPF_CELF2.4.8	[BBH] CELF2_DANRE (sp|Q6P0B1) CUGBP Elavlike family member 2 OS=Danio rerio GN=celf2 PE=2 SV=1	0.0421	-0.3762	down	-0.0385	down	0.6511	up	0.3377	up	1.0273	up	0.6896	up
MPF_LOC101472081.1.1	XM_004564098.1 PREDICTED: Maylandia zebra probable ATPdependent RNA helicase DDX4-like (LOC101472081), transcript variant X1, mRNA	0.0421	-0.0860	down	-0.4856	down	0.8904	up	-0.3995	down	0.9764	up	1.3759	up
MPF_LOC101163898.2.2	XP_004070391.1 PREDICTED: ATP synthase subunit epsilon, mitochondrial-like [Oryzias latipes]	0.0421	-0.0360	down	0.0434	up	0.6920	up	0.0794	up	0.7280	up	0.6486	up
MPF_LOC101469266.2.2	XM_004548320.1 PREDICTED: Maylandia zebra SCY1-like protein 2like (LOC101469266), mRNA	0.0421	-0.1406	down	0.0881	up	0.8803	up	0.2287	up	1.0209	up	0.7921	up
MPF_LOC101470756.1.1	XM_004540502.1 PREDICTED: Maylandia zebra membrane-bound Oacyltransferase domaincontaining protein 2-like (LOC101470756), mRNA	0.0421	-0.1896	down	-0.1151	down	0.8621	up	0.0746	up	1.0517	up	0.9771	up

MPF_LOC101468420.1.2	XM_004559700.1 PREDICTED: Maylandia zebra inactive tyrosineprotein kinase 7-like (LOC101468420), mRNA	0.0421	0.2825	up	0.4400	up	0.9860	up	0.1576	up	0.7035	up	0.5460	up
MPF_LOC101484486.1.1	XM_004571906.1 PREDICTED: Maylandia zebra protein FAM83D-like (LOC101484486), mRNA	0.0421	0.0749	up	0.1374	up	0.9164	up	0.0625	up	0.8415	up	0.7790	up
MPF_LOC101465889.2.3	XM_004563621.1 PREDICTED: Maylandia zebra rho guanine nucleotide exchange factor 37-like (LOC101465889), transcript variant X5, mRNA	0.0422	-0.1410	down	0.0192	up	0.6560	up	0.1602	up	0.7970	up	0.6368	up
MPF_LOC100695994.36.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.0422	-0.1207	down	0.0886	up	0.9248	up	0.2093	up	1.0455	up	0.8362	up
MPF_LOC101173672.1.1	XM_004084030.1 PREDICTED: Oryzias latipes protein SCO2 homolog, mitochondrial-like (LOC101173672), mRNA	0.0422	-0.0293	down	0.0548	up	0.8445	up	0.0841	up	0.8739	up	0.7898	up
MPF_LOC101466805.1.1	XM_004574191.1 PREDICTED: Maylandia zebra general transcription factor IIH subunit 2-like (LOC101466805), transcript variant X2, mRNA	0.0422	-0.0954	down	0.1836	up	1.1785	up	0.2790	up	1.2740	up	0.9950	up
MPF_LOC100706031.1.1	XP_003449200.1 PREDICTED: PQ-loop repeatcontaining protein 2-like [Oreochromis niloticus]	0.0424	-0.0962	down	0.3260	up	0.7774	up	0.4222	up	0.8737	up	0.4514	up

MPF_LOC101471734.2.2	XM_004545073.1 PREDICTED: Maylandia zebra dual specificity tyrosinephosphorylation-regulated kinase 2-like (LOC101471734), transcript variant X3, mRNA	0.0424	0.4228	up	0.2938	up	0.9633	up	-0.1290	down	0.5405	up	0.6695	up
MPF_LEG8.1.2	NP_001133778.1 Galectin-8 [Salmo salar]	0.0424	-0.2331	down	0.1357	up	0.5844	up	0.3689	up	0.8175	up	0.4486	up
MPF_contig_029570		0.0424	-0.0163	down	-0.9105	down	-2.8057	down	-0.8942	down	-2.7894	down	-1.8952	down
MPF_LOC101169293.5.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0.0424	-0.1674	down	0.1713	up	-1.8773	down	0.3388	up	-1.7099	down	-2.0486	down
MPF_LOC101478340.1.2	XM_004540060.1 PREDICTED: Maylandia zebra dual specificity protein phosphatase 23-like (LOC101478340), transcript variant X3, mRNA	0.0424	0.0087	up	0.0317	up	0.5094	up	0.0230	up	0.5007	up	0.4777	up
MPF_LOC101484591.2.3	XM_004552405.1 PREDICTED: Maylandia zebra ataxin-7-like protein 3like (LOC101484591), transcript variant X2, mRNA	0.0424	-0.1372	down	0.3996	up	1.3952	up	0.5368	up	1.5325	up	0.9957	up
MPF_contig_044710		0.0424	0.0147	up	0.2702	up	0.6345	up	0.2555	up	0.6198	up	0.3643	up
MPF_LOC101479185.1.1	XM_004540346.1 PREDICTED: Maylandia zebra phospholipase DDHD1like (LOC101479185), transcript variant X2, mRNA	0.0424	-0.3613	down	0.0036	up	0.8138	up	0.3648	up	1.1751	up	0.8102	up

MPF_LOC101466761.1.1	XM_004564446.1 PREDICTED: Maylandia zebra transmembrane and TPR repeat-containing protein 3-like (LOC101466761), transcript variant X2, mRNA	0.0424	-0.0499	down	-0.0166	down	0.8067	up	0.0334	up	0.8566	up	0.8232	up
MPF_contig_019019		0.0424	-0.1363	down	0.0750	up	0.7273	up	0.2113	up	0.8636	up	0.6523	up
MPF_LOC101474859.5.2 1	XM_004575478.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 4like (LOC101474859), transcript variant X2, mRNA	0.0424	0.1564	up	0.0869	up	-0.5994	down	-0.0694	down	-0.7558	down	-0.6863	down
MPF_LOC100701856.1.1	XP_003455042.1 PREDICTED: V-type proton ATPase subunit B, brain isoform-like [Oreochromis niloticus]	0.0424	0.0831	up	0.3179	up	0.5927	up	0.2348	up	0.5096	up	0.2747	up
MPF_contig_029673		0.0424	0.2148	up	-0.3308	down	-2.3148	down	-0.5456	down	-2.5296	down	-1.9840	down
MPF_LOC101163263.1.1	XP_004075057.1 PREDICTED: galactose-1phosphate uridylyltransferaselike [Oryzias latipes]	0.0425	0.0224	up	0.2778	up	0.6212	up	0.2553	up	0.5988	up	0.3434	up
MPF_contig_005052		0.0425	-0.1807	down	0.5820	up	1.2512	up	0.7628	up	1.4319	up	0.6692	up
MPF_contig_032375		0.0425	-0.0259	down	0.1691	up	0.8276	up	0.1951	up	0.8535	up	0.6584	up
MPF_LOC101071953.1.2	XP_003966121.1 PREDICTED: maternal B9.15 protein-like [Takifugu rubripes]	0.0425	-0.0325	down	0.2222	up	0.7539	up	0.2546	up	0.7864	up	0.5317	up
MPF_ZN345.1.3	ZN345_HUMAN (sp|Q14585) Zinc finger protein 345 OS=Homo sapiens GN=ZNF345 PE=2 SV=1	0.0425	0.0471	up	0.5499	up	1.8342	up	0.5028	up	1.7871	up	1.2843	up

MPF_LOC101484189.1.1	XM_004542778.1 PREDICTED: Maylandia zebra zinc finger protein 830like (LOC101484189), mRNA	0.0425	-0.0095	down	0.4162	up	0.7175	up	0.4256	up	0.7270	up	0.3014	up
MPF_contig_019453	XM_004546174.1 PREDICTED: Maylandia zebra RAF proto-oncogene serine/threonine-protein kinase-like (LOC101470685), transcript variant X1, mRNA	0.0426	0.2484	up	0.3134	up	1.2981	up	0.0650	up	1.0497	up	0.9847	up
MPF_LOC101466143.10.18	XM_004574840.1 PREDICTED: Maylandia zebra 40S ribosomal protein S18-like (LOC101466143), mRNA	0.0426	0.0979	up	0.1983	up	0.5855	up	0.1004	up	0.4876	up	0.3872	up
MPF_LOC100693501.1.2	XP_003440491.1 PREDICTED: 3-hydroxyacylCoA dehydratase-like [Oreochromis niloticus]	0.0426	0.0352	up	0.3484	up	0.5811	up	0.3133	up	0.5459	up	0.2326	up
MPF_contig_044700		0.0426	-0.1778	down	0.0128	up	0.6322	up	0.1906	up	0.8100	up	0.6194	up
MPF_LOC101464577.1.1	XM_004547080.1 PREDICTED: Maylandia zebra betaine--homocysteine S-methyltransferase 1-like (LOC101464577), mRNA	0.0427	-0.1471	down	-0.1003	down	0.9042	up	0.0468	up	1.0513	up	1.0044	up
MPF_LOC101464185.3.11	XM_004543268.1 PREDICTED: Maylandia zebra ferritin, heavy subunitlike (LOC101464185), transcript variant X1, mRNA	0.0427	-0.2068	down	0.1300	up	0.7410	up	0.3368	up	0.9478	up	0.6110	up

MPF_LOC101473634.1.1	XM_004559539.1 PREDICTED: Maylandia zebra queuine tRNAribosyltransferase-like (LOC101473634), mRNA	0.0428	0.0739	up	0.3650	up	0.9266	up	0.2910	up	0.8527	up	0.5616	up
MPF_LOC100694159.1.1	XM_003448615.1 PREDICTED: Oreochromis niloticus hexokinase-2-like (LOC100694159), mRNA	0.0428	0.0055	up	0.4535	up	1.2394	up	0.4480	up	1.2339	up	0.7859	up
MPF_LOC101475607.1.1	XM_004566845.1 PREDICTED: Maylandia zebra basic helix-loop-helix transcription factor scleraxislike (LOC101475607), mRNA	0.0428	-0.1337	down	-0.2267	down	0.5673	up	-0.0930	down	0.7009	up	0.7940	up
MPF_LOC101484010.1.1	XR_190959.1 PREDICTED: Maylandia zebra homeoboxcontaining protein 1-like (LOC101484010), transcript variant X6, misc_RNA	0.0428	0.0455	up	0.0846	up	0.9791	up	0.0391	up	0.9336	up	0.8945	up
MPF_TEKT2.4.5	NM_001017432.3 Danio rerio tektin 2 (testicular) (tekt2), mRNA gb|BC093125.1| Danio rerio zgc:111885, mRNA (cDNA clone MGC:111885 IMAGE:7402307), complete cds	0.0428	-0.2200	down	0.1128	up	-1.1544	down	0.3329	up	-0.9343	down	-1.2672	down
MPF_LOC101473750.1.1	XM_004564384.1 PREDICTED: Maylandia zebra uncharacterized LOC101473750 (LOC101473750), mRNA	0.0428	-0.1339	down	0.3080	up	1.1743	up	0.4418	up	1.3081	up	0.8663	up

MPF_LOC101480346.1.4	XM_004567337.1 PREDICTED: Maylandia zebra myotubularin-related protein 3-like (LOC101480346), transcript variant X4, mRNA	0.0428	0.1075	up	0.2356	up	0.9450	up	0.1281	up	0.8375	up	0.7094	up
MPF_LOC100695509.1.1	XM_003454804.1 PREDICTED: Oreochromis niloticus rab5 GDP/GTP exchange factor-like (LOC100695509), mRNA	0.0428	0.0262	up	0.4066	up	0.8296	up	0.3804	up	0.8034	up	0.4230	up
MPF_contig_020782		0.0428	0.0009	up	0.1186	up	0.4879	up	0.1177	up	0.4870	up	0.3693	up
MPF_LOC101464117.1.1	XM_004572292.1 PREDICTED: Maylandia zebra solute carrier family 12 member 7-like (LOC101464117), transcript variant X3, mRNA	0.0428	-0.3063	down	-1.0835	down	-2.6162	down	-0.7772	down	-2.3099	down	-1.5327	down
MPF_LOC101078738.1.1	XP_003961123.1 PREDICTED: syntaxin-4-like [Takifugu rubripes]	0.0428	0.1828	up	-0.2494	down	1.0813	up	-0.4321	down	0.8985	up	1.3307	up
MPF_LOC101471132.1.1	XM_004541239.1 PREDICTED: Maylandia zebra 28S ribosomal protein S29, mitochondrial-like (LOC101471132), transcript variant X1, mRNA	0.0428	0.0239	up	0.4172	up	1.1502	up	0.3932	up	1.1263	up	0.7331	up
MPF_RS15A.1.5	[BBH] RS15A_RAT (sp|P62246) 40S ribosomal protein S15a OS=Rattus norvegicus GN=Rps15a PE=1 SV=2	0.0429	-0.0502	down	-0.4858	down	-1.6153	down	-0.4356	down	-1.5651	down	-1.1295	down
MPF_LOC100702817.2.3	XM_003449140.1 PREDICTED: Oreochromis niloticus intermediate filament protein ON3-like	0.0429	-0.3336	down	-2.5040	down	-4.6758	down	-2.1704	down	-4.3422	down	-2.1719	down

	(LOC100702817), mRNA													
MPF_LOC101482455.1.1	XM_004559215.1 PREDICTED: Maylandia zebra gap junction gamma-1 protein-like (LOC101482455), mRNA	0.0429	-0.0811	down	0.0616	up	0.7090	up	0.1427	up	0.7902	up	0.6475	up
MPF_LOC101471187.1.1	XM_004552253.1 PREDICTED: Maylandia zebra ADP-ribosylation factor 1-like (LOC101471187), mRNA	0.0429	-0.1649	down	0.3013	up	0.5948	up	0.4662	up	0.7597	up	0.2935	up
MPF_FUK.2.2	FUK_HUMAN (sp|Q8N0W3) L-fucose kinase OS=Homo sapiens GN=FUK PE=2 SV=2	0.0429	-0.2751	down	-0.4715	down	-1.2365	down	-0.1964	down	-0.9614	down	-0.7650	down
MPF_contig_003872		0.0429	-0.0243	down	-0.0954	down	0.8901	up	-0.0711	down	0.9144	up	0.9855	up
MPF_SI_DKEYP38G8.5.1.1	NP_001116762.1 uncharacterized protein LOC568385 [Danio rerio]	0.0429	0.0406	up	0.2567	up	0.6863	up	0.2161	up	0.6457	up	0.4296	up
MPF_contig_015414		0.0429	-0.0022	down	0.2312	up	0.8039	up	0.2334	up	0.8062	up	0.5728	up
MPF_contig_031726		0.0429	-0.0034	down	0.2705	up	0.9465	up	0.2739	up	0.9498	up	0.6760	up
MPF_POL3.2.3	POL3_DROME (sp|P04323) Retrovirus-related Pol polyprotein from transposon 17.6 OS=Drosophila melanogaster GN=pol PE=4 SV=1	0.0429	-0.0244	down	0.2606	up	0.9335	up	0.2851	up	0.9579	up	0.6729	up

MPF_LOC100634711.1.2	XP_003391247.1 PREDICTED: hypothetical protein LOC100634711 [Amphimedon queenslandica]	0.0429	-0.1524	down	-0.6072	down	-1.9294	down	-0.4548	down	-1.7770	down	-1.3222	down
MPF_ZN845.1.1	ZN845_HUMAN (sp|Q96IR2) Zinc finger protein 845 OS=Homo sapiens GN=ZNF845 PE=2 SV=3	0.0429	0.3003	up	0.3483	up	0.8654	up	0.0480	up	0.5651	up	0.5171	up
MPF_LOC100710520.3.3	XM_003451402.1 PREDICTED: Oreochromis niloticus transcription factor 7like 2-like (LOC100710520), mRNA	0.0429	0.1234	up	0.1834	up	0.8474	up	0.0600	up	0.7240	up	0.6640	up
MPF_LOC101473238.1.1	XM_004575788.1 PREDICTED: Maylandia zebra homocysteineresponsive endoplasmic reticulum-resident ubiquitinlike domain member 1 proteinlike (LOC101473238), mRNA	0.0429	0.2890	up	0.6040	up	1.5044	up	0.3150	up	1.2154	up	0.9003	up
MPF_contig_039665	XM_004573329.1 PREDICTED: Maylandia zebra poliovirus receptorrelated protein 3-like (LOC101479710), transcript variant X1, mRNA	0.0429	0.2816	up	0.3250	up	1.2359	up	0.0433	up	0.9543	up	0.9109	up

MPF_LOC100709151.1.1	XM_003443494.1 PREDICTED: Oreochromis niloticus forkhead box protein H1-like (LOC100709151), mRNA	0.0429	-0.1959	down	0.0970	up	-0.9755	down	0.2929	up	-0.7796	down	-1.0725	down

MPF_LOC100706747.1.1	XM_003446414.1 PREDICTED: Oreochromis niloticus enoyl-CoA delta isomerase 1, mitochondriallike (LOC100706747), mRNA	0.0430	0.0655	up	0.0128	up	0.6408	up	-0.0527	down	0.5753	up	0.6280	up
MPF_LOC101487987.1.1	XM_004543163.1 PREDICTED: Maylandia zebra switch-associated protein 70-like (LOC101487987), mRNA	0.0430	0.1167	up	-0.0219	down	1.0712	up	-0.1386	down	0.9545	up	1.0931	up
MPF_contig_010205		0.0430	-0.0577	down	0.0926	up	0.5771	up	0.1503	up	0.6349	up	0.4846	up
MPF_LOC100711796.2.4	XM_003459356.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100711796 (LOC100711796), mRNA	0.0430	-0.0748	down	-0.9090	down	-2.7785	down	-0.8342	down	-2.7037	down	-1.8695	down
MPF_LOC101482482.5.5	XM_004566239.1 PREDICTED: Maylandia zebra TGF-beta-activated kinase 1 and MAP3K7binding protein 2-like (LOC101482482), transcript variant X5, mRNA	0.0430	0.2031	up	0.1743	up	0.7820	up	-0.0288	down	0.5789	up	0.6077	up
MPF_contig_039525		0.0430	-0.0662	down	-0.1240	down	0.9529	up	-0.0578	down	1.0192	up	1.0770	up
MPF_LOC101480149.1.1	XM_004542668.1 PREDICTED: Maylandia zebra serine--pyruvate aminotransferase, mitochondrial-like (LOC101480149), mRNA	0.0430	-0.1611	down	0.2587	up	0.7765	up	0.4198	up	0.9376	up	0.5178	up
MPF_contig_042980		0.0431	0.0708	up	0.1129	up	0.9681	up	0.0420	up	0.8973	up	0.8552	up

MPF_LOC101475504.1.1	XM_004544142.1 PREDICTED: Maylandia zebra solute carrier family 15 member 4-like (LOC101475504), mRNA	0.0431	-0.1246	down	-0.3818	down	1.0729	up	-0.2572	down	1.1975	up	1.4546	up
MPF_LOC101481563.1.1	XM_004556453.1 PREDICTED: Maylandia zebra heat shock 70 kDa protein 1-like (LOC101481563), mRNA	0.0431	0.0927	up	0.0771	up	0.4780	up	-0.0156	down	0.3853	up	0.4010	up
MPF_LOC101062709.2.3	XM_003972629.1 PREDICTED: Takifugu rubripes beta-2-microglobulinlike (LOC101062709), mRNA	0.0431	0.5880	up	-0.7402	down	-1.6706	down	-1.3282	down	-2.2587	down	-0.9305	down
MPF_LOC101470559.5.6	XM_004542366.1 PREDICTED: Maylandia zebra ATPase family AAA domain-containing protein 2Blike (LOC101470559), mRNA	0.0431	-0.1481	down	0.2451	up	0.7571	up	0.3932	up	0.9052	up	0.5120	up
MPF_LOC100701273.22.44	XM_003444228.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 12-like (LOC100701273), mRNA	0.0431	0.1249	up	0.5103	up	0.5482	up	0.3854	up	0.4233	up	0.0379	up
MPF_ZG57.7.12	ZG57_XENLA (sp|P18729) Gastrula zinc finger protein XlCGF57.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.0432	0.3154	up	0.5220	up	1.1271	up	0.2065	up	0.8116	up	0.6051	up

MPF_LOC101078751.2.2	XM_003963635.1 PREDICTED: Takifugu rubripes cytoplasmic tRNA 2thiolation protein 2-like (LOC101078751), mRNA	0.0432	-0.0708	down	0.0228	up	0.7487	up	0.0936	up	0.8195	up	0.7259	up
MPF_LOC101473980.1.1	XM_004546842.1 PREDICTED: Maylandia zebra leucine-rich repeatcontaining protein 14-like (LOC101473980), transcript variant X1, mRNA	0.0432	0.0118	up	0.3164	up	0.6991	up	0.3046	up	0.6873	up	0.3827	up
MPF_contig_019882		0.0432	0.4944	up	-0.0275	down	1.4068	up	-0.5219	down	0.9124	up	1.4343	up
MPF_contig_037397		0.0432	0.1714	up	0.0808	up	0.6342	up	-0.0906	down	0.4628	up	0.5534	up
MPF_LOC100695994.19.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.0432	0.1931	up	0.3152	up	2.0123	up	0.1222	up	1.8193	up	1.6971	up
MPF_LOC100694614.1.1	XP_003449742.1 PREDICTED: protein FRG1like isoform 1 [Oreochromis niloticus]	0.0432	0.2642	up	0.0811	up	0.7669	up	-0.1831	down	0.5027	up	0.6858	up
MPF_contig_023161		0.0432	-0.0705	down	0.1154	up	0.7331	up	0.1859	up	0.8035	up	0.6177	up
MPF_LOC101483484.1.1	XM_004553053.1 PREDICTED: Maylandia zebra mortality factor 4-like protein 1-like (LOC101483484), transcript variant X2, mRNA	0.0432	-0.2366	down	0.1638	up	0.5330	up	0.4003	up	0.7695	up	0.3692	up
MPF_contig_028611		0.0432	-0.1089	down	0.0464	up	0.4618	up	0.1553	up	0.5707	up	0.4154	up
MPF_contig_018990		0.0432	-0.0713	down	0.1517	up	0.5989	up	0.2230	up	0.6703	up	0.4473	up
MPF_contig_045500		0.0432	0.0019	up	0.6754	up	1.3906	up	0.6736	up	1.3887	up	0.7151	up

MPF_LOC101476588.2.2	XM_004569767.1 PREDICTED: Maylandia zebra CCR4-NOT transcription complex subunit 3-like (LOC101476588), transcript variant X2, mRNA	0.0432	0.0477	up	0.2759	up	0.6914	up	0.2282	up	0.6437	up	0.4155	up
MPF_ZN234.2.2	ZN234_HUMAN (sp|Q14588) Zinc finger protein 234 OS=Homo sapiens GN=ZNF234 PE=2 SV=3	0.0432	-0.2957	down	0.0150	up	1.6964	up	0.3107	up	1.9921	up	1.6814	up
MPF_contig_028802		0.0432	-0.1336	down	0.0438	up	0.4228	up	0.1775	up	0.5564	up	0.3789	up
MPF_LOC100697737.1.1	XP_003458594.1 PREDICTED: zinc finger MYM-type protein 4-like [Oreochromis niloticus]	0.0432	-0.0219	down	-0.0267	down	0.8048	up	-0.0047	down	0.8267	up	0.8315	up
MPF_LOC101474478.2.3	XM_004572875.1 PREDICTED: Maylandia zebra neuritin-like (LOC101474478), mRNA	0.0432	0.0674	up	-0.0125	down	-0.5664	down	-0.0799	down	-0.6338	down	-0.5539	down
MPF_contig_024477		0.0432	-0.0095	down	0.2566	up	1.5213	up	0.2661	up	1.5308	up	1.2647	up
MPF_LOC100696954.1.1	XM_003439695.1 PREDICTED: Oreochromis niloticus minor histocompatibility protein HA-1-like (LOC100696954), mRNA	0.0432	-0.0818	down	0.1591	up	0.7138	up	0.2409	up	0.7956	up	0.5548	up
MPF_LOC100703135.1.1	XM_003439550.1 PREDICTED: Oreochromis niloticus DNA replication complex GINS protein PSF3like (LOC100703135), mRNA	0.0432	-0.0059	down	0.4054	up	0.9160	up	0.4113	up	0.9219	up	0.5106	up

MPF_LOC101470650.1.2	XM_004540130.1 PREDICTED: Maylandia zebra nesprin-1-like (LOC101470650), transcript variant X2, mRNA	0.0433	-0.0275	down	-0.2500	down	-1.4095	down	-0.2225	down	-1.3819	down	-1.1595	down
MPF_contig_018225		0.0433	-0.0296	down	0.1329	up	0.5251	up	0.1624	up	0.5546	up	0.3922	up
MPF_LOC100694446.1.1	XP_003455177.1 PREDICTED: 3-hydroxy-3methylglutaryl-coenzyme A reductase-like [Oreochromis niloticus]	0.0433	-0.1889	down	0.2188	up	-0.8566	down	0.4077	up	-0.6677	down	-1.0754	down
MPF_contig_032386		0.0433	-0.0432	down	0.3977	up	1.0493	up	0.4409	up	1.0925	up	0.6516	up
MPF_LOC100707328.3.3	XM_003459711.1 PREDICTED: Oreochromis niloticus splicing factor 1-like, transcript variant 1 (LOC100707328), mRNA	0.0434	-0.1484	down	0.0769	up	1.2364	up	0.2253	up	1.3849	up	1.1596	up
MPF_contig_036640		0.0434	-0.0250	down	0.1219	up	0.4379	up	0.1469	up	0.4629	up	0.3160	up
MPF_LOC100703894.1.1	XP_003447861.1 PREDICTED: rho GTPaseactivating protein 11A-like [Oreochromis niloticus]	0.0434	-0.1835	down	0.1819	up	1.3797	up	0.3653	up	1.5632	up	1.1978	up
MPF_contig_035266		0.0434	0.0743	up	0.6150	up	1.1717	up	0.5407	up	1.0974	up	0.5567	up
MPF_LOC101157892.1.1	XM_004080497.1 PREDICTED: Oryzias latipes serine protease 27-like (LOC101157892), mRNA	0.0434	-0.0153	down	0.2614	up	1.0222	up	0.2767	up	1.0375	up	0.7608	up
MPF_contig_047370		0.0435	-0.1361	down	0.1184	up	0.5603	up	0.2545	up	0.6964	up	0.4419	up

MPF_LOC101476280.1.1	XM_004563657.1 PREDICTED: Maylandia zebra tRNA (cytosine(34)C(5))-methyltransferase-like (LOC101476280), transcript variant X1, mRNA	0.0435	-0.1724	down	0.1991	up	0.8560	up	0.3715	up	1.0284	up	0.6569	up
MPF_LOC101471926.2.2	XM_004543101.1 PREDICTED: Maylandia zebra zinc finger protein 821like (LOC101471926), transcript variant X5, mRNA	0.0435	-0.1695	down	0.2863	up	1.2152	up	0.4558	up	1.3847	up	0.9290	up
MPF_contig_044118		0.0435	0.0673	up	-0.0379	down	0.8987	up	-0.1051	down	0.8314	up	0.9365	up
MPF_ZNF84.5.14	ZNF84_HUMAN (sp|P51523) Zinc finger protein 84 OS=Homo sapiens GN=ZNF84 PE=1 SV=2	0.0435	0.0187	up	0.1309	up	1.0715	up	0.1123	up	1.0528	up	0.9405	up
MPF_LOC101071815.1.1	XP_003969208.1 PREDICTED: lysosomal protein NCU-G1-like [Takifugu rubripes]	0.0435	-0.0995	down	0.2806	up	0.7079	up	0.3801	up	0.8074	up	0.4273	up
MPF_contig_036850		0.0436	-1.3550	down	-0.9905	down	-2.7036	down	0.3645	up	-1.3486	down	-1.7131	down
MPF_LOC100711483.3.3	XP_003448809.1 PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11-like [Oreochromis niloticus]	0.0437	-0.1328	down	0.2061	up	0.9040	up	0.3389	up	1.0368	up	0.6979	up
MPF_LOC101474911.1.1	XM_004566844.1 PREDICTED: Maylandia zebra B-cell receptor CD22like (LOC101474911), transcript variant X3, mRNA	0.0437	-0.4039	down	-1.6449	down	-2.9634	down	-1.2410	down	-2.5595	down	-1.3185	down

MPF_contig_031014	XM_004549212.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 10like (LOC101485347), transcript variant X1, mRNA	0.0437	-0.2140	down	-0.1445	down	0.8394	up	0.0695	up	1.0533	up	0.9839	up
MPF_LOC100708962.1.1	XP_003442474.1 PREDICTED: importin subunit beta-1-like [Oreochromis niloticus]	0.0438	-0.1285	down	0.1804	up	0.7288	up	0.3089	up	0.8573	up	0.5484	up
MPF_LOC101467994.1.1	XR_191159.1 PREDICTED: Maylandia zebra synaptotagmin-14-like (LOC101467994), transcript variant X3, misc_RNA	0.0438	-0.1311	down	-0.2924	down	0.9896	up	-0.1614	down	1.1206	up	1.2820	up
MPF_LOC101481996.5.6	XM_004569599.1 PREDICTED: Maylandia zebra interferon regulatory factor 2-binding protein 1-like (LOC101481996), mRNA	0.0438	-0.1768	down	0.0391	up	0.5862	up	0.2160	up	0.7630	up	0.5471	up
MPF_LOC101075613.2.2	XP_003971057.1 PREDICTED: folliculininteracting protein 1-like [Takifugu rubripes]	0.0438	-0.0636	down	0.0420	up	0.9301	up	0.1056	up	0.9937	up	0.8881	up
MPF_LOC101467735.1.2	XM_004564544.1 PREDICTED: Maylandia zebra secretory carrierassociated membrane protein 2-like (LOC101467735), mRNA	0.0438	-0.1114	down	0.5913	up	1.2925	up	0.7028	up	1.4039	up	0.7012	up
MPF_LOC101470951.1.1	XM_004541051.1 PREDICTED: Maylandia zebra heterogeneous nuclear ribonucleoprotein H-like (LOC101470951), mRNA	0.0438	0.0592	up	0.1202	up	0.9685	up	0.0610	up	0.9093	up	0.8483	up

MPF_PPIA.1.6	PPIA_BLAGE (sp|P54985) Peptidyl-prolyl cis-trans isomerase OS=Blattella germanica GN=CYPA PE=2 SV=1	0.0438	0.0194	up	-0.0233	down	1.0068	up	-0.0428	down	0.9874	up	1.0302	up
MPF_LOC101077970.1.2	XM_003974514.1 PREDICTED: Takifugu rubripes tight junction protein ZO-2-like (LOC101077970), mRNA	0.0438	-0.0542	down	0.3612	up	0.5981	up	0.4154	up	0.6523	up	0.2369	up
MPF_contig_016470		0.0438	0.1062	up	0.1371	up	0.7365	up	0.0309	up	0.6303	up	0.5994	up
MPF_LOC100701988.2.2	XM_003442403.1 PREDICTED: Oreochromis niloticus CD2 antigen cytoplasmic tail-binding protein 2-like (LOC100701988), mRNA	0.0438	-0.0315	down	0.1405	up	1.1199	up	0.1720	up	1.1513	up	0.9793	up
MPF_LOC101471713.1.1	XM_004564280.1 PREDICTED: Maylandia zebra maternal embryonic leucine zipper kinase-like (LOC101471713), mRNA	0.0438	0.0640	up	0.5214	up	1.0537	up	0.4575	up	0.9898	up	0.5323	up
MPF_contig_025134	XM_004548413.1 PREDICTED: Maylandia zebra forkhead box protein M1-like (LOC101468468), transcript variant X1, mRNA	0.0438	-0.1374	down	-0.0391	down	0.7542	up	0.0983	up	0.8916	up	0.7934	up
MPF_LOC101174705.1.1	XP_004080443.1 PREDICTED: adenosine kinase-like isoform 2 [Oryzias latipes]	0.0438	0.2132	up	0.1490	up	0.8859	up	-0.0642	down	0.6727	up	0.7369	up
MPF_LOC101475728.1.1	XM_004547700.1 PREDICTED: Maylandia zebra immunoglobulin superfamily member 8-like	0.0438	-0.0961	down	0.3777	up	0.7494	up	0.4738	up	0.8455	up	0.3717	up

	(LOC101475728), mRNA													

MPF_contig_024716	XM_004542915.1 PREDICTED: Maylandia zebra FYVE and coiled-coil domain-containing protein 1like (LOC101469042), transcript variant X1, mRNA	0.0438	-0.0323	down	0.3640	up	0.9631	up	0.3963	up	0.9954	up	0.5991	up
MPF_contig_033328	XM_004545071.1 PREDICTED: Maylandia zebra dual specificity tyrosinephosphorylation-regulated kinase 2-like (LOC101471734), transcript variant X1, mRNA	0.0438	-0.1404	down	0.1683	up	0.7038	up	0.3087	up	0.8442	up	0.5355	up
MPF_LOC100701421.1.2	XM_003438032.1 PREDICTED: Oreochromis niloticus putative glycerol kinase 5-like (LOC100701421), mRNA	0.0438	0.0167	up	0.0980	up	0.8447	up	0.0813	up	0.8279	up	0.7467	up
MPF_LOC101171598.1.1	XM_004074880.1 PREDICTED: Oryzias latipes uncharacterized LOC101171598 (LOC101171598), mRNA	0.0438	0.1452	up	0.4514	up	1.0379	up	0.3063	up	0.8927	up	0.5865	up
MPF_contig_028002		0.0438	-0.1717	down	0.0946	up	0.7294	up	0.2663	up	0.9011	up	0.6347	up
MPF_LOC100701568.2.2	XP_003450260.1 PREDICTED: copine-3-like [Oreochromis niloticus]	0.0438	-0.2922	down	-0.1305	down	-1.5271	down	0.1617	up	-1.2349	down	-1.3966	down

MPF_LOC101477726.1.1	XM_004547886.1 PREDICTED: Maylandia zebra transformer-2 protein homolog alpha-like (LOC101477726), transcript variant X2, mRNA	0.0439	-0.6885	down	0.1946	up	1.0176	up	0.8832	up	1.7061	up	0.8229	up
MPF_contig_046161	XM_004559166.1 PREDICTED: Maylandia zebra PTB domain-containing engulfment adapter protein 1like (LOC101471107), transcript variant X1, mRNA	0.0439	0.0586	up	0.0768	up	0.8179	up	0.0182	up	0.7593	up	0.7411	up
MPF_contig_044372		0.0439	0.0867	up	-0.1667	down	-0.5174	down	-0.2534	down	-0.6041	down	-0.3507	down
MPF_contig_037717	XM_004569413.1 PREDICTED: Maylandia zebra seizure 6-like proteinlike (LOC101478650), transcript variant X2, mRNA	0.0439	-0.2034	down	0.6684	up	-0.9122	down	0.8718	up	-0.7087	down	-1.5805	down
MPF_contig_028414		0.0440	0.0337	up	0.2112	up	0.4175	up	0.1776	up	0.3838	up	0.2063	up
MPF_LOC100704053.4.12	XP_003440700.1 PREDICTED: ubiquitin-like protein FUBI-like [Oreochromis niloticus]	0.0440	-0.0295	down	-0.6049	down	-1.7907	down	-0.5753	down	-1.7612	down	-1.1858	down
MPF_LOC101486203.1.2	XM_004572644.1 PREDICTED: Maylandia zebra flotillin-1-like (LOC101486203), mRNA	0.0440	0.1220	up	-0.0009	down	1.4508	up	-0.1228	down	1.3288	up	1.4517	up
MPF_LOC100704115.1.1	XP_003457092.1 PREDICTED: E3 ubiquitinprotein ligase DTX3L-like [Oreochromis niloticus]	0.0440	-0.0299	down	0.2673	up	0.6760	up	0.2972	up	0.7058	up	0.4087	up

MPF_LOC101478656.1.1	XM_004546945.1 PREDICTED: Maylandia zebra terminal uridylyltransferase 7-like (LOC101478656), transcript variant X1, mRNA	0.0440	-0.1606	down	0.1438	up	0.8111	up	0.3044	up	0.9717	up	0.6673	up
MPF_contig_004034		0.0441	-0.0109	down	0.3082	up	0.5884	up	0.3190	up	0.5993	up	0.2802	up
MPF_contig_043239		0.0441	-0.2145	down	-0.0162	down	0.6555	up	0.1983	up	0.8700	up	0.6717	up
MPF_contig_011873		0.0442	-0.1451	down	0.6110	up	-0.8640	down	0.7561	up	-0.7188	down	-1.4750	down
MPF_contig_024970		0.0442	-0.1818	down	0.3157	up	0.7948	up	0.4975	up	0.9766	up	0.4792	up
MPF_LIN1.3.14	LIN1_NYCCO (sp|P08548) LINE-1 reverse transcriptase homolog OS=Nycticebus coucang PE=1 SV=1	0.0442	-0.0954	down	0.2119	up	0.3600	up	0.3073	up	0.4555	up	0.1481	up
MPF_RL13A.2.2	RL13A_SALTR (sp|Q91487) 60S ribosomal protein L13a (Fragment) OS=Salmo trutta GN=rpl13a PE=2 SV=1	0.0442	-0.1736	down	-0.3636	down	0.6656	up	-0.1900	down	0.8392	up	1.0292	up
MPF_LOC101165224.1.1	XP_004068265.1 PREDICTED: desmoplakin-like [Oryzias latipes]	0.0442	-0.4044	down	0.4066	up	0.6067	up	0.8111	up	1.0112	up	0.2001	up
MPF_LOC101161784.1.1	XP_004086111.1 PREDICTED: stathmin-4-like [Oryzias latipes]	0.0443	-0.1017	down	-0.0750	down	0.7497	up	0.0267	up	0.8514	up	0.8247	up
MPF_LOC101463600.1.1	XM_004544939.1 PREDICTED: Maylandia zebra class E basic helix-loophelix protein 40-like (LOC101463600), mRNA	0.0444	-0.2197	down	-0.2300	down	-1.4458	down	-0.0103	down	-1.2261	down	-1.2158	down

MPF_contig_033595	XM_004575490.1 PREDICTED: Maylandia zebra histone acetyltransferase p300-like (LOC101478121), transcript variant X2, mRNA	0.0444	0.1900	up	0.2639	up	0.8491	up	0.0739	up	0.6590	up	0.5852	up
MPF_contig_019803	XM_004548264.1 PREDICTED: Maylandia zebra plasma membrane calcium-transporting ATPase 1-like (LOC101479313), transcript variant X1, mRNA	0.0445	0.2239	up	0.3975	up	1.1204	up	0.1737	up	0.8965	up	0.7228	up
MPF_LOC101482272.1.1	XM_004564790.1 PREDICTED: Maylandia zebra probable ATPdependent RNA helicase DDX49-like (LOC101482272), mRNA	0.0445	-0.0329	down	-0.5209	down	-2.4199	down	-0.4881	down	-2.3871	down	-1.8990	down
MPF_LOC101112592.3.4	XP_004015912.1 PREDICTED: 40S ribosomal protein S15a-like [Ovis aries]	0.0445	0.2011	up	-0.2185	down	-1.0801	down	-0.4196	down	-1.2812	down	-0.8617	down
MPF_LOC100703703.2.2	XM_003443559.1 PREDICTED: Oreochromis niloticus ribosome biogenesis regulatory protein homolog (LOC100703703), mRNA	0.0445	0.2511	up	0.2736	up	0.6481	up	0.0225	up	0.3970	up	0.3745	up
MPF_LOC100703656.1.1	XP_003456112.1 PREDICTED: WD repeatcontaining protein 54-like [Oreochromis niloticus]	0.0445	0.2893	up	0.3337	up	0.7518	up	0.0444	up	0.4625	up	0.4181	up
MPF_contig_000095		0.0445	-0.2872	down	0.1876	up	0.8483	up	0.4747	up	1.1354	up	0.6607	up

MPF_LOC101167972.1.1	XM_004075428.1 PREDICTED: Oryzias latipes coiled-coil-helix-coiled-coilhelix domain-containing protein 2, mitochondrial-like (LOC101167972), mRNA	0.0445	0.1525	up	0.2883	up	0.8674	up	0.1358	up	0.7149	up	0.5791	up
MPF_LOC101487291.1.6	XM_004560239.1 PREDICTED: Maylandia zebra constitutive coactivator of PPAR-gamma-like protein 2-like (LOC101487291), mRNA	0.0445	0.2812	up	-0.0875	down	1.1826	up	-0.3687	down	0.9014	up	1.2702	up
MPF_EF1A.5.11	EF1A_ORYLA (sp|Q9YIC0) Elongation factor 1-alpha OS=Oryzias latipes GN=eef1a PE=2 SV=1	0.0445	0.0751	up	0.0224	up	-0.2340	down	-0.0527	down	-0.3091	down	-0.2564	down
MPF_LOC100701582.9.9	XP_003455288.1 PREDICTED: zinc finger protein 236-like [Oreochromis niloticus]	0.0445	-0.0785	down	0.1140	up	1.1253	up	0.1925	up	1.2038	up	1.0113	up
MPF_LOC101078280.1.1	XP_003977524.1 PREDICTED: ELAV-like protein 1-like isoform 2 [Takifugu rubripes]	0.0445	0.0569	up	0.3819	up	1.0319	up	0.3250	up	0.9750	up	0.6500	up
MPF_LOC101158596.1.1	XM_004067963.1 PREDICTED: Oryzias latipes probable cation-transporting ATPase 13A3-like (LOC101158596), mRNA	0.0445	0.0387	up	0.3708	up	0.8542	up	0.3321	up	0.8155	up	0.4834	up
MPF_LOC101482044.2.2	XM_004554969.1 PREDICTED: Maylandia zebra ubiquitin-conjugating enzyme E2 R2-like (LOC101482044), mRNA	0.0445	-0.2591	down	0.0783	up	0.8351	up	0.3374	up	1.0943	up	0.7569	up

MPF_LOC101475774.1.1	XM_004538970.1 PREDICTED: Maylandia zebra stromal membraneassociated protein 1-like (LOC101475774), mRNA	0.0446	-0.0373	down	0.0914	up	0.7126	up	0.1287	up	0.7499	up	0.6212	up
MPF_LOC101468177.1.1	XM_004548960.1 PREDICTED: Maylandia zebra histone-lysine Nmethyltransferase EHMT2like (LOC101468177), mRNA	0.0446	-0.0604	down	0.3133	up	0.9569	up	0.3737	up	1.0173	up	0.6435	up
MPF_LOC101485709.1.4	XM_004548564.1 PREDICTED: Maylandia zebra synapsin-1-like (LOC101485709), mRNA	0.0446	0.2250	up	0.3848	up	0.8977	up	0.1597	up	0.6727	up	0.5129	up
MPF_contig_039074	XM_004553126.1 PREDICTED: Maylandia zebra 40S ribosomal protein S27-like (LOC101477750), transcript variant X1, mRNA	0.0446	0.0917	up	0.1175	up	0.6780	up	0.0258	up	0.5863	up	0.5605	up
MPF_contig_018476		0.0446	-0.0924	down	0.8176	up	0.9683	up	0.9101	up	1.0608	up	0.1507	up
MPF_LOC100707420.1.1	XP_003439114.1 PREDICTED: UBX domain- containing protein 10-like [Oreochromis niloticus]	0.0446	-0.1156	down	-0.3729	down	0.9308	up	-0.2573	down	1.0464	up	1.3037	up
MPF_DDC.1.5	NM_213342.1 Danio rerio dopa decarboxylase (ddc), mRNA gb|BC056292.1| Danio rerio dopa decarboxylase, mRNA (cDNA clone MGC:65801 IMAGE:6791927), complete cds	0.0446	-0.0555	down	0.1193	up	0.7051	up	0.1749	up	0.7606	up	0.5857	up

MPF_LOC101476630.1.2	XM_004554857.1 PREDICTED: Maylandia zebra UDP-Nacetylhexosamine pyrophosphorylase-like (LOC101476630), transcript variant X2, mRNA	0.0449	0.2051	up	0.7010	up	1.3355	up	0.4959	up	1.1304	up	0.6345	up
MPF_contig_013999	XM_004567628.1 PREDICTED: Maylandia zebra regulator of G-protein signaling 20-like (LOC101484195), transcript variant X4, mRNA	0.0449	-0.3442	down	-1.2689	down	-2.3024	down	-0.9246	down	-1.9581	down	-1.0335	down
MPF_contig_037242		0.0449	-0.0451	down	-0.4049	down	-2.0128	down	-0.3598	down	-1.9677	down	-1.6080	down
MPF_LOC101474972.4.4	XM_004576316.1 PREDICTED: Maylandia zebra zinc finger protein 771like (LOC101474972), partial mRNA	0.0449	0.0072	up	0.1155	up	1.1377	up	0.1084	up	1.1306	up	1.0222	up
MPF_LOC101465139.2.2	XM_004544582.1 PREDICTED: Maylandia zebra WSC domain-containing protein 2-like (LOC101465139), transcript variant X2, mRNA	0.0449	0.0137	up	0.0536	up	0.7309	up	0.0399	up	0.7173	up	0.6774	up
MPF_LOC101479252.2.3	XM_004555147.1 PREDICTED: Maylandia zebra transmembrane protein 55B-A-like (LOC101479252), mRNA	0.0449	0.0993	up	0.2326	up	0.9353	up	0.1333	up	0.8360	up	0.7028	up
MPF_CICA.1.1	XP_003200581.1 PREDICTED: hypothetical protein LOC560266 [Danio rerio]	0.0449	0.0276	up	-0.5327	down	-0.9977	down	-0.5603	down	-1.0252	down	-0.4650	down

MPF_LOC101468902.2.2	XM_004561019.1 PREDICTED: Maylandia zebra thyroid hormone receptor beta-like (LOC101468902), transcript variant X5, mRNA	0.0449	-0.1697	down	-0.0225	down	0.9266	up	0.1473	up	1.0963	up	0.9491	up
MPF_LOC100701016.1.1	XP_003448688.1 PREDICTED: hypothetical protein LOC100701016 [Oreochromis niloticus]	0.0449	-0.0604	down	0.3314	up	0.9037	up	0.3918	up	0.9641	up	0.5723	up
MPF_contig_042733		0.0449	0.2936	up	0.2203	up	1.0973	up	-0.0732	down	0.8038	up	0.8770	up
MPF_LOC100702845.1.1	XP_003457274.1 PREDICTED: REST corepressor 1-like [Oreochromis niloticus]	0.0450	-0.1733	down	0.1548	up	0.7461	up	0.3281	up	0.9194	up	0.5913	up
MPF_UBC.1.5	UBC_RAT (sp|Q63429) Polyubiquitin-C OS=Rattus norvegicus GN=Ubc PE=1 SV=1	0.0450	0.2013	up	0.2593	up	0.3981	up	0.0580	up	0.1968	up	0.1388	up
MPF_contig_044782		0.0450	-0.1408	down	0.1493	up	0.6124	up	0.2901	up	0.7532	up	0.4631	up
MPF_LOC101479771.1.1	XM_004543232.1 PREDICTED: Maylandia zebra protein CASC4-like (LOC101479771), transcript variant X4, mRNA	0.0450	-0.1076	down	0.1711	up	0.7170	up	0.2787	up	0.8246	up	0.5459	up
MPF_contig_006233		0.0450	-0.1312	down	-0.2345	down	0.6975	up	-0.1033	down	0.8287	up	0.9320	up
MPF_MTA2.1.1	XP_003458453.1 PREDICTED: metastasisassociated protein MTA2 [Oreochromis niloticus]	0.0450	0.3056	up	0.3285	up	0.8017	up	0.0229	up	0.4961	up	0.4732	up
MPF_LOC100691137.1.1	XM_003455036.1 PREDICTED: Oreochromis niloticus golgin subfamily A member 1-like (LOC100691137), mRNA	0.0450	0.0207	up	0.3023	up	1.4623	up	0.2816	up	1.4416	up	1.1600	up

MPF_contig_023491		0.0450	0.0295	up	-0.0660	down	0.5268	up	-0.0955	down	0.4973	up	0.5928	up
MPF_contig_000307		0.0450	0.0505	up	0.1597	up	0.9008	up	0.1092	up	0.8503	up	0.7411	up
MPF_LOC100933241.19.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.0450	-0.3526	down	0.0771	up	1.2007	up	0.4297	up	1.5533	up	1.1236	up
MPF_LOC100705419.1.1	XP_003446703.1 PREDICTED: protein midA homolog, mitochondrial-like [Oreochromis niloticus]	0.0450	-0.0879	down	0.0601	up	0.9420	up	0.1480	up	1.0299	up	0.8819	up
MPF_LOC101474198.2.2	XM_004572414.1 PREDICTED: Maylandia zebra zinc finger protein 709like (LOC101474198), mRNA	0.0450	0.4440	up	0.7451	up	1.5814	up	0.3011	up	1.1375	up	0.8363	up
MPF_LOC101476819.6.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0.0450	0.3409	up	-0.4760	down	-2.2337	down	-0.8168	down	-2.5745	down	-1.7577	down
MPF_LOC101467663.1.1	XM_004545403.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 5like (LOC101467663), mRNA	0.0450	0.1882	up	0.4386	up	0.7563	up	0.2504	up	0.5682	up	0.3177	up
MPF_LOC100695149.1.1	XP_003450236.1 PREDICTED: ubiquitin carboxyl-terminal hydrolase 16-like [Oreochromis niloticus]	0.0450	-0.2115	down	-0.4933	down	-1.8228	down	-0.2818	down	-1.6113	down	-1.3295	down
MPF_contig_026549		0.0450	-0.0657	down	0.1327	up	0.3955	up	0.1984	up	0.4612	up	0.2628	up

MPF_contig_010356		0.0450	-0.1113	down	-0.1153	down	0.8003	up	-0.0040	down	0.9115	up	0.9155	up
MPF_LOC101474919.1.1	XM_004544715.1 PREDICTED: Maylandia zebra bone morphogenetic protein 1-like (LOC101474919), mRNA	0.0450	-0.0938	down	0.1129	up	1.1085	up	0.2067	up	1.2023	up	0.9956	up
MPF_contig_015804		0.0450	-0.0245	down	0.0285	up	0.5633	up	0.0530	up	0.5878	up	0.5348	up
MPF_LOC100703097.1.1	XM_003452630.1 PREDICTED: Oreochromis niloticus aspartate aminotransferase, cytoplasmic-like (LOC100703097), mRNA	0.0450	0.1060	up	0.2043	up	0.8007	up	0.0984	up	0.6947	up	0.5963	up
MPF_LOC101475765.2.2	XM_004558538.1 PREDICTED: Maylandia zebra peroxisome proliferatoractivated receptor gamma coactivator-related protein 1like (LOC101475765), transcript variant X2, mRNA	0.0450	0.4686	up	0.4443	up	1.4052	up	-0.0243	down	0.9366	up	0.9609	up
MPF_contig_018739		0.0450	0.3515	up	0.7468	up	-0.2323	down	0.3953	up	-0.5838	down	-0.9791	down
MPF_LOC100701849.3.5	XP_003453244.1 PREDICTED: hypothetical protein LOC100701849 [Oreochromis niloticus]	0.0450	0.4179	up	0.0985	up	0.8487	up	-0.3194	down	0.4307	up	0.7502	up
MPF_LOC100618182.3.3	XP_003340880.1 PREDICTED: zinc finger protein 345-like [Monodelphis domestica]	0.0451	-0.0028	down	0.0645	up	0.8204	up	0.0673	up	0.8232	up	0.7559	up

MPF_LOC101464118.1.2	XM_004548946.1 PREDICTED: Maylandia zebra sterile alpha motif domain-containing protein 12like (LOC101464118), transcript variant X2, mRNA	0.0451	0.0327	up	-0.1224	down	0.9426	up	-0.1551	down	0.9099	up	1.0650	up
MPF_LOC101485532.1.1	XM_004573748.1 PREDICTED: Maylandia zebra nuclear receptorinteracting protein 2-like (LOC101485532), mRNA	0.0451	0.2442	up	0.4392	up	1.1196	up	0.1950	up	0.8754	up	0.6804	up
MPF_contig_037253	XM_004575055.1 PREDICTED: Maylandia zebra probable palmitoyltransferase ZDHHC12-like (LOC101478118), transcript variant X1, mRNA	0.0451	-0.1892	down	0.6010	up	0.4242	up	0.7902	up	0.6135	up	-0.1768	down
MPF_LOC101466836.2.3	XM_004537932.1 PREDICTED: Maylandia zebra pleckstrin homologylike domain family B member 1-like (LOC101466836), mRNA	0.0451	0.0255	up	-0.0381	down	0.7446	up	-0.0636	down	0.7192	up	0.7828	up
MPF_MGN.1.1	MGN_RAT (sp|Q27W02) Protein mago nashi homolog OS=Rattus norvegicus GN=Magoh PE=2 SV=1	0.0451	-0.4352	down	-0.1870	down	0.5071	up	0.2482	up	0.9423	up	0.6941	up
MPF_LOC101074201.1.1	XM_003971402.1 PREDICTED: Takifugu rubripes creatine kinase Btype-like (LOC101074201), mRNA	0.0451	-0.0007	down	0.0632	up	1.0262	up	0.0639	up	1.0269	up	0.9630	up
MPF_LOC100689854.9.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0.0451	0.0674	up	0.1795	up	1.1552	up	0.1121	up	1.0878	up	0.9757	up

MPF_LOC101478400.1.4	XR_191224.1 PREDICTED: Maylandia zebra uncharacterized LOC101478400 (LOC101478400), misc_RNA	0.0451	0.6005	up	0.6925	up	-0.4533	down	0.0920	up	-1.0538	down	-1.1458	down
MPF_LOC100693621.3.4	XM_003448445.1 PREDICTED: Oreochromis niloticus medium-chain specific acyl-CoA dehydrogenase, mitochondrial-like (LOC100693621), mRNA	0.0451	-0.1202	down	-0.1214	down	0.8072	up	-0.0012	down	0.9274	up	0.9286	up
MPF_LOC101463657.2.2	XM_004557477.1 PREDICTED: Maylandia zebra cerebellar degeneration-related protein 2-like (LOC101463657), mRNA	0.0451	0.1027	up	0.0499	up	1.1123	up	-0.0528	down	1.0097	up	1.0625	up
MPF_contig_032110		0.0451	0.7041	up	-0.0492	down	1.3986	up	-0.7533	down	0.6945	up	1.4479	up
MPF_LOC100696950.1.1	XM_003438941.1 PREDICTED: Oreochromis niloticus sal-like protein 3-like (LOC100696950), mRNA	0.0451	0.1126	up	0.3130	up	0.8167	up	0.2003	up	0.7040	up	0.5037	up
MPF_LOC101074895.1.1	XP_003977078.1 PREDICTED: nocturnin-like [Takifugu rubripes]	0.0451	-0.2374	down	0.0670	up	0.8656	up	0.3044	up	1.1031	up	0.7986	up
MPF_LOC100706126.1.2	XM_003447163.1 PREDICTED: Oreochromis niloticus mediator of RNA polymerase II transcription subunit 30-like (LOC100706126), mRNA	0.0451	0.0933	up	0.1848	up	0.7540	up	0.0915	up	0.6607	up	0.5692	up

MPF_LOC101480339.1.7	XM_004565589.1 PREDICTED: Maylandia zebra neoverrucotoxin subunit alpha-like (LOC101480339), mRNA	0.0452	0.1225	up	0.4696	up	0.5529	up	0.3471	up	0.4304	up	0.0833	up
MPF_LOC100690062.1.2	XP_003454755.1 PREDICTED: CLIP-associating protein 1-like [Oreochromis niloticus]	0.0452	-0.0861	down	0.3149	up	1.4205	up	0.4009	up	1.5066	up	1.1057	up
MPF_contig_023396		0.0452	-0.1288	down	0.0339	up	0.5144	up	0.1627	up	0.6432	up	0.4805	up
MPF_LOC100705654.1.1	XM_003460057.1 PREDICTED: Oreochromis niloticus echinoderm microtubule-associated protein-like 6-like (LOC100705654), mRNA	0.0453	-0.0747	down	0.2348	up	0.8267	up	0.3096	up	0.9014	up	0.5919	up
MPF_contig_036789		0.0453	-1.0097	down	-1.2231	down	-2.5241	down	-0.2134	down	-1.5144	down	-1.3010	down
MPF_LOC100693211.1.1	XM_003437922.1 PREDICTED: Oreochromis niloticus kinesin-like protein KIF2C-like (LOC100693211), mRNA	0.0453	0.0046	up	0.1189	up	0.7302	up	0.1143	up	0.7256	up	0.6113	up
MPF_contig_014649		0.0453	-0.0145	down	0.0288	up	0.7441	up	0.0432	up	0.7586	up	0.7153	up
MPF_contig_041724		0.0453	0.4267	up	0.5350	up	1.2815	up	0.1083	up	0.8548	up	0.7464	up
MPF_contig_021646	XM_004551947.1 PREDICTED: Maylandia zebra protein CDV3 homolog (LOC101486605), transcript variant X1, mRNA	0.0453	0.2297	up	0.2473	up	0.8015	up	0.0176	up	0.5718	up	0.5542	up
MPF_contig_014860		0.0453	-0.0491	down	0.0957	up	0.7690	up	0.1448	up	0.8181	up	0.6733	up
MPF_contig_018885		0.0453	0.3684	up	0.2887	up	1.1329	up	-0.0797	down	0.7646	up	0.8442	up

MPF_contig_024739	XM_004075770.1 PREDICTED: Oryzias latipes arf-GAP domain and FG repeat-containing protein 1like, transcript variant 1 (LOC101155131), mRNA	0.0453	0.0423	up	0.1051	up	0.8125	up	0.0628	up	0.7702	up	0.7074	up
MPF_RNF220.1.3	XM_003456173.1 PREDICTED: Oreochromis niloticus ring finger protein 220 (RNF220), mRNA	0.0453	-0.0812	down	-0.1472	down	0.4825	up	-0.0660	down	0.5638	up	0.6297	up
MPF_LOC101484400.1.5	XM_004572910.1 PREDICTED: Maylandia zebra 60S ribosomal protein L22-like 1-like (LOC101484400), mRNA	0.0453	-0.2220	down	-1.2921	down	-2.7279	down	-1.0701	down	-2.5059	down	-1.4358	down
MPF_LOC100701951.1.1	XP_003454875.1 PREDICTED: tripartite motifcontaining protein 59-like [Oreochromis niloticus]	0.0453	-0.1633	down	0.0862	up	0.6091	up	0.2495	up	0.7724	up	0.5230	up
MPF_LOC100690119.15.18	XP_003448733.1 PREDICTED: zinc finger protein 16-like [Oreochromis niloticus]	0.0453	0.0258	up	0.1662	up	1.2040	up	0.1404	up	1.1782	up	1.0378	up
MPF_LOC100705745.3.3	XM_003442416.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100705745 (LOC100705745), mRNA	0.0453	-0.3938	down	-0.1285	down	-0.8309	down	0.2653	up	-0.4371	down	-0.7024	down
MPF_contig_031544	XM_004572462.1 PREDICTED: Maylandia zebra amphiphysin-like (LOC101485160), transcript variant X5, mRNA	0.0453	-0.2039	down	0.4471	up	0.5065	up	0.6510	up	0.7103	up	0.0593	up

MPF_LOC100702006.1.1	XM_003446313.1 PREDICTED: Oreochromis niloticus transmembrane protein 214-B-like (LOC100702006), mRNA	0.0453	-0.0033	down	0.2358	up	0.8397	up	0.2392	up	0.8431	up	0.6039	up
MPF_LOC101467444.3.3	XM_004569104.1 PREDICTED: Maylandia zebra RWD domain-containing protein 1-like (LOC101467444), mRNA	0.0453	0.0949	up	0.5942	up	-0.4129	down	0.4993	up	-0.5078	down	-1.0071	down
MPF_LOC101168690.1.1	XP_004086876.1 PREDICTED: acyl-CoAbinding domain-containing protein 5-like [Oryzias latipes]	0.0453	-0.0182	down	0.2358	up	0.7676	up	0.2541	up	0.7859	up	0.5318	up
MPF_LOC101487019.2.2	XM_004540473.1 PREDICTED: Maylandia zebra antimicrobial peptide NK-lysin-like (LOC101487019), mRNA	0.0454	-0.0451	down	-0.3779	down	-1.0805	down	-0.3328	down	-1.0354	down	-0.7026	down
MPF_LOC100696496.2.2	XM_003458306.1 PREDICTED: Oreochromis niloticus nucleolar protein 11like (LOC100696496), mRNA	0.0454	-0.0303	down	0.1772	up	0.7826	up	0.2076	up	0.8130	up	0.6054	up
MPF_ZO20.1.1	ZO20_XENLA (sp|P18744) Oocyte zinc finger protein XlCOF20 (Fragment) OS=Xenopus laevis PE=3 SV=1	0.0454	-0.0597	down	0.3140	up	0.8369	up	0.3737	up	0.8965	up	0.5228	up

MPF_LOC101464215.1.1	XM_004550655.1 PREDICTED: Maylandia zebra protein broad-mindedlike (LOC101464215), transcript variant X3, mRNA	0.0454	-0.0324	down	0.5333	up	1.0497	up	0.5657	up	1.0821	up	0.5164	up
MPF_LOC100699477.1.3	XM_003446549.1 PREDICTED: Oreochromis niloticus sodium/potassiumtransporting ATPase subunit alpha-1-like (LOC100699477), mRNA	0.0454	0.1646	up	0.3282	up	0.6747	up	0.1636	up	0.5101	up	0.3466	up
MPF_LOC101167345.3.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA	0.0454	0.0004	up	0.1574	up	1.3644	up	0.1570	up	1.3641	up	1.2071	up
MPF_LOC101478249.1.1	XM_004561870.1 PREDICTED: Maylandia zebra calcyphosin-like protein-like (LOC101478249), transcript variant X2, mRNA	0.0454	-0.0018	down	0.1213	up	0.5843	up	0.1231	up	0.5862	up	0.4631	up
MPF_TRIP4.1.1	XM_003450755.1 PREDICTED: Oreochromis niloticus thyroid hormone receptor interactor 4 (TRIP4), mRNA	0.0454	0.0547	up	0.2611	up	0.7864	up	0.2064	up	0.7317	up	0.5253	up
MPF_contig_010216		0.0454	-0.1452	down	0.1299	up	0.6575	up	0.2751	up	0.8026	up	0.5275	up
MPF_contig_018259		0.0454	0.2190	up	0.2923	up	1.0729	up	0.0733	up	0.8539	up	0.7806	up
MPF_LOC101069698.1.1	XM_003976368.1 PREDICTED: Takifugu rubripes ubiquitin carboxylterminal hydrolase CYLD-like	0.0454	0.0048	up	0.2579	up	0.6828	up	0.2530	up	0.6780	up	0.4250	up

	(LOC101069698), mRNA													
MPF_LOC101476871.1.3	XM_004569314.1 PREDICTED: Maylandia zebra nuclear factor 1 C-typelike (LOC101476871), transcript variant X2, mRNA	0.0454	0.4265	up	-0.4742	down	-2.5250	down	-0.9007	down	-2.9515	down	-2.0508	down
MPF_ZN425.2.2	ZN425_MACFA (sp|Q9N003) Zinc finger protein 425 (Fragment) OS=Macaca fascicularis GN=ZNF425 PE=2 SV=2	0.0454	0.1631	up	0.2225	up	1.2979	up	0.0595	up	1.1349	up	1.0754	up
MPF_LOC101474972.3.4	XM_004576316.1 PREDICTED: Maylandia zebra zinc finger protein 771like (LOC101474972), partial mRNA	0.0454	-0.0577	down	0.0382	up	1.0449	up	0.0959	up	1.1027	up	1.0068	up
MPF_LOC100711274.1.1	XP_003440891.1 PREDICTED: protein dispatched homolog 1-like [Oreochromis niloticus]	0.0454	-0.1242	down	-0.0632	down	0.7367	up	0.0610	up	0.8609	up	0.7999	up
MPF_LOC100689854.3.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0.0454	0.0451	up	0.1458	up	1.0690	up	0.1007	up	1.0239	up	0.9232	up
MPF_LOC101470644.1.1	XM_004561929.1 PREDICTED: Maylandia zebra pyrin-like (LOC101470644), mRNA	0.0454	-0.0781	down	0.2866	up	0.7362	up	0.3646	up	0.8143	up	0.4496	up
MPF_LOC100690401.3.3	XP_003454006.1 PREDICTED: hypothetical protein LOC100690401 [Oreochromis niloticus]	0.0454	0.1775	up	0.0581	up	0.6150	up	-0.1194	down	0.4375	up	0.5569	up

MPF_LOC101478855.1.1	XM_004550336.1 PREDICTED: Maylandia zebra leucine--tRNA ligase, cytoplasmic-like (LOC101478855), mRNA	0.0454	-0.0711	down	0.0616	up	0.5672	up	0.1327	up	0.6383	up	0.5056	up
MPF_LOC101469733.1.2	XM_004551213.1 PREDICTED: Maylandia zebra ubiquitin carboxylterminal hydrolase 2-like (LOC101469733), mRNA	0.0454	-0.1646	down	0.2541	up	0.5901	up	0.4187	up	0.7547	up	0.3361	up
MPF_LOC100709421.7.10	XM_003444588.1 PREDICTED: Oreochromis niloticus elongation factor 1gamma-like (LOC100709421), mRNA	0.0454	-0.6783	down	-0.5374	down	-1.2410	down	0.1410	up	-0.5627	down	-0.7036	down
MPF_contig_013193	XM_004563683.1 PREDICTED: Maylandia zebra KH domain-containing, RNA-binding, signal transduction-associated protein 1-like (LOC101482948), transcript variant X1, mRNA	0.0455	-0.2207	down	-0.0388	down	0.8235	up	0.1819	up	1.0442	up	0.8623	up
MPF_LOC101487020.1.1	XM_004540662.1 PREDICTED: Maylandia zebra autophagy-related protein 2 homolog B-like (LOC101487020), mRNA	0.0455	-0.2928	down	0.2001	up	0.5741	up	0.4929	up	0.8669	up	0.3739	up
MPF_LOC101468017.1.1	XM_004558791.1 PREDICTED: Maylandia zebra major facilitator superfamily domaincontaining protein 5-like (LOC101468017), mRNA	0.0455	-0.2299	down	0.2229	up	0.7925	up	0.4528	up	1.0224	up	0.5695	up

MPF_LOC101474977.2.2	XM_004554494.1 PREDICTED: Maylandia zebra collagen alpha-1(XXV) chain-like (LOC101474977), mRNA	0.0455	0.2968	up	0.3493	up	1.0452	up	0.0525	up	0.7484	up	0.6960	up
MPF_LOC100710689.1.1	XM_003452076.1 PREDICTED: Oreochromis niloticus GPN-loop GTPase 2like (LOC100710689), mRNA	0.0455	0.0639	up	0.1264	up	0.7371	up	0.0624	up	0.6732	up	0.6107	up
MPF_LOC100697359.1.1	XP_003451740.1 PREDICTED: rab5 GDP/GTP exchange factor-like [Oreochromis niloticus]	0.0455	-0.1363	down	0.2183	up	0.7817	up	0.3546	up	0.9179	up	0.5633	up
MPF_LOC101484888.2.2	XM_004556830.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 7-like (LOC101484888), mRNA	0.0455	0.4884	up	0.6169	up	1.0120	up	0.1284	up	0.5235	up	0.3951	up
MPF_LOC101169321.1.1	XP_004080336.1 PREDICTED: myosin regulatory light chain 2, skeletal muscle isoform-like [Oryzias latipes]	0.0455	0.2968	up	-0.1106	down	1.5413	up	-0.4074	down	1.2445	up	1.6518	up
MPF_LOC100690119.9.1 8	XP_003448733.1 PREDICTED: zinc finger protein 16-like [Oreochromis niloticus]	0.0455	-0.0555	down	0.0673	up	0.9464	up	0.1227	up	1.0019	up	0.8791	up
MPF_LOC101487433.1.2	XM_004546237.1 PREDICTED: Maylandia zebra poly(rC)-binding protein 2-like (LOC101487433), transcript variant X3, mRNA	0.0455	0.0998	up	-0.1511	down	0.8200	up	-0.2509	down	0.7202	up	0.9712	up

MPF_LOC100703996.2.2	XM_003450220.1 PREDICTED: Oreochromis niloticus armadillo repeatcontaining protein 4-like (LOC100703996), mRNA	0.0455	0.4464	up	0.7388	up	1.2373	up	0.2924	up	0.7908	up	0.4985	up
MPF_LOC100696893.2.2	XM_003447708.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100696893 (LOC100696893), mRNA	0.0455	-0.2418	down	-0.0881	down	0.8320	up	0.1537	up	1.0738	up	0.9201	up
MPF_LOC101157468.1.1	XM_004074359.1 PREDICTED: Oryzias latipes uncharacterized LOC101157468 (LOC101157468), mRNA	0.0455	-0.0851	down	0.0497	up	0.8383	up	0.1348	up	0.9234	up	0.7886	up
MPF_LOC101483918.1.2	XM_004543720.1 PREDICTED: Maylandia zebra serine/threonineprotein kinase SIK2-like (LOC101483918), mRNA	0.0455	-0.0662	down	0.1391	up	0.9998	up	0.2053	up	1.0661	up	0.8608	up
MPF_LOC101155548.2.3	XM_004080009.1 PREDICTED: Oryzias latipes eukaryotic initiation factor 4AI-like (LOC101155548), mRNA	0.0455	-0.0155	down	0.2907	up	0.4130	up	0.3062	up	0.4285	up	0.1223	up
MPF_LOC100697328.1.1	XM_003443448.1 PREDICTED: Oreochromis niloticus cathepsin O-like (LOC100697328), mRNA	0.0456	0.0919	up	0.5163	up	1.2137	up	0.4244	up	1.1218	up	0.6974	up
MPF_LOC100535897.1.1	XP_003198487.1 PREDICTED: zinc finger protein 729-like [Danio rerio]	0.0456	-0.0396	down	0.0451	up	0.6117	up	0.0846	up	0.6513	up	0.5667	up

MPF_NBEAL1.1.1	XP_003440955.1 PREDICTED: neurobeachinlike protein 1 [Oreochromis niloticus]	0.0456	0.0481	up	0.4871	up	1.3668	up	0.4390	up	1.3187	up	0.8797	up
MPF_LOC100701582.4.9	XP_003455288.1 PREDICTED: zinc finger protein 236-like [Oreochromis niloticus]	0.0456	-0.0647	down	0.0398	up	1.0643	up	0.1045	up	1.1290	up	1.0245	up
MPF_contig_029864	XM_004540792.1 PREDICTED: Maylandia zebra centrosomal protein of 170 kDa protein B-like (LOC101470655), transcript variant X1, mRNA	0.0457	-0.1753	down	0.1802	up	0.9528	up	0.3555	up	1.1281	up	0.7726	up
MPF_ZN714.1.1	ZN714_HUMAN (sp|Q96N38) Zinc finger protein 714 OS=Homo sapiens GN=ZNF714 PE=2 SV=2	0.0457	0.1779	up	0.3418	up	1.1310	up	0.1639	up	0.9531	up	0.7892	up
MPF_PVRL1.6.9	NM_001146661.1 Salmo salar Poliovirus receptorrelated protein 1 (pvrl1), mRNA gb|BT057409.1| Salmo salar clone ssal-rgb2614-164 Poliovirus receptorrelated protein 1 precursor putative mRNA, complete cds	0.0457	0.1037	up	0.3402	up	0.6302	up	0.2365	up	0.5264	up	0.2900	up
MPF_contig_007341		0.0457	-0.0005	down	-0.0955	down	0.6556	up	-0.0949	down	0.6562	up	0.7511	up
MPF_LOC101479287.2.2	XM_004542104.1 PREDICTED: Maylandia zebra N-alphaacetyltransferase 30-like (LOC101479287), mRNA	0.0457	-0.1168	down	0.2647	up	1.0409	up	0.3815	up	1.1577	up	0.7763	up
MPF_LOC101472185.1.1	XM_004540318.1 PREDICTED: Maylandia zebra small ubiquitin-related modifier 3-like (LOC101472185), mRNA	0.0457	-0.1820	down	0.2528	up	0.5673	up	0.4348	up	0.7493	up	0.3145	up

MPF_LOC100695046.1.1	XM_003449864.1 PREDICTED: Oreochromis niloticus pleckstrin homology domain-containing family G member 1-like (LOC100695046), mRNA	0.0457	0.1618	up	0.2994	up	1.3511	up	0.1376	up	1.1894	up	1.0518	up
MPF_ZN271.2.19	ZN271_HUMAN (sp|Q14591) Zinc finger protein 271 OS=Homo sapiens GN=ZNF271 PE=2 SV=4	0.0457	0.0188	up	0.1979	up	0.8320	up	0.1791	up	0.8132	up	0.6341	up
MPF_LOC101476629.1.1	XM_004554227.1 PREDICTED: Maylandia zebra SPRY domain-containing SOCS box protein 1-like (LOC101476629), mRNA	0.0457	-0.2044	down	0.0581	up	0.8205	up	0.2624	up	1.0248	up	0.7624	up
MPF_contig_047843		0.0457	-0.0683	down	0.0629	up	0.5306	up	0.1312	up	0.5989	up	0.4677	up
MPF_LOC100712032.1.1	XM_003451995.1 PREDICTED: Oreochromis niloticus centrosomal protein of 55 kDa-like (LOC100712032), mRNA	0.0457	0.0049	up	0.1321	up	0.8974	up	0.1273	up	0.8925	up	0.7652	up
MPF_LOC579970.1.1	XP_785151.3 PREDICTED: uncharacterized protein LOC579970 [Strongylocentrotus purpuratus]	0.0458	-0.1381	down	-0.4347	down	0.9425	up	-0.2966	down	1.0806	up	1.3772	up
MPF_LOC101478456.1.1	XM_004545288.1 PREDICTED: Maylandia zebra prickle-like protein 2like (LOC101478456), transcript variant X2, mRNA	0.0458	-0.1992	down	0.0151	up	0.8329	up	0.2144	up	1.0321	up	0.8177	up

MPF_contig_023536		0.0458	-0.0730	down	0.0231	up	0.6712	up	0.0961	up	0.7442	up	0.6481	up
MPF_LECG.42.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.0458	0.2824	up	-2.6250	down	-4.1395	down	-2.9073	down	-4.4219	down	-1.5145	down
MPF_LOC101473888.1.1	XM_004545269.1 PREDICTED: Maylandia zebra otopetrin-1-like (LOC101473888), mRNA	0.0458	-0.1292	down	0.2366	up	0.7797	up	0.3657	up	0.9088	up	0.5431	up
MPF_contig_045776		0.0458	-0.0279	down	0.0641	up	0.7175	up	0.0920	up	0.7454	up	0.6534	up
MPF_LOC101472031.3.3	XM_004571147.1 PREDICTED: Maylandia zebra exosome complex component RRP40-like (LOC101472031), mRNA	0.0458	-0.0849	down	0.2024	up	0.8674	up	0.2873	up	0.9523	up	0.6650	up
MPF_LRP2.2.4	LRP2_HUMAN (sp|P98164) Low-density lipoprotein receptor-related protein 2 OS=Homo sapiens GN=LRP2 PE=1 SV=3	0.0459	-0.0094	down	-0.3116	down	1.0533	up	-0.3022	down	1.0626	up	1.3649	up
MPF_contig_008801		0.0459	0.0222	up	0.0907	up	0.9683	up	0.0684	up	0.9461	up	0.8776	up
MPF_contig_048765		0.0459	0.0402	up	0.1752	up	0.6597	up	0.1349	up	0.6194	up	0.4845	up
MPF_LOC101170497.8.8	XP_004086004.1 PREDICTED: oocyte zinc finger protein XlCOF6-like [Oryzias latipes]	0.0459	-0.1405	down	-0.0445	down	1.2223	up	0.0960	up	1.3629	up	1.2669	up
MPF_contig_017500		0.0459	0.0260	up	0.3286	up	0.8421	up	0.3026	up	0.8162	up	0.5135	up
MPF_LOC100704418.1.1	XM_003445158.1 PREDICTED: Oreochromis niloticus transmembrane 9 superfamily member 2-like	0.0459	-0.0732	down	-0.0613	down	0.5302	up	0.0119	up	0.6034	up	0.5915	up

	(LOC100704418), mRNA													
MPF_LOC101475483.1.1	XM_004539773.1 PREDICTED: Maylandia zebra bifunctional glutamate/proline--tRNA ligase-like (LOC101475483), transcript variant X2, mRNA	0.0459	-0.0652	down	0.1738	up	0.6182	up	0.2390	up	0.6834	up	0.4444	up
MPF_NEMVEDRAFT_V1G74223.1.1	XP_001630293.1 predicted protein [Nematostella vectensis]	0.0459	0.0171	up	0.1808	up	0.4567	up	0.1637	up	0.4396	up	0.2760	up
MPF_LOC101475658.2.4	XM_004552544.1 PREDICTED: Maylandia zebra neurobeachin-like protein 1-like (LOC101475658), mRNA	0.0460	-0.1425	down	0.2172	up	0.8696	up	0.3597	up	1.0121	up	0.6524	up
MPF_contig_030947	XM_004572764.1 PREDICTED: Maylandia zebra agrin-like (LOC101470011), transcript variant X2, mRNA	0.0460	0.1830	up	-1.0749	down	-2.7576	down	-1.2579	down	-2.9405	down	-1.6827	down
MPF_contig_028400		0.0460	-0.0934	down	-0.0147	down	0.6601	up	0.0787	up	0.7536	up	0.6748	up
MPF_contig_035217		0.0460	-0.1480	down	0.4498	up	1.4923	up	0.5977	up	1.6403	up	1.0426	up
MPF_LOC101467051.1.1	XM_004544493.1 PREDICTED: Maylandia zebra ectopic P granules protein 5 homolog (LOC101467051), transcript variant X2, mRNA	0.0460	-0.2361	down	0.2207	up	0.9433	up	0.4568	up	1.1795	up	0.7227	up
MPF_LOC101484014.1.1	XM_004566976.1 PREDICTED: Maylandia zebra metal transporter CNNM4-like	0.0460	0.1860	up	0.3448	up	0.8151	up	0.1588	up	0.6291	up	0.4703	up

	(LOC101484014), transcript variant X2, mRNA													
MPF_LOC101468137.1.1	XM_004540589.1 PREDICTED: Maylandia zebra charged multivesicular body protein 3-like (LOC101468137), mRNA	0.0460	0.1332	up	0.2605	up	0.9215	up	0.1273	up	0.7883	up	0.6610	up
MPF_LOC100692693.1.1	XP_003442669.1 PREDICTED: protein SANDlike [Oreochromis niloticus]	0.0460	0.0213	up	0.1560	up	0.7357	up	0.1347	up	0.7145	up	0.5797	up
MPF_contig_015041		0.0460	0.2594	up	0.2543	up	1.5125	up	-0.0051	down	1.2530	up	1.2582	up
MPF_LOC101473574.7.7	XM_004564566.1 PREDICTED: Maylandia zebra 60S ribosomal protein L27a-like (LOC101473574), mRNA	0.0460	-0.2498	down	-0.8767	down	-2.1382	down	-0.6269	down	-1.8884	down	-1.2615	down
MPF_LOC101476819.5.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0.0460	0.7274	up	-0.7437	down	-2.7832	down	-1.4711	down	-3.5107	down	-2.0396	down
MPF_LOC101482421.1.1	XM_004551262.1 PREDICTED: Maylandia zebra MIT domain-containing protein 1-like (LOC101482421), mRNA	0.0460	-0.0628	down	0.4432	up	0.8427	up	0.5061	up	0.9055	up	0.3995	up
MPF_LOC101064361.1.1	XM_003976044.1 PREDICTED: Takifugu	0.0460	-0.1205	down	1.2062	up	0.6398	up	1.3267	up	0.7603	up	-0.5664	down

	rubripes tetraspanin-9-like (LOC101064361), mRNA													
MPF_LOC101473258.1.1	XM_004556246.1 PREDICTED: Maylandia zebra craniofacial development protein 1-like (LOC101473258), mRNA	0.0460	-0.1159	down	-0.0873	down	0.8812	up	0.0286	up	0.9971	up	0.9685	up
MPF_LOC101485847.1.1	XR_190889.1 PREDICTED: Maylandia zebra hematological and neurological expressed 1 protein-like (LOC101485847), transcript variant X2, misc_RNA	0.0460	-0.3385	down	0.5142	up	0.3696	up	0.8527	up	0.7081	up	-0.1446	down
MPF_LOC101479961.1.1	XM_004544000.1 PREDICTED: Maylandia zebra bromodomain and WD repeat-containing protein 1like (LOC101479961), transcript variant X2, mRNA	0.0460	0.0057	up	-0.1051	down	0.7898	up	-0.1109	down	0.7841	up	0.8949	up
MPF_LOC101077384.1.1	XP_003961117.1 PREDICTED: receptor activity-modifying protein 3like [Takifugu rubripes]	0.0460	0.0239	up	0.2447	up	0.4524	up	0.2208	up	0.4285	up	0.2077	up
MPF_LOC100695345.1.1	XP_003457247.1 PREDICTED: protein transport protein Sec23A-like [Oreochromis niloticus]	0.0460	0.1652	up	0.1695	up	0.4688	up	0.0043	up	0.3036	up	0.2993	up
MPF_LOC100709523.1.2	XP_003448801.1 PREDICTED: UPF0539 protein C7orf59 homolog isoform 1 [Oreochromis niloticus] ref|XP_003448802.1| PREDICTED: UPF0539	0.0460	-0.0683	down	0.2816	up	0.5694	up	0.3499	up	0.6376	up	0.2878	up

	protein C7orf59 homolog isoform 2 [Oreochromis niloticus]													
MPF_LOC101466250.1.1	XM_004575281.1 PREDICTED: Maylandia zebra apoptotic chromatin condensation inducer in the nucleus-like (LOC101466250), mRNA	0.0460	-0.0237	down	0.2836	up	0.9145	up	0.3072	up	0.9381	up	0.6309	up
MPF_LOC101169532.18.45	XP_004070110.1 PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Oryzias latipes]	0.0460	-0.8877	down	-0.3838	down	-2.3487	down	0.5039	up	-1.4610	down	-1.9649	down
MPF_LOC101467393.6.6	XM_004557584.1 PREDICTED: Maylandia zebra zinc finger CCCH domain-containing protein 7Blike (LOC101467393), mRNA	0.0460	-0.1778	down	0.1532	up	0.5789	up	0.3311	up	0.7567	up	0.4257	up
MPF_LOC101484509.1.3	XM_004552208.1 PREDICTED: Maylandia zebra ubiquitin carboxylterminal hydrolase 31-like (LOC101484509), mRNA	0.0460	-0.1219	down	0.3036	up	1.7337	up	0.4254	up	1.8556	up	1.4301	up
MPF_LOC101483861.2.2	XM_004549388.1 PREDICTED: Maylandia zebra centlein-like (LOC101483861), transcript variant X2, mRNA	0.0460	0.0490	up	0.3585	up	0.9111	up	0.3095	up	0.8621	up	0.5526	up

MPF_contig_035224	XM_004568483.1 PREDICTED: Maylandia zebra copine-3-like (LOC101469901), transcript variant X1, mRNA	0.0460	-0.1888	down	-0.1602	down	-1.4278	down	0.0285	up	-1.2390	down	-1.2675	down
MPF_LOC100691446.1.1	XM_003443937.1 PREDICTED: Oreochromis niloticus Fanconi anemia group F protein-like (LOC100691446), mRNA	0.0461	-0.0252	down	0.2870	up	1.0203	up	0.3122	up	1.0456	up	0.7334	up
MPF_LOC101472936.1.2	XM_004553303.1 PREDICTED: Maylandia zebra FERM domain-containing protein 4A-like (LOC101472936), mRNA	0.0461	0.1015	up	-0.3759	down	-2.0257	down	-0.4775	down	-2.1272	down	-1.6498	down
MPF_LOC101478089.1.1	XM_004544632.1 PREDICTED: Maylandia zebra S-adenosylmethionine synthase isoform type-2-like (LOC101478089), mRNA	0.0461	-0.1834	down	-0.1212	down	0.8858	up	0.0622	up	1.0692	up	1.0070	up
MPF_LOC101480093.2.8	XM_004574589.1 PREDICTED: Maylandia zebra tripartite motifcontaining protein 16-like (LOC101480093), mRNA	0.0461	0.1531	up	0.1101	up	0.7622	up	-0.0430	down	0.6090	up	0.6521	up
MPF_LOC100689895.3.13	XP_003459184.1 PREDICTED: coxsackievirus and adenovirus receptor homolog [Oreochromis niloticus]	0.0461	-0.2144	down	-0.3444	down	-2.1010	down	-0.1300	down	-1.8866	down	-1.7565	down
MPF_LOC101159718.1.1	XM_004084187.1 PREDICTED: Oryzias latipes protein preY, mitochondriallike (LOC101159718), mRNA	0.0461	0.0171	up	0.2455	up	0.6691	up	0.2284	up	0.6520	up	0.4236	up

MPF_LOC100690793.1.3	XP_003459914.1 PREDICTED: hypothetical protein LOC100690793 [Oreochromis niloticus]	0.0461	0.3809	up	-1.2503	down	-4.2741	down	-1.6312	down	-4.6550	down	-3.0238	down
MPF_LOC101172338.1.1	XP_004072456.1 PREDICTED: leucine-zipper- like transcriptional regulator 1like [Oryzias latipes]	0.0461	-0.1906	down	-0.0706	down	0.6357	up	0.1200	up	0.8262	up	0.7063	up
MPF_LOC100708676.1.3	XP_003459898.1 PREDICTED: ribosomal RNA processing protein 36 homolog [Oreochromis niloticus]	0.0461	-0.3166	down	0.0171	up	0.7271	up	0.3337	up	1.0437	up	0.7101	up
MPF_LOC101463957.1.1	XM_004559680.1 PREDICTED: Maylandia zebra fibroblast growth factor receptor 2-like (LOC101463957), transcript variant X1, mRNA	0.0461	-0.1047	down	0.6178	up	0.4915	up	0.7225	up	0.5962	up	-0.1263	down
MPF_LOC101482347.1.1	XR_191458.1 PREDICTED: Maylandia zebra TBC1 domain family member 13like (LOC101482347), transcript variant X2, misc_RNA	0.0461	0.0073	up	0.0596	up	-2.0301	down	0.0523	up	-2.0374	down	-2.0897	down
MPF_LOC101170724.1.1	XP_004083423.1 PREDICTED: G-protein coupled receptor 126-like [Oryzias latipes]	0.0461	-0.1825	down	-0.2153	down	0.7723	up	-0.0328	down	0.9548	up	0.9875	up
MPF_LOC101476292.1.1	XM_004567039.1 PREDICTED: Maylandia zebra transgelin-like (LOC101476292), transcript variant X2, mRNA	0.0461	-0.8633	down	-2.9215	down	-5.8780	down	-2.0582	down	-5.0147	down	-2.9565	down
MPF_LOC100694178.1.1	XP_003454020.1 PREDICTED: DNA	0.0462	0.0090	up	0.1843	up	0.6755	up	0.1753	up	0.6665	up	0.4912	up

	polymerase delta catalytic subunit-like [Oreochromis niloticus]													
MPF_ISK1.1.1	ISK1_STRCA (sp|Q9PSM2) Pancreatic secretory trypsin inhibitor OS=Struthio camelus GN=SPINK1 PE=1 SV=1	0.0462	-0.2845	down	-0.1230	down	0.6194	up	0.1615	up	0.9039	up	0.7424	up
MPF_LOC101479761.1.1	XM_004564407.1 PREDICTED: Maylandia zebra CTP synthase 1-like (LOC101479761), transcript variant X2, mRNA	0.0462	-0.2312	down	0.2584	up	0.6836	up	0.4896	up	0.9149	up	0.4252	up

MPF_LOC100692512.1.1	XM_003440027.1 PREDICTED: Oreochromis niloticus torsin-1A-interacting protein 2-like (LOC100692512), mRNA	0.0462	-0.2205	down	0.0681	up	0.5948	up	0.2886	up	0.8153	up	0.5267	up
MPF_LOC101475776.4.7	XM_004539154.1 PREDICTED: Maylandia zebra ATP synthase subunit d, mitochondrial-like (LOC101475776), transcript variant X2, mRNA	0.0462	0.2630	up	0.2590	up	0.8066	up	-0.0040	down	0.5436	up	0.5476	up
MPF_LOC101077559.1.1	XP_003966852.1 PREDICTED: uncharacterized protein LOC101077559 [Takifugu rubripes]	0.0462	0.1088	up	0.4138	up	0.8717	up	0.3050	up	0.7629	up	0.4579	up
MPF_ZSCA2.1.1	ZSCA2_MOUSE (sp|Q07230) Zinc finger and SCAN domaincontaining protein 2 OS=Mus musculus GN=Zscan2 PE=1 SV=1	0.0462	0.0709	up	0.2671	up	0.8843	up	0.1963	up	0.8134	up	0.6172	up

MPF_LOC100933241.4.24	XM_003771971.1 PREDICTED: Sarcophilus harrisii uncharacterized LOC100933241 (LOC100933241), mRNA	0.0462	-0.0830	down	0.1652	up	0.7633	up	0.2482	up	0.8464	up	0.5981	up
MPF_contig_006542		0.0463	0.2492	up	0.2165	up	0.8940	up	-0.0328	down	0.6447	up	0.6775	up
MPF_contig_031055	XM_004564782.1 PREDICTED: Maylandia zebra arrestin domaincontaining protein 2-like (LOC101479940), transcript variant X3, mRNA	0.0463	0.0986	up	-0.2612	down	-2.1128	down	-0.3597	down	-2.2114	down	-1.8516	down
MPF_LOC100699721.1.2	XP_003460016.1 PREDICTED: bifunctional protein NCOAT-like, partial [Oreochromis niloticus]	0.0463	-0.7598	down	-1.4072	down	-4.5936	down	-0.6474	down	-3.8338	down	-3.1864	down
MPF_LOC101481365.1.1	XM_004554151.1 PREDICTED: Maylandia zebra early endosome antigen 1-like (LOC101481365), transcript variant X4, mRNA	0.0463	-0.4281	down	0.1436	up	0.9849	up	0.5717	up	1.4130	up	0.8413	up
MPF_LOC101475750.1.3	XM_004552928.1 PREDICTED: Maylandia zebra serine/threonineprotein kinase Kist-like (LOC101475750), mRNA	0.0464	-0.0924	down	-0.0688	down	0.4329	up	0.0236	up	0.5253	up	0.5017	up
MPF_contig_020723		0.0464	0.1076	up	0.5301	up	2.1376	up	0.4225	up	2.0300	up	1.6074	up
MPF_LOC100694075.1.1	XM_003449860.1 PREDICTED: Oreochromis niloticus histidine triad nucleotide-binding protein 3like (LOC100694075), mRNA	0.0464	-0.1242	down	0.0971	up	1.1087	up	0.2213	up	1.2330	up	1.0116	up

MPF_contig_024313		0.0464	-0.1900	down	-0.3587	down	-1.0556	down	-0.1686	down	-0.8655	down	-0.6969	down
MPF_LOC101485582.2.4	XM_004540190.1 PREDICTED: Maylandia zebra polypyrimidine tractbinding protein 1-like (LOC101485582), mRNA	0.0464	0.0016	up	0.0254	up	0.5470	up	0.0238	up	0.5454	up	0.5216	up
MPF_LOC101464588.1.1	XM_004572198.1 PREDICTED: Maylandia zebra serpin H1-like (LOC101464588), transcript variant X3, mRNA	0.0464	0.1183	up	0.3215	up	0.9937	up	0.2031	up	0.8753	up	0.6722	up
MPF_contig_026897		0.0464	-0.0641	down	0.1022	up	-0.9908	down	0.1663	up	-0.9267	down	-1.0930	down
MPF_LOC101485743.1.3	XM_004554347.1 PREDICTED: Maylandia zebra uncharacterized LOC101485743 (LOC101485743), mRNA	0.0464	-0.1086	down	-0.1774	down	0.4570	up	-0.0688	down	0.5656	up	0.6345	up
MPF_LOC101466198.1.1	XM_004542903.1 PREDICTED: Maylandia zebra tripartite motifcontaining protein 47-like (LOC101466198), mRNA	0.0464	0.0246	up	0.3288	up	0.5752	up	0.3041	up	0.5505	up	0.2464	up
MPF_LOC100693515.2.2	XM_003443433.1 PREDICTED: Oreochromis niloticus uncharacterized protein C4orf14 homolog (LOC100693515), mRNA	0.0464	0.2782	up	0.4534	up	1.0631	up	0.1751	up	0.7849	up	0.6097	up
MPF_LOC101481244.1.1	XM_004547901.1 PREDICTED: Maylandia zebra cytoplasmic dynein 1 intermediate chain 1-like (LOC101481244), transcript variant X3, mRNA	0.0464	-0.1012	down	0.7716	up	1.2851	up	0.8728	up	1.3862	up	0.5135	up

MPF_EZH2.1.1	NM_001105101.1 Oryzias latipes enhancer of zeste homolog 2 (ezh2), mRNA dbj|AB195561.1| Oryzias latipes olezh2 mRNA for Enhancer of zeste homolog 2, complete cds	0.0464	0.3550	up	0.5670	up	1.2712	up	0.2121	up	0.9162	up	0.7041	up
MPF_LOC100700981.1.1	XM_003440559.1 PREDICTED: Oreochromis niloticus rab-like protein 2Alike (LOC100700981), mRNA	0.0464	-0.0666	down	0.1374	up	0.8940	up	0.2040	up	0.9606	up	0.7566	up
MPF_contig_011613		0.0464	-0.0544	down	0.3959	up	0.9325	up	0.4503	up	0.9869	up	0.5366	up
MPF_LOC100693183.1.1	XM_003453248.1 PREDICTED: Oreochromis niloticus doublecortin domaincontaining protein 2-like (LOC100693183), mRNA	0.0464	-0.5347	down	-0.5655	down	1.0037	up	-0.0309	down	1.5384	up	1.5692	up
MPF_contig_034805		0.0464	-0.1467	down	0.1218	up	0.8299	up	0.2685	up	0.9766	up	0.7080	up
MPF_LOC101486883.2.2	XM_004552510.1 PREDICTED: Maylandia zebra granulins-like (LOC101486883), transcript variant X2, mRNA	0.0465	0.4679	up	-0.3967	down	-1.9050	down	-0.8646	down	-2.3729	down	-1.5082	down
MPF_LOC101469342.3.6	XM_004544216.1 PREDICTED: Maylandia zebra serine protease inhibitor A3K-like (LOC101469342), mRNA	0.0465	-0.0114	down	0.2846	up	0.9545	up	0.2960	up	0.9658	up	0.6699	up
MPF_LOC101469584.2.2	XM_004559799.1 PREDICTED: Maylandia zebra serum response factorlike (LOC101469584), mRNA	0.0465	0.1970	up	0.2322	up	1.1169	up	0.0352	up	0.9199	up	0.8847	up

MPF_LOC101486817.1.1	XM_004561164.1 PREDICTED: Maylandia zebra potassium channel subfamily K member 1-like (LOC101486817), mRNA	0.0466	-0.0054	down	0.0493	up	0.9515	up	0.0547	up	0.9569	up	0.9022	up
MPF_contig_034810		0.0466	0.5458	up	0.4981	up	1.1762	up	-0.0477	down	0.6304	up	0.6781	up
MPF_LOC101479560.2.2	XM_004560219.1 PREDICTED: Maylandia zebra calpain-7-like (LOC101479560), mRNA	0.0466	-0.0172	down	0.2006	up	0.8004	up	0.2178	up	0.8176	up	0.5999	up
MPF_contig_028881		0.0466	0.0310	up	0.0807	up	0.3285	up	0.0496	up	0.2975	up	0.2479	up
MPF_contig_020753		0.0466	-0.1251	down	0.1182	up	0.7271	up	0.2432	up	0.8521	up	0.6089	up
MPF_contig_043319		0.0466	-0.4908	down	-0.4739	down	1.0190	up	0.0169	up	1.5099	up	1.4929	up
MPF_contig_048986		0.0466	0.2328	up	0.4086	up	1.1109	up	0.1759	up	0.8782	up	0.7023	up
MPF_contig_014173		0.0466	-0.1902	down	0.0549	up	0.5940	up	0.2451	up	0.7842	up	0.5391	up
MPF_LOC101478211.2.2	XM_004575724.1 PREDICTED: Maylandia zebra atrial natriuretic peptide-converting enzymelike (LOC101478211), mRNA	0.0466	0.0223	up	0.1984	up	0.5514	up	0.1761	up	0.5292	up	0.3530	up
MPF_LOC101073081.1.1	XP_003971526.1 PREDICTED: clavesin-2-like [Takifugu rubripes]	0.0466	-0.2612	down	-0.4256	down	0.8965	up	-0.1644	down	1.1576	up	1.3221	up
MPF_LOC101480831.3.3	XM_004565417.1 PREDICTED: Maylandia zebra putative 60S ribosomal protein L37a-like (LOC101480831), mRNA	0.0466	-0.1454	down	-1.1789	down	-3.0644	down	-1.0335	down	-2.9190	down	-1.8855	down
MPF_contig_020187		0.0466	-0.0350	down	0.1634	up	0.5768	up	0.1983	up	0.6118	up	0.4134	up

MPF_RPS7.1.12	XM_003971400.1 PREDICTED: Takifugu rubripes 40S ribosomal protein S7-like (LOC101073757), mRNA	0.0466	-0.2146	down	-0.9003	down	-2.2636	down	-0.6858	down	-2.0491	down	-1.3633	down
MPF_LOC101478996.1.1	XM_004562235.1 PREDICTED: Maylandia zebra F-box only protein 8like (LOC101478996), transcript variant X1, mRNA	0.0466	0.3067	up	0.3408	up	1.0881	up	0.0341	up	0.7814	up	0.7473	up
MPF_contig_019188		0.0467	-0.1031	down	0.1147	up	1.1581	up	0.2179	up	1.2612	up	1.0434	up
MPF_LOC101465276.5.8	XM_004553799.1 PREDICTED: Maylandia zebra MAP kinase-interacting serine/threonine-protein kinase 2-like (LOC101465276), mRNA	0.0467	-0.0545	down	0.0877	up	0.6941	up	0.1422	up	0.7485	up	0.6063	up
MPF_LOC101076727.1.1	XP_003966453.1 PREDICTED: centrosomal protein of 70 kDa-like [Takifugu rubripes]	0.0467	-0.0075	down	0.1678	up	0.7202	up	0.1753	up	0.7277	up	0.5524	up
MPF_LOC101468983.2.2	XR_191999.1 PREDICTED: Maylandia zebra uncharacterized LOC101468983 (LOC101468983), misc_RNA	0.0467	-0.4087	down	-1.0396	down	-2.0102	down	-0.6309	down	-1.6015	down	-0.9707	down
MPF_LOC101470374.1.1	XM_004568489.1 PREDICTED: Maylandia zebra WD repeat-containing protein 37-like (LOC101470374), transcript variant X5, mRNA	0.0467	0.1389	up	0.2412	up	0.8861	up	0.1023	up	0.7472	up	0.6449	up

MPF_LOC101476760.3.8	XM_004562605.1 PREDICTED: Maylandia zebra SLAIN motif-containing protein 1-like (LOC101476760), transcript variant X4, mRNA	0.0467	-0.4494	down	0.3148	up	0.6577	up	0.7642	up	1.1071	up	0.3429	up
MPF_LOC101468014.1.1	XM_004557773.1 PREDICTED: Maylandia zebra alkyldihydroxyacetonephosphate synthase, peroxisomallike (LOC101468014), mRNA	0.0467	0.2828	up	0.8867	up	1.3477	up	0.6039	up	1.0649	up	0.4610	up
MPF_ZN271.13.19	ZN271_HUMAN (sp|Q14591) Zinc finger protein 271 OS=Homo sapiens GN=ZNF271 PE=2 SV=4	0.0467	-0.0178	down	0.2276	up	0.7570	up	0.2454	up	0.7749	up	0.5294	up
MPF_LOC101470075.1.5	XM_004567108.1 PREDICTED: Maylandia zebra fragile X mental retardation syndrome-related protein 2-like (LOC101470075), transcript variant X2, mRNA	0.0467	0.0974	up	0.2930	up	0.6332	up	0.1956	up	0.5358	up	0.3403	up
MPF_HARB1.10.14	HARB1_MOUSE (sp|Q8BR93) Putative nuclease HARBI1 OS=Mus musculus GN=Harbi1 PE=2 SV=1	0.0467	-0.0612	down	0.2155	up	0.8132	up	0.2767	up	0.8744	up	0.5977	up
MPF_contig_016016		0.0467	0.2228	up	0.3612	up	0.6931	up	0.1383	up	0.4703	up	0.3319	up

MPF_SI_DKEY93N13.2.1.2	XP_002661155.1 PREDICTED: hypothetical protein LOC100334554 [Danio rerio]	0.0467	0.0215	up	0.1822	up	0.4028	up	0.1607	up	0.3813	up	0.2206	up

MPF_contig_035685		0.0467	-0.1387	down	-0.0013	down	0.5464	up	0.1374	up	0.6852	up	0.5478	up
MPF_LOC101464301.1.2	XM_004571738.1 PREDICTED: Maylandia zebra PH domain leucine-rich repeat protein phosphatase 1like (LOC101464301), mRNA	0.0467	0.0707	up	-0.0175	down	0.7275	up	-0.0882	down	0.6567	up	0.7449	up
MPF_LOC100697921.1.1	XM_003439274.1 PREDICTED: Oreochromis niloticus uncharacterized protein C8orf59 homolog (LOC100697921), mRNA	0.0467	0.0651	up	0.1212	up	0.5398	up	0.0561	up	0.4747	up	0.4186	up
MPF_LOC100712101.2.2	XP_003445149.1 PREDICTED: poly [ADPribose] polymerase 12-like [Oreochromis niloticus]	0.0467	0.1797	up	0.4112	up	0.5925	up	0.2315	up	0.4128	up	0.1813	up
MPF_LOC100709351.10.10	XM_003449499.1 PREDICTED: Oreochromis niloticus integral membrane protein 2B-like (LOC100709351), mRNA	0.0467	0.1316	up	0.1524	up	0.7185	up	0.0208	up	0.5869	up	0.5661	up
MPF_contig_031243		0.0467	-1.0903	down	0.6502	up	-1.0480	down	1.7405	up	0.0423	up	-1.6982	down
MPF_LOC101475732.4.4	XM_004548444.1 PREDICTED: Maylandia zebra ankyrin repeat and BTB/POZ domain-containing protein BTBD11-A-like (LOC101475732), transcript variant X2, mRNA	0.0467	-0.0070	down	-0.0072	down	0.6396	up	-0.0003	down	0.6466	up	0.6468	up
MPF_LOC101482440.1.2	XM_004553601.1 PREDICTED: Maylandia zebra macrophage erythroblast attacher-like (LOC101482440), mRNA	0.0467	0.1184	up	0.2849	up	0.8353	up	0.1665	up	0.7168	up	0.5504	up
MPF_contig_011476		0.0467	-0.2006	down	0.3755	up	0.9127	up	0.5762	up	1.1134	up	0.5372	up

MPF_LOC101167345.20.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA	0.0467	-0.1124	down	0.1085	up	0.5370	up	0.2209	up	0.6494	up	0.4286	up
MPF_LOC101475619.1.1	XM_004568507.1 PREDICTED: Maylandia zebra cullin-2-like (LOC101475619), transcript variant X1, mRNA	0.0467	0.2249	up	-0.1726	down	-1.7121	down	-0.3975	down	-1.9370	down	-1.5395	down
MPF_LOC100534757.1.1	XP_003200191.1 PREDICTED: hypothetical protein LOC100534757 [Danio rerio]	0.0467	0.3052	up	0.2442	up	1.1436	up	-0.0610	down	0.8384	up	0.8994	up
MPF_LOC100698649.3.10	XP_003460222.1 PREDICTED: complement C1q tumor necrosis factorrelated protein 3-like [Oreochromis niloticus]	0.0467	-0.2402	down	-1.7262	down	-3.9627	down	-1.4860	down	-3.7226	down	-2.2366	down
MPF_LOC101477178.1.1	XM_004575319.1 PREDICTED: Maylandia zebra hippocampus abundant transcript-like protein 1-like (LOC101477178), mRNA	0.0467	-0.2348	down	0.2105	up	0.5923	up	0.4453	up	0.8271	up	0.3818	up
MPF_contig_028794		0.0467	-0.2548	down	-0.2267	down	-1.1759	down	0.0280	up	-0.9212	down	-0.9492	down
MPF_LOC101484593.1.1	XM_004552501.1 PREDICTED: Maylandia zebra potassium voltagegated channel subfamily A member 3-like (LOC101484593), transcript variant X2, mRNA	0.0467	-0.5034	down	0.3843	up	1.7458	up	0.8877	up	2.2492	up	1.3615	up
MPF_contig_032441		0.0467	-0.4584	down	-0.0578	down	-2.2603	down	0.4006	up	-1.8018	down	-2.2025	down

MPF_contig_006725		0.0467	-0.2165	down	-0.0966	down	-1.1745	down	0.1199	up	-0.9580	down	-1.0779	down
MPF_LOC101467006.1.1	XM_004557214.1 PREDICTED: Maylandia zebra transmembrane emp24 domain-containing protein 5like (LOC101467006), mRNA	0.0467	-0.0639	down	0.2964	up	0.8998	up	0.3603	up	0.9637	up	0.6034	up
MPF_LOC101481571.1.1	XM_004561800.1 PREDICTED: Maylandia zebra Down syndrome critical region protein 3 homolog (LOC101481571), mRNA	0.0467	0.0358	up	0.2817	up	0.5653	up	0.2459	up	0.5295	up	0.2836	up
MPF_LOC101466717.1.1	XM_004574276.1 PREDICTED: Maylandia zebra BTB/POZ domaincontaining protein KCTD21like (LOC101466717), mRNA	0.0467	-0.0188	down	0.3288	up	0.6475	up	0.3477	up	0.6663	up	0.3187	up
MPF_contig_004068		0.0468	0.0716	up	0.2737	up	0.7689	up	0.2021	up	0.6972	up	0.4952	up
MPF_contig_034929		0.0468	-0.1780	down	-0.0035	down	-1.1133	down	0.1745	up	-0.9353	down	-1.1098	down
MPF_LOC100708000.1.1	XP_003448879.1 PREDICTED: lon protease homolog, mitochondrial-like [Oreochromis niloticus]	0.0468	-0.1356	down	0.1038	up	0.7097	up	0.2394	up	0.8452	up	0.6058	up
MPF_LOC101467618.1.3	XM_004560729.1 PREDICTED: Maylandia zebra ubiquitin carboxylterminal hydrolase 7-like (LOC101467618), transcript variant X4, mRNA	0.0468	0.1137	up	0.2486	up	0.6988	up	0.1349	up	0.5851	up	0.4502	up
MPF_LOC101485578.1.1	XM_004539623.1 PREDICTED: Maylandia zebra CD276 antigen-like (LOC101485578), mRNA	0.0468	-0.4496	down	-1.1312	down	-2.8262	down	-0.6815	down	-2.3765	down	-1.6950	down
MPF_contig_010571		0.0468	-0.1513	down	0.0482	up	0.4447	up	0.1995	up	0.5960	up	0.3965	up

MPF_LOC101079375.1.1	XP_003968437.1 PREDICTED: rho guanine nucleotide exchange factor 26-like [Takifugu rubripes]	0.0468	-0.1850	down	0.1319	up	0.5325	up	0.3170	up	0.7175	up	0.4005	up
MPF_contig_031403		0.0468	-0.0157	down	0.1469	up	0.4771	up	0.1626	up	0.4927	up	0.3302	up
MPF_GORAB.1.1	GORAB_MOUSE (sp|Q8BRM2) RAB6interacting golgin OS=Mus musculus GN=Gorab PE=1 SV=1	0.0468	-0.0986	down	0.0756	up	0.9683	up	0.1741	up	1.0669	up	0.8927	up
MPF_RL13.5.5	RL13_DANRE (sp|Q90Z10) 60S ribosomal protein L13 OS=Danio rerio GN=rpl13 PE=2 SV=3	0.0469	0.0357	up	-0.7928	down	-1.9501	down	-0.8285	down	-1.9858	down	-1.1573	down
MPF_LOC100701582.7.9	XP_003455288.1 PREDICTED: zinc finger protein 236-like [Oreochromis niloticus]	0.0469	-0.0270	down	0.0573	up	1.0218	up	0.0843	up	1.0488	up	0.9645	up
MPF_LOC101475263.1.1	XM_004553405.1 PREDICTED: Maylandia zebra synemin-like (LOC101475263), mRNA	0.0469	-0.1477	down	-0.3303	down	0.8140	up	-0.1825	down	0.9618	up	1.1443	up
MPF_LOC101479453.3.6	XM_004555525.1 PREDICTED: Maylandia zebra myosin light chain 1, skeletal muscle isoform-like (LOC101479453), transcript variant X2, mRNA	0.0469	0.0654	up	0.1977	up	0.6260	up	0.1323	up	0.5606	up	0.4283	up
MPF_LOC100699007.2.2	XM_003442225.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100699007, transcript variant 2 (LOC100699007), mRNA	0.0469	0.3285	up	-1.2139	down	-4.0041	down	-1.5424	down	-4.3326	down	-2.7903	down

MPF_contig_016646	XM_004564866.1 PREDICTED: Maylandia zebra 60S ribosomal protein L18a-like (LOC101477695), transcript variant X1, mRNA	0.0469	0.0588	up	0.3401	up	0.7497	up	0.2813	up	0.6910	up	0.4097	up
MPF_LOC100692340.3.3	XM_003443685.1 PREDICTED: Oreochromis niloticus FXYD domaincontaining ion transport regulator 3-like (LOC100692340), mRNA	0.0469	-0.1597	down	-0.1895	down	-1.3667	down	-0.0298	down	-1.2070	down	-1.1772	down
MPF_LOC101476475.1.1	XM_004562669.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 3-like (LOC101476475), mRNA	0.0469	-0.9958	down	-2.9008	down	-5.3271	down	-1.9051	down	-4.3314	down	-2.4263	down

MPF_LOC101465900.1.2	XM_004541867.1 PREDICTED: Maylandia zebra YLP motif-containing protein 1-like (LOC101465900), transcript variant X3, mRNA	0.0469	0.2152	up	0.2919	up	0.8712	up	0.0767	up	0.6559	up	0.5792	up
MPF_contig_008514		0.0470	-0.0010	down	0.1086	up	0.8624	up	0.1096	up	0.8634	up	0.7538	up
MPF_LOC101477198.1.1	XM_004557340.1 PREDICTED: Maylandia zebra histamine H2 receptorlike (LOC101477198), mRNA	0.0470	0.0570	up	0.1554	up	0.5324	up	0.0983	up	0.4754	up	0.3770	up
MPF_contig_015723		0.0470	-0.0629	down	0.4350	up	0.8319	up	0.4979	up	0.8948	up	0.3969	up
MPF_LOC101467113.3.4	XM_004559889.1 PREDICTED: Maylandia zebra nuclear ubiquitous casein and cyclin-dependent kinase substrate 1-like (LOC101467113), mRNA	0.0470	0.1843	up	0.0936	up	0.5897	up	-0.0907	down	0.4054	up	0.4961	up

MPF_contig_008944	XM_004556098.1 PREDICTED: Maylandia zebra transforming acidic coiled-coil-containing protein 2-like (LOC101481661), transcript variant X12, mRNA	0.0470	-0.0833	down	0.1288	up	0.9193	up	0.2121	up	1.0026	up	0.7905	up
MPF_LOC101483704.1.1	XM_004559123.1 PREDICTED: Maylandia zebra mannose-1-phosphate guanyltransferase beta-like (LOC101483704), mRNA	0.0470	-0.1574	down	-0.0335	down	0.7229	up	0.1239	up	0.8803	up	0.7564	up
MPF_LOC100708084.3.4	XM_003447339.1 PREDICTED: Oreochromis niloticus uridine phosphorylase 2-like (LOC100708084), mRNA	0.0470	-0.3891	down	-0.7836	down	-2.3257	down	-0.3945	down	-1.9366	down	-1.5420	down
MPF_LOC100693122.1.3	XP_003459042.1 PREDICTED: hypothetical protein LOC100693122 [Oreochromis niloticus]	0.0470	0.2893	up	-0.4365	down	-2.4497	down	-0.7258	down	-2.7390	down	-2.0132	down
MPF_LOC101465293.1.1	XM_004559783.1 PREDICTED: Maylandia zebra sorting nexin-5-like (LOC101465293), mRNA	0.0470	0.0854	up	0.3335	up	0.8624	up	0.2482	up	0.7770	up	0.5288	up
MPF_LOC101471646.1.1	XM_004571230.1 PREDICTED: Maylandia zebra WW domain-binding protein 4-like (LOC101471646), mRNA	0.0471	-0.0489	down	0.1236	up	1.2569	up	0.1725	up	1.3058	up	1.1333	up
MPF_LOC101478371.2.2	XM_004568698.1 PREDICTED: Maylandia zebra ankyrin repeat and SOCS box protein 7-like (LOC101478371), mRNA	0.0471	-0.1438	down	0.1649	up	0.9684	up	0.3086	up	1.1122	up	0.8036	up

MPF_LOC101062026.1.1	XP_003968842.1 PREDICTED: alpha-2macroglobulin-like [Takifugu rubripes]	0.0471	-0.0746	down	0.2419	up	0.7298	up	0.3166	up	0.8045	up	0.4879	up
MPF_LOC101484522.1.1	XM_004554979.1 PREDICTED: Maylandia zebra transducin-like enhancer protein 1-like (LOC101484522), mRNA	0.0471	0.1090	up	0.1247	up	0.9690	up	0.0157	up	0.8600	up	0.8443	up
MPF_LOC101487058.1.1	XM_004548476.1 PREDICTED: Maylandia zebra protein bicaudal D homolog 2-like (LOC101487058), mRNA	0.0471	0.3055	up	0.1087	up	0.9715	up	-0.1969	down	0.6659	up	0.8628	up
MPF_LOC101466982.1.2	XM_004574455.1 PREDICTED: Maylandia zebra pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondriallike (LOC101466982), mRNA	0.0471	-0.2313	down	0.3121	up	1.1587	up	0.5433	up	1.3900	up	0.8466	up
MPF_LOC100691772.1.7	XM_003438667.1 PREDICTED: Oreochromis niloticus histone H3.3-like (LOC100691772), mRNA	0.0471	-0.1286	down	0.3007	up	0.5636	up	0.4293	up	0.6922	up	0.2629	up
MPF_contig_002825	XM_004549786.1 PREDICTED: Maylandia zebra rap guanine nucleotide exchange factor 1-like (LOC101486972), transcript variant X3, mRNA	0.0471	-0.0735	down	0.1184	up	0.9337	up	0.1919	up	1.0072	up	0.8153	up
MPF_LOC101486559.2.2	XM_004565435.1 PREDICTED: Maylandia zebra keratin, type I cytoskeletal 18-like (LOC101486559), mRNA	0.0471	-0.9076	down	-2.1337	down	-4.5403	down	-1.2261	down	-3.6327	down	-2.4066	down

MPF_contig_040085		0.0471	-0.1412	down	0.0042	up	0.6445	up	0.1453	up	0.7856	up	0.6403	up
MPF_LOC100710354.1.1	XM_003456492.1 PREDICTED: Oreochromis niloticus DNA-directed RNA polymerase III subunit RPC6like (LOC100710354), mRNA	0.0471	-0.2279	down	0.1706	up	1.3905	up	0.3985	up	1.6184	up	1.2199	up
MPF_LOC101485385.2.2	XM_004537995.1 PREDICTED: Maylandia zebra zinc finger protein 618like (LOC101485385), mRNA	0.0471	-0.0733	down	0.2006	up	1.4750	up	0.2740	up	1.5483	up	1.2744	up
MPF_LOC100691014.1.1	XP_003449060.1 PREDICTED: clusterinassociated protein 1 homolog [Oreochromis niloticus]	0.0471	-0.0077	down	0.2035	up	0.8322	up	0.2112	up	0.8399	up	0.6287	up
MPF_LOC101476946.4.4	XM_004542655.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 5-like (LOC101476946), mRNA	0.0471	-0.2883	down	-0.2218	down	0.5960	up	0.0665	up	0.8844	up	0.8179	up
MPF_LOC101487061.1.1	XM_004548940.1 PREDICTED: Maylandia zebra protein phosphatase 1 regulatory subunit 36-like (LOC101487061), transcript variant X2, mRNA	0.0471	0.2461	up	0.5194	up	0.8738	up	0.2732	up	0.6276	up	0.3544	up
MPF_contig_038161		0.0472	-0.2857	down	-0.0813	down	1.3752	up	0.2043	up	1.6609	up	1.4566	up
MPF_LOC100697098.2.2	XM_003455635.1 PREDICTED: Oreochromis niloticus transmembrane BAX inhibitor motif-containing protein 4-like (LOC100697098), mRNA	0.0472	-0.2006	down	0.2204	up	0.5728	up	0.4210	up	0.7733	up	0.3523	up

MPF_LOC101485892.5.16	XM_004549780.1 PREDICTED: Maylandia zebra phytanoyl-CoA dioxygenase domaincontaining protein 1-like (LOC101485892), mRNA	0.0472	-0.0357	down	0.0847	up	0.6906	up	0.1204	up	0.7263	up	0.6058	up
MPF_contig_037690		0.0472	-0.1527	down	0.4834	up	0.9378	up	0.6360	up	1.0905	up	0.4545	up
MPF_LOC101465129.2.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNAbinding protein A-like (LOC101465129), transcript variant X4, mRNA	0.0472	0.3349	up	0.5123	up	0.9753	up	0.1774	up	0.6404	up	0.4630	up
MPF_BM1_14085.2.5	XP_001894282.1 T-cell receptor beta chain ANA 11 [Brugia malayi]	0.0472	0.0126	up	0.0816	up	0.6224	up	0.0690	up	0.6098	up	0.5408	up
MPF_contig_049099		0.0472	0.0205	up	0.1169	up	0.4536	up	0.0964	up	0.4331	up	0.3367	up
MPF_LOC101474349.1.1	XM_004541348.1 PREDICTED: Maylandia zebra uncharacterized LOC101474349 (LOC101474349), mRNA	0.0472	-0.0166	down	0.2655	up	1.1239	up	0.2821	up	1.1405	up	0.8584	up
MPF_contig_005551	XM_004568985.1 PREDICTED: Maylandia zebra mitogen-activated protein kinase kinase kinase kinase 4-like (LOC101483446), transcript variant X3, mRNA	0.0472	-0.1489	down	0.0611	up	0.6651	up	0.2100	up	0.8140	up	0.6041	up
MPF_LOC100703657.12.12	XM_003456466.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100703657), mRNA	0.0472	0.1183	up	0.3138	up	0.9001	up	0.1955	up	0.7818	up	0.5863	up

MPF_PTT_12042.1.2	XP_003300709.1 hypothetical protein PTT_12042 [Pyrenophora teres f. teres 0-1]	0.0472	-0.0223	down	0.1568	up	0.3557	up	0.1791	up	0.3780	up	0.1989	up
MPF_contig_038868		0.0472	0.0387	up	0.1550	up	0.5674	up	0.1163	up	0.5287	up	0.4124	up
MPF_LOC101467642.1.1	XM_004565102.1 PREDICTED: Maylandia zebra ubiquitin-likeconjugating enzyme ATG10like (LOC101467642), transcript variant X3, mRNA	0.0472	0.2142	up	0.6467	up	0.3963	up	0.4325	up	0.1821	up	-0.2503	down
MPF_contig_015519	XM_004555587.1 PREDICTED: Maylandia zebra LIM and senescent cell antigen-like-containing domain protein 1-like (LOC101469398), transcript variant X3, mRNA	0.0472	0.0384	up	0.1022	up	0.5049	up	0.0639	up	0.4665	up	0.4026	up
MPF_LOC101471367.5.5	XM_004573481.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase CBL-like (LOC101471367), mRNA	0.0472	-0.0895	down	-0.0504	down	0.9392	up	0.0390	up	1.0287	up	0.9897	up
MPF_LOC100696395.1.1	XM_003454890.1 PREDICTED: Oreochromis niloticus protein DVR-1-like (LOC100696395), mRNA	0.0472	-0.2303	down	0.2264	up	0.5747	up	0.4567	up	0.8050	up	0.3483	up
MPF_LOC101469156.2.2	XM_004568928.1 PREDICTED: Maylandia zebra zinc finger CCHC domain-containing protein 2like (LOC101469156), mRNA	0.0472	0.0411	up	0.2124	up	1.1693	up	0.1712	up	1.1282	up	0.9570	up

MPF_LOC100538336.1.1	XP_003198555.1 PREDICTED: zinc finger protein 729-like [Danio rerio]	0.0472	-0.0124	down	0.2203	up	1.1780	up	0.2327	up	1.1905	up	0.9578	up
MPF_LOC101464537.3.3	XM_004563077.1 PREDICTED: Maylandia zebra trinucleotide repeatcontaining gene 6B proteinlike (LOC101464537), mRNA	0.0472	-0.0090	down	0.0376	up	0.8460	up	0.0466	up	0.8549	up	0.8084	up
MPF_LOC101473574.6.7	XM_004564566.1 PREDICTED: Maylandia zebra 60S ribosomal protein L27a-like (LOC101473574), mRNA	0.0472	-0.8302	down	-0.2846	down	-1.0879	down	0.5456	up	-0.2577	down	-0.8033	down
MPF_LOC101466982.2.2	XM_004574455.1 PREDICTED: Maylandia zebra pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondriallike (LOC101466982), mRNA	0.0472	-0.3573	down	0.2747	up	1.1452	up	0.6320	up	1.5025	up	0.8705	up
MPF_CLAP1.1.2	CLAP1_HUMAN (sp|Q7Z460) CLIP-associating protein 1 OS=Homo sapiens GN=CLASP1 PE=1 SV=1	0.0472	-0.0898	down	0.2876	up	1.4070	up	0.3775	up	1.4968	up	1.1193	up
MPF_LOC100698949.1.1	XM_003448716.1 PREDICTED: Oreochromis niloticus acyl-CoA synthetase family member 2, mitochondrial-like (LOC100698949), mRNA	0.0472	-0.0211	down	0.2251	up	0.7928	up	0.2462	up	0.8138	up	0.5676	up

MPF_LOC101472043.6.14	XM_004573789.1 PREDICTED: Maylandia zebra tight junctionassociated protein 1-like (LOC101472043), transcript variant X4, mRNA	0.0472	-0.1208	down	0.2603	up	1.1182	up	0.3811	up	1.2390	up	0.8579	up
MPF_LOC101162897.1.2	XP_004085175.1 PREDICTED: complement factor H-like [Oryzias latipes]	0.0472	0.0314	up	-1.2537	down	-3.6601	down	-1.2850	down	-3.6915	down	-2.4064	down
MPF_LOC101465639.1.2	XM_004549991.1 PREDICTED: Maylandia zebra protein FAM64A-like (LOC101465639), transcript variant X1, mRNA	0.0472	-0.0800	down	0.1902	up	0.8350	up	0.2702	up	0.9149	up	0.6447	up
MPF_contig_044432		0.0472	0.1734	up	0.2657	up	0.8229	up	0.0923	up	0.6495	up	0.5572	up
MPF_LOC101463588.1.1	XM_004542794.1 PREDICTED: Maylandia zebra uncharacterized LOC101463588 (LOC101463588), mRNA	0.0472	0.2916	up	0.3665	up	0.8703	up	0.0749	up	0.5788	up	0.5039	up
MPF_LOC101467410.1.1	XM_004562377.1 PREDICTED: Maylandia zebra protein FAM20A-like (LOC101467410), mRNA	0.0472	0.0192	up	0.0734	up	1.0242	up	0.0541	up	1.0050	up	0.9509	up
MPF_contig_044713		0.0472	-0.0366	down	0.2057	up	1.4976	up	0.2424	up	1.5342	up	1.2919	up
MPF_LOC101476820.2.2	XM_004554033.1 PREDICTED: Maylandia zebra transketolase-like (LOC101476820), mRNA	0.0472	-0.0524	down	-0.3170	down	0.7263	up	-0.2645	down	0.7787	up	1.0432	up
MPF_LOC100708393.1.1	XM_003457059.1 PREDICTED: Oreochromis niloticus SPRY domaincontaining protein 3-like (LOC100708393), mRNA	0.0472	0.3032	up	0.0365	up	1.0516	up	-0.2667	down	0.7484	up	1.0151	up

MPF_contig_027380		0.0472	0.0269	up	0.2170	up	0.4586	up	0.1900	up	0.4316	up	0.2416	up
MPF_contig_046271		0.0472	0.1934	up	0.4215	up	1.1217	up	0.2281	up	0.9283	up	0.7002	up
MPF_contig_007710		0.0472	0.0403	up	0.3147	up	0.9127	up	0.2743	up	0.8724	up	0.5980	up
MPF_contig_015580		0.0472	0.1035	up	0.2178	up	1.1454	up	0.1143	up	1.0419	up	0.9276	up
MPF_LOC100694365.1.1	XM_003454723.1 PREDICTED: Oreochromis niloticus sodium/potassiumtransporting ATPase subunit beta-233-like (LOC100694365), mRNA	0.0472	-0.3382	down	-0.2705	down	0.7369	up	0.0676	up	1.0751	up	1.0075	up
MPF_contig_048091		0.0472	0.1126	up	0.5860	up	1.6410	up	0.4734	up	1.5285	up	1.0550	up
MPF_contig_004261		0.0472	-0.6164	down	-1.1324	down	-3.0272	down	-0.5160	down	-2.4108	down	-1.8948	down
MPF_MUC5A.2.3	MUC5A_HUMAN (sp|P98088) Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3	0.0472	-0.1139	down	0.1157	up	0.7683	up	0.2296	up	0.8822	up	0.6525	up
MPF_contig_016218		0.0472	-0.0366	down	0.4186	up	1.5995	up	0.4552	up	1.6361	up	1.1808	up
MPF_contig_015005		0.0472	0.2124	up	0.3201	up	1.0453	up	0.1078	up	0.8329	up	0.7251	up
MPF_LOC100703657.7.12	XM_003456466.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100703657), mRNA	0.0472	-0.0215	down	-0.0060	down	-0.9442	down	0.0155	up	-0.9227	down	-0.9382	down

MPF_LOC100701544.9.20	XM_003444229.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 3-like (LOC100701544), mRNA	0.0472	0.0442	up	0.3629	up	0.5044	up	0.3188	up	0.4602	up	0.1415	up
MPF_LOC100692618.2.2	XM_003444944.1 PREDICTED: Oreochromis niloticus protein BTG1-like (LOC100692618), mRNA	0.0472	-0.1376	down	-0.4236	down	0.8154	up	-0.2860	down	0.9530	up	1.2390	up
MPF_LOC100692146.1.1	XP_003441574.1 PREDICTED: serine/threonine-protein kinase SRPK1-like [Oreochromis niloticus]	0.0472	-0.1695	down	0.0413	up	0.7081	up	0.2108	up	0.8775	up	0.6668	up
MPF_LOC100695994.1.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.0472	0.1634	up	0.1330	up	0.8962	up	-0.0304	down	0.7328	up	0.7632	up
MPF_LOC101474586.1.5	XM_004553213.1 PREDICTED: Maylandia zebra chromodomain-helicase-DNA-binding protein 2-like (LOC101474586), transcript variant X4, mRNA	0.0472	-0.3064	down	-0.1714	down	1.3638	up	0.1349	up	1.6701	up	1.5352	up
MPF_LOC100708289.1.2	XP_003455567.1 PREDICTED: serine/threonine-protein kinase Chk2-like [Oreochromis niloticus]	0.0472	0.4118	up	0.6048	up	1.0278	up	0.1930	up	0.6160	up	0.4229	up
MPF_LOC101480552.1.1	XM_004544820.1 PREDICTED: Maylandia zebra protein polybromo-1like (LOC101480552), transcript variant X3, mRNA	0.0472	0.0309	up	0.3640	up	0.7675	up	0.3331	up	0.7365	up	0.4034	up
MPF_contig_023617		0.0473	0.0064	up	0.0141	up	0.9022	up	0.0077	up	0.8958	up	0.8881	up

MPF_RL37A.1.1	RL37A_XENLA (sp|Q7SZB4) 60S ribosomal protein L37a OS=Xenopus laevis GN=rpl37a PE=3 SV=3	0.0473	-0.0966	down	-1.1451	down	-3.0397	down	-1.0485	down	-2.9430	down	-1.8945	down
MPF_LOC101465961.3.3	XM_004575014.1 PREDICTED: Maylandia zebra actin filamentassociated protein 1-like (LOC101465961), transcript variant X4, mRNA	0.0473	-0.0601	down	0.0715	up	0.5086	up	0.1316	up	0.5687	up	0.4371	up
MPF_LOC101480353.2.2	XM_004545546.1 PREDICTED: Maylandia zebra zinc finger protein ubid4-like (LOC101480353), transcript variant X4, mRNA	0.0473	-0.2056	down	0.3347	up	0.7792	up	0.5403	up	0.9848	up	0.4445	up
MPF_contig_020856		0.0474	-0.0488	down	0.1425	up	0.9874	up	0.1912	up	1.0362	up	0.8450	up
MPF_ZN239.2.2	ZN239_MOUSE (sp|P24399) Zinc finger protein 239 OS=Mus musculus GN=Znf239 PE=2 SV=2	0.0474	0.0742	up	0.2388	up	0.9100	up	0.1646	up	0.8358	up	0.6713	up
MPF_contig_000715		0.0474	-0.0575	down	0.1312	up	0.5853	up	0.1886	up	0.6428	up	0.4542	up
MPF_LOC100706202.1.1	XM_003443483.1 PREDICTED: Oreochromis niloticus E3 ubiquitin-protein ligase MARCH6-like (LOC100706202), mRNA	0.0474	0.0010	up	0.1082	up	0.8347	up	0.1072	up	0.8337	up	0.7265	up
MPF_LOC101466143.5.18	XM_004574840.1 PREDICTED: Maylandia zebra 40S ribosomal protein S18-like (LOC101466143), mRNA	0.0474	-0.2095	down	-0.8331	down	-2.2106	down	-0.6236	down	-2.0011	down	-1.3775	down
MPF_contig_041939		0.0474	-0.0441	down	-0.0312	down	0.5969	up	0.0129	up	0.6411	up	0.6281	up

MPF_contig_017496	XM_004556285.1 PREDICTED: Maylandia zebra bromodomain-containing protein 1-like (LOC101482734), transcript variant X2, mRNA	0.0474	0.2250	up	0.2512	up	0.9206	up	0.0262	up	0.6956	up	0.6694	up
MPF_contig_002418	XM_004543995.1 PREDICTED: Maylandia zebra tumor necrosis factor receptor superfamily member 19-like (LOC101479020), transcript variant X1, mRNA	0.0474	-0.0759	down	0.1083	up	0.6251	up	0.1842	up	0.7010	up	0.5168	up

MPF_DCAM.1.3	NM_001165344.1 Salmo salar S-adenosylmethionine decarboxylase proenzyme (dcam), mRNA gb|BT058814.1| Salmo salar clone ssal-rgf-504-333 Sadenosylmethionine decarboxylase proenzyme putative mRNA, complete cds	0.0474	-0.1401	down	0.1253	up	1.0184	up	0.2654	up	1.1584	up	0.8931	up
MPF_contig_038107	XM_004542238.1 PREDICTED: Maylandia zebra neurexin-3b-like (LOC101486071), transcript variant X2, mRNA	0.0474	0.0327	up	-0.0284	down	1.2129	up	-0.0611	down	1.1802	up	1.2413	up
		0.0474	-0.9678	down	-0.5025	down	0.9701	up	0.4653	up	1.9379	up	1.4726	up
MPF_LOC101479192.1.1	XM_004541915.1 PREDICTED: Maylandia zebra lebercilin-like (LOC101479192), transcript variant X1, mRNA	0.0474	-0.6639	down	-1.4727	down	-3.6301	down	-0.8089	down	-2.9662	down	-2.1574	down
MPF_contig_010614	XM_004573501.1 PREDICTED: Maylandia zebra disks large homolog 1like (LOC101473605), transcript variant X14, mRNA	0.0474	-0.0522	down	0.3231	up	1.1427	up	0.3753	up	1.1949	up	0.8196	up

MPF_LOC100706131.1.1	XM_003448741.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L18a-like (LOC100706131), mRNA	0.0474	-0.0793	down	-0.6105	down	-1.6144	down	-0.5311	down	-1.5351	down	-1.0040	down
MPF_LOC101467616.1.2	XM_004560174.1 PREDICTED: Maylandia zebra protein dpy-19 homolog 1-like (LOC101467616), transcript variant X2, mRNA	0.0474	0.0260	up	0.3862	up	0.9055	up	0.3602	up	0.8795	up	0.5193	up
MPF_AP4E1.1.1	XM_003443945.1 PREDICTED: Oreochromis niloticus adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), mRNA	0.0474	0.0873	up	0.4813	up	0.8626	up	0.3940	up	0.7753	up	0.3813	up
MPF_LOC101468136.1.1	XM_004564171.1 PREDICTED: Maylandia zebra gamma-aminobutyric acid receptor subunit gamma1-like (LOC101468136), transcript variant X2, mRNA	0.0474	-0.2106	down	-0.1297	down	0.6322	up	0.0809	up	0.8427	up	0.7618	up
MPF_LOC101473555.2.3	XM_004560383.1 PREDICTED: Maylandia zebra CDP-diacylglycerol-serine Ophosphatidyltransferase-like (LOC101473555), transcript variant X8, mRNA	0.0474	-0.1637	down	-0.5732	down	-1.7770	down	-0.4094	down	-1.6133	down	-1.2039	down
MPF_contig_007962		0.0474	0.5562	up	0.4248	up	1.0101	up	-0.1314	down	0.4539	up	0.5853	up
MPF_contig_044633		0.0474	-0.1917	down	0.1203	up	1.3002	up	0.3120	up	1.4919	up	1.1799	up

MPF_LOC100700626.1.1	XM_003441138.1 PREDICTED: Oreochromis niloticus probable methyltransferase TARBP1like (LOC100700626), mRNA	0.0474	-0.1289	down	0.2489	up	0.9738	up	0.3778	up	1.1028	up	0.7250	up
MPF_LOC100694157.1.1	XP_003448416.1 PREDICTED: endoplasmic reticulum-Golgi intermediate compartment protein 3-like isoform 2 [Oreochromis niloticus]	0.0474	-0.0982	down	0.1915	up	0.9386	up	0.2897	up	1.0368	up	0.7471	up
MPF_LOC101465326.1.1	XM_004542254.1 PREDICTED: Maylandia zebra protein FAM177A1-like (LOC101465326), transcript variant X3, mRNA	0.0474	-0.1572	down	0.1512	up	0.7999	up	0.3083	up	0.9571	up	0.6488	up
MPF_LOC101470075.3.5	XM_004567108.1 PREDICTED: Maylandia zebra fragile X mental retardation syndrome-related protein 2-like (LOC101470075), transcript variant X2, mRNA	0.0474	-0.0530	down	-0.1042	down	0.4873	up	-0.0511	down	0.5404	up	0.5915	up
MPF_LOC100689789.1.1	XP_003454260.1 PREDICTED: choline transporter-like protein 1-like [Oreochromis niloticus]	0.0474	-0.2889	down	0.3647	up	1.2299	up	0.6536	up	1.5188	up	0.8652	up
MPF_LOC101062526.1.1	XP_003962815.1 PREDICTED: d-2hydroxyglutarate dehydrogenase, mitochondrial-like [Takifugu rubripes]	0.0474	0.0634	up	0.5737	up	0.8169	up	0.5103	up	0.7535	up	0.2432	up

MPF_contig_011672	XM_004550791.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 6-like (LOC101478586), transcript variant X1, mRNA	0.0474	0.4261	up	-0.4283	down	-2.5318	down	-0.8544	down	-2.9578	down	-2.1035	down
MPF_LOC101174419.1.1	XP_004069338.1 PREDICTED: phosphatidate phosphatase LPIN2-like [Oryzias latipes]	0.0474	-0.0191	down	0.3022	up	0.7503	up	0.3214	up	0.7694	up	0.4480	up
MPF_MK67I.1.1	MK67I_DANRE (sp|Q8JIY8) MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Danio rerio GN=mki67ip PE=2 SV=2	0.0474	-0.1976	down	-0.3193	down	0.9089	up	-0.1217	down	1.1064	up	1.2282	up
MPF_contig_015779		0.0474	-0.0810	down	0.0308	up	0.7890	up	0.1118	up	0.8700	up	0.7582	up
MPF_AP2MB.1.1	[BBH] AP2MB_DANRE (sp|Q7ZW98) AP-2 complex subunit mu-B OS=Danio rerio GN=ap2m1b PE=2 SV=1	0.0474	0.0840	up	0.1281	up	0.7214	up	0.0441	up	0.6374	up	0.5933	up
MPF_RL37P.1.1	RL37P_RAT (sp|P61515) Putative 60S ribosomal protein L37a OS=Rattus norvegicus GN=Rpl37a-ps1 PE=5 SV=2	0.0474	-0.0862	down	-1.1490	down	-3.0276	down	-1.0628	down	-2.9414	down	-1.8785	down
MPF_LOC101487317.1.1	XM_004567081.1 PREDICTED: Maylandia zebra UPF0696 protein C11orf68 homolog (LOC101487317), transcript variant X3, mRNA	0.0474	-0.1389	down	0.2180	up	0.7441	up	0.3568	up	0.8830	up	0.5262	up

MPF_LOC100693952.1.2	XP_003442761.1 PREDICTED: hypothetical protein LOC100693952 [Oreochromis niloticus]	0.0474	0.0466	up	0.3390	up	0.7600	up	0.2924	up	0.7134	up	0.4210	up
MPF_LOC101465834.2.2	XM_004547185.1 PREDICTED: Maylandia zebra UPF0600 protein C5orf51 homolog (LOC101465834), transcript variant X1, mRNA	0.0474	0.0610	up	0.0167	up	0.7763	up	-0.0443	down	0.7153	up	0.7596	up
MPF_contig_029502		0.0474	0.0243	up	0.5544	up	1.0747	up	0.5301	up	1.0504	up	0.5203	up
MPF_contig_041819		0.0474	-0.0986	down	0.0489	up	0.6168	up	0.1475	up	0.7154	up	0.5679	up
MPF_LOC100703013.1.1	XM_003452384.1 PREDICTED: Oreochromis niloticus HAUS augmin-like complex subunit 6-like (LOC100703013), mRNA	0.0474	0.0226	up	0.1299	up	0.6683	up	0.1074	up	0.6458	up	0.5384	up
MPF_contig_009740		0.0474	-0.3990	down	-0.3454	down	-1.0058	down	0.0536	up	-0.6068	down	-0.6605	down
MPF_contig_010874	XM_004556645.1 PREDICTED: Maylandia zebra RING finger protein 157-like (LOC101483028), transcript variant X3, mRNA	0.0475	0.0705	up	0.2610	up	0.8234	up	0.1905	up	0.7529	up	0.5624	up
MPF_LOC101486821.3.3	XM_004562174.1 PREDICTED: Maylandia zebra vacuolar protein sorting-associated protein 54like (LOC101486821), transcript variant X4, mRNA	0.0475	0.1618	up	0.2881	up	0.6638	up	0.1263	up	0.5020	up	0.3757	up
MPF_LOC101474929.1.4	XM_004569492.1 PREDICTED: Maylandia zebra platelet binding protein GspB-like (LOC101474929),	0.0475	-0.0138	down	0.0945	up	0.4806	up	0.1083	up	0.4944	up	0.3860	up

	mRNA													
MPF_LOC101472753.1.1	XM_004557041.1 PREDICTED: Maylandia zebra ELAV-like protein 1like (LOC101472753), mRNA	0.0476	-0.2364	down	0.1130	up	0.6681	up	0.3494	up	0.9045	up	0.5552	up
MPF_MLL3.1.1	MLL3_HUMAN (sp|Q8NEZ4) Histone-lysine Nmethyltransferase MLL3 OS=Homo sapiens GN=MLL3 PE=1 SV=3	0.0476	0.0878	up	0.0282	up	0.9485	up	-0.0596	down	0.8607	up	0.9203	up
MPF_LOC100697269.1.1	XP_003450244.1 PREDICTED: RCC1 and BTB domain-containing protein 2like [Oreochromis niloticus]	0.0476	-0.2407	down	0.3893	up	0.8127	up	0.6300	up	1.0533	up	0.4234	up
MPF_USP24.1.1	XP_003439791.1 PREDICTED: ubiquitin carboxyl-terminal hydrolase 24 [Oreochromis niloticus]	0.0476	-0.1198	down	-0.0152	down	0.8093	up	0.1046	up	0.9291	up	0.8245	up
MPF_LOC101468354.1.1	XM_004544958.1 PREDICTED: Maylandia zebra retinoic acid receptor gamma-A-like (LOC101468354), transcript variant X4, mRNA	0.0476	0.1227	up	0.3170	up	0.6409	up	0.1944	up	0.5183	up	0.3239	up
MPF_LOC100690746.2.2	XM_003448354.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S23-like (LOC100690746), mRNA	0.0476	0.0701	up	0.0874	up	0.6920	up	0.0173	up	0.6219	up	0.6046	up
MPF_LOC101476571.1.3	XM_004540817.1 PREDICTED: Maylandia zebra uncharacterized LOC101476571	0.0476	0.0579	up	0.1913	up	0.9617	up	0.1333	up	0.9038	up	0.7704	up

	(LOC101476571), transcript variant X3, mRNA													
MPF_LOC100618223.1.2	XP_003340934.1 PREDICTED: zinc finger protein 879-like [Monodelphis domestica]	0.0476	0.1263	up	0.1936	up	1.0221	up	0.0673	up	0.8958	up	0.8285	up
MPF_LOC100702190.6.6	XM_003448143.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L10a-like (LOC100702190), mRNA	0.0476	0.1149	up	0.2219	up	0.5910	up	0.1070	up	0.4762	up	0.3692	up
MPF_LOC100703046.1.1	XM_003439129.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100703046 (LOC100703046), mRNA	0.0476	-0.1676	down	0.0169	up	0.5774	up	0.1845	up	0.7450	up	0.5606	up
MPF_LOC101465807.1.1	XM_004541220.1 PREDICTED: Maylandia zebra aryl hydrocarbon receptor nuclear translocatorlike (LOC101465807), transcript variant X2, mRNA	0.0476	-0.0940	down	0.2229	up	1.1121	up	0.3169	up	1.2061	up	0.8892	up
MPF_LOC101466459.12.29	XM_004554283.1 PREDICTED: Maylandia zebra semaphorin-3G-like (LOC101466459), mRNA	0.0477	-0.0093	down	0.2594	up	0.4729	up	0.2687	up	0.4822	up	0.2135	up
MPF_LOC101480885.1.1	XM_004553596.1 PREDICTED: Maylandia zebra probable E3 SUMOprotein ligase RNF212-like (LOC101480885), transcript variant X2, mRNA	0.0477	0.0848	up	0.1743	up	0.7642	up	0.0895	up	0.6794	up	0.5899	up

MPF_LOC101475930.1.1	XM_004549175.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF19A-like (LOC101475930), mRNA	0.0477	-0.0601	down	0.0889	up	0.6297	up	0.1490	up	0.6898	up	0.5407	up
MPF_LOC101075598.1.1	XP_003967399.1 PREDICTED: GRAM domaincontaining protein 2-like [Takifugu rubripes]	0.0477	0.0149	up	0.1771	up	0.5019	up	0.1623	up	0.4870	up	0.3247	up
MPF_LOC101077496.1.1	XM_003968940.1 PREDICTED: Takifugu rubripes gamma-glutamylcyclotransferase-like (LOC101077496), mRNA	0.0477	-2.0850	down	-1.3112	down	-2.4980	down	0.7738	up	-0.4129	down	-1.1867	down
MPF_contig_040368		0.0477	-0.4297	down	-1.1866	down	-2.8639	down	-0.7569	down	-2.4343	down	-1.6774	down
MPF_contig_029430		0.0477	-0.1284	down	-0.0003	down	0.9316	up	0.1281	up	1.0600	up	0.9319	up
MPF_LOC100708302.1.1	XP_003458003.1 PREDICTED: F-box only protein 3-like [Oreochromis niloticus]	0.0477	0.1232	up	0.2361	up	1.0910	up	0.1129	up	0.9678	up	0.8549	up
MPF_LOC101485207.2.2	XM_004538633.1 PREDICTED: Maylandia zebra ewing's tumorassociated antigen 1 homolog (LOC101485207), mRNA	0.0477	0.0153	up	0.2105	up	0.4693	up	0.1951	up	0.4540	up	0.2589	up
MPF_LOC101159044.1.1	XM_004078726.1 PREDICTED: Oryzias latipes zinc finger protein 644-like (LOC101159044), mRNA	0.0477	-0.0171	down	0.2722	up	0.8210	up	0.2893	up	0.8382	up	0.5489	up

MPF_LOC101476003.1.3	XM_004567127.1 PREDICTED: Maylandia zebra plasminogen activator inhibitor 1 RNA-binding protein-like (LOC101476003), mRNA	0.0478	-0.0341	down	0.0440	up	0.6598	up	0.0781	up	0.6939	up	0.6158	up
MPF_contig_019715		0.0478	-0.0145	down	0.1027	up	0.7554	up	0.1172	up	0.7699	up	0.6527	up
MPF_ZGC_113983.2.4	NM_001025171.1 Danio rerio zgc:113983 (zgc:113983), mRNA gb|BC097059.1| Danio rerio zgc:113983, mRNA (cDNA clone MGC:113983 IMAGE:7226638), complete cds	0.0478	-0.0506	down	0.5434	up	0.9189	up	0.5939	up	0.9695	up	0.3756	up
MPF_LOC101475114.2.2	XM_004544525.1 PREDICTED: Maylandia zebra apoptosis-inducing factor 3-like (LOC101475114), transcript variant X2, mRNA	0.0478	0.0225	up	0.5527	up	0.6483	up	0.5302	up	0.6258	up	0.0956	up
MPF_LOC100700213.1.2	XM_003451195.1 PREDICTED: Oreochromis niloticus WD repeatcontaining protein 89-like (LOC100700213), mRNA	0.0478	-0.0793	down	0.1474	up	0.7885	up	0.2267	up	0.8678	up	0.6411	up
		0.0478	-1.0506	down	-0.5907	down	0.8918	up	0.4599	up	1.9423	up	1.4824	up
MPF_LECG.9.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0.0478	-0.0856	down	0.2530	up	0.9984	up	0.3386	up	1.0840	up	0.7454	up
MPF_LOC101481998.2.2	XM_004546414.1 PREDICTED: Maylandia zebra oxysterol-binding protein-related protein 2-like (LOC101481998), mRNA	0.0478	-0.0472	down	0.2445	up	1.2241	up	0.2917	up	1.2713	up	0.9796	up

MPF_LOC101486169.4.4	XM_004566076.1 PREDICTED: Maylandia zebra cyclin-T2-like (LOC101486169), mRNA	0.0478	-1.1590	down	-3.0355	down	-5.6013	down	-1.8764	down	-4.4422	down	-2.5658	down
MPF_LOC101481296.1.1	XM_004562691.1 PREDICTED: Maylandia zebra protocadherin-7-like (LOC101481296), transcript variant X4, mRNA	0.0478	-0.3729	down	-0.3560	down	1.1108	up	0.0169	up	1.4837	up	1.4668	up

MPF_contig_031009	XM_004546030.1 PREDICTED: Maylandia zebra dystroglycan-like (LOC101485248), transcript variant X1, mRNA	0.0479	0.0149	up	-0.0469	down	0.7902	up	-0.0617	down	0.7754	up	0.8371	up
MPF_LOC100703732.1.4	XP_003451339.1 PREDICTED: proximal tubules-expressed gene protein-like [Oreochromis niloticus]	0.0479	-0.0873	down	0.1845	up	0.9923	up	0.2717	up	1.0796	up	0.8079	up
MPF_contig_016010		0.0479	-0.1180	down	0.1630	up	0.5556	up	0.2810	up	0.6736	up	0.3925	up
MPF_LOC101479891.1.1	XM_004552094.1 PREDICTED: Maylandia zebra shootin-1-like (LOC101479891), mRNA	0.0479	-0.0405	down	0.1851	up	0.3874	up	0.2256	up	0.4279	up	0.2023	up
MPF_LOC100709491.1.2	XM_003440416.1 PREDICTED: Oreochromis niloticus tetraspanin-3-like, transcript variant 1 (LOC100709491), mRNA	0.0479	0.0932	up	0.3787	up	0.7442	up	0.2855	up	0.6510	up	0.3655	up
MPF_LOC100711971.2.2	XM_003437578.1 PREDICTED: Oreochromis niloticus probable RNA polymerase II nuclear localization protein SLC7A6OS-like	0.0479	-0.0053	down	0.3184	up	0.6443	up	0.3237	up	0.6496	up	0.3259	up

	(LOC100711971), mRNA													
MPF_LOC101465372.1.1	XM_004553174.1 PREDICTED: Maylandia zebra zinc finger protein 592like (LOC101465372), mRNA	0.0479	0.0002	up	-0.2278	down	1.3082	up	-0.2281	down	1.3079	up	1.5360	up
MPF_LOC100690119.5.18	XP_003448733.1 PREDICTED: zinc finger protein 16-like [Oreochromis niloticus]	0.0479	0.2126	up	0.4387	up	1.2410	up	0.2262	up	1.0284	up	0.8023	up
MPF_contig_004801	XM_004544584.1 PREDICTED: Maylandia zebra sodium- and chloridedependent GABA transporter ine-like (LOC101465611), transcript variant X2, mRNA	0.0479	-0.0912	down	0.0738	up	0.5233	up	0.1650	up	0.6145	up	0.4495	up
MPF_LOC100699367.1.1	XM_003441300.1 PREDICTED: Oreochromis niloticus receptor tyrosineprotein kinase erbB-3-like (LOC100699367), mRNA	0.0480	-0.0243	down	0.0197	up	-0.9575	down	0.0439	up	-0.9332	down	-0.9772	down
MPF_contig_037969		0.0480	0.1247	up	0.2556	up	0.5915	up	0.1309	up	0.4669	up	0.3359	up
MPF_contig_032361		0.0480	-0.2260	down	0.3105	up	0.4569	up	0.5366	up	0.6829	up	0.1463	up
MPF_contig_020726		0.0480	0.0797	up	0.4633	up	0.8709	up	0.3836	up	0.7911	up	0.4076	up

MPF_LOC100692360.1.1	XM_003449271.1 PREDICTED: Oreochromis niloticus seryl-tRNA synthetase, mitochondrial-like (LOC100692360), mRNA	0.0480	0.1064	up	0.3409	up	0.8835	up	0.2345	up	0.7771	up	0.5426	up
MPF_C1GTB.1.1	C1GTB_DANRE (sp|Q7SYI5) Glycoprotein-Nacetylgalactosamine 3-betagalactosyltransferase 1-B OS=Danio rerio GN=c1galt1b PE=2 SV=1	0.0480	-0.0045	down	0.1357	up	0.5005	up	0.1402	up	0.5049	up	0.3648	up
MPF_LOC100709639.2.2	XP_003455728.1 PREDICTED: hypothetical protein LOC100709639 [Oreochromis niloticus]	0.0481	-0.1352	down	-0.1794	down	1.1504	up	-0.0442	down	1.2856	up	1.3298	up
MPF_LOC101476003.2.3	XM_004567127.1 PREDICTED: Maylandia zebra plasminogen activator inhibitor 1 RNA-binding protein-like (LOC101476003), mRNA	0.0481	-0.0998	down	-0.2205	down	0.4709	up	-0.1207	down	0.5707	up	0.6914	up
MPF_BKRB2.1.1	BKRB2_RAT (sp|P25023) B2 bradykinin receptor OS=Rattus norvegicus GN=Bdkrb2 PE=1 SV=4	0.0481	-0.0915	down	0.1794	up	0.6566	up	0.2709	up	0.7481	up	0.4772	up
MPF_LOC101472026.1.1	XM_004570479.1 PREDICTED: Maylandia zebra TSC22 domain family protein 2-like (LOC101472026), transcript variant X2, mRNA	0.0481	0.0665	up	0.2196	up	0.7465	up	0.1531	up	0.6800	up	0.5269	up
MPF_LOC101066523.1.1	XM_003975754.1 PREDICTED: Takifugu rubripes eukaryotic initiation factor 4A-II-like (LOC101066523), mRNA	0.0481	-0.2069	down	-0.1863	down	0.5254	up	0.0206	up	0.7323	up	0.7117	up

MPF_LOC100708211.3.3	XM_003457561.1 PREDICTED: Oreochromis niloticus GON-4-like proteinlike (LOC100708211), mRNA	0.0481	0.0449	up	0.2289	up	1.1094	up	0.1840	up	1.0645	up	0.8805	up
MPF_LOC101067309.1.3	XP_003962755.1 PREDICTED: antimicrobial peptide NK-lysin-like [Takifugu rubripes]	0.0481	-0.0942	down	0.1316	up	0.7417	up	0.2258	up	0.8359	up	0.6101	up
MPF_LOC101484349.1.2	XM_004538184.1 PREDICTED: Maylandia zebra sorting nexin-24-like (LOC101484349), mRNA	0.0481	0.0067	up	-0.0554	down	0.8359	up	-0.0621	down	0.8291	up	0.8912	up
MPF_contig_032648		0.0481	-0.2800	down	-0.5655	down	-1.0256	down	-0.2855	down	-0.7456	down	-0.4600	down
MPF_contig_010321		0.0481	-0.1636	down	0.1641	up	0.7522	up	0.3276	up	0.9157	up	0.5881	up
MPF_LOC101078289.1.1	XP_003961121.1 PREDICTED: armadillo repeat-containing protein 7like [Takifugu rubripes]	0.0481	-0.2946	down	-0.2017	down	0.8111	up	0.0929	up	1.1058	up	1.0129	up
MPF_contig_037577		0.0481	-0.2681	down	0.9280	up	0.0673	up	1.1961	up	0.3354	up	-0.8607	down
MPF_LOC100693952.2.2	XM_003442713.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693952 (LOC100693952), mRNA	0.0481	0.1048	up	0.3558	up	0.7709	up	0.2510	up	0.6661	up	0.4151	up
MPF_LOC101471500.2.2	XM_004562486.1 PREDICTED: Maylandia zebra telomere length regulation protein TEL2 homolog (LOC101471500), mRNA	0.0481	-0.1102	down	0.0536	up	0.8317	up	0.1638	up	0.9419	up	0.7781	up

MPF_RTJK.7.23	RTJK_DROME (sp|P21328) RNA-directed DNA polymerase from mobile element jockey OS=Drosophila melanogaster GN=pol PE=1 SV=1	0.0481	-0.0988	down	-0.7216	down	-1.8723	down	-0.6228	down	-1.7735	down	-1.1507	down
MPF_LOC100705401.1.1	XM_003441917.1 PREDICTED: Oreochromis niloticus delta-1-pyrroline-5carboxylate synthase-like (LOC100705401), mRNA	0.0481	0.0497	up	0.1829	up	1.4220	up	0.1332	up	1.3724	up	1.2391	up
MPF_LOC101485782.1.1	XM_004542236.1 PREDICTED: Maylandia zebra SNW domain-containing protein 1-like (LOC101485782), mRNA	0.0482	0.0168	up	-0.0090	down	0.4949	up	-0.0258	down	0.4782	up	0.5040	up
MPF_LOC100705238.1.1	XM_003448656.1 PREDICTED: Oreochromis niloticus 39S ribosomal protein L10, mitochondriallike (LOC100705238), mRNA	0.0482	0.0628	up	0.3062	up	1.0601	up	0.2434	up	0.9974	up	0.7539	up
MPF_LOC100707794.1.1	XM_003441925.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100707794 (LOC100707794), mRNA	0.0482	-0.1428	down	0.1652	up	0.9609	up	0.3080	up	1.1038	up	0.7958	up
MPF_contig_012834	XM_004569635.1 PREDICTED: Maylandia zebra serine/threonineprotein kinase PAK 4-like (LOC101465929), transcript variant X3, mRNA	0.0482	0.0714	up	0.2496	up	1.1377	up	0.1782	up	1.0663	up	0.8881	up

MPF_LOC101479698.2.3	XM_004547798.1 PREDICTED: Maylandia zebra small integral membrane protein 12-like (LOC101479698), transcript variant X2, mRNA	0.0482	0.1038	up	0.1681	up	0.8356	up	0.0643	up	0.7318	up	0.6675	up

MPF_LOC101062855.1.1	XM_003970797.1 PREDICTED: Takifugu rubripes polyubiquitin-B-like, transcript variant 2 (LOC101062855), mRNA	0.0482	0.2332	up	0.2245	up	0.3907	up	-0.0087	down	0.1575	up	0.1661	up
MPF_LOC101065561.13.19	XM_003978943.1 PREDICTED: Takifugu rubripes NACHT, LRR and PYD domains-containing protein 12-like (LOC101065561), partial mRNA	0.0482	0.1699	up	0.4385	up	-0.2272	down	0.2685	up	-0.3971	down	-0.6657	down
MPF_contig_044830		0.0482	-0.0345	down	0.4579	up	1.2091	up	0.4924	up	1.2436	up	0.7512	up
MPF_LOC100711371.1.1	XM_003443926.1 PREDICTED: Oreochromis niloticus transmembrane protein 168-like (LOC100711371), mRNA	0.0482	-0.0514	down	0.0172	up	0.8018	up	0.0686	up	0.8532	up	0.7846	up
MPF_LOC100706800.1.1	XM_003439818.1 PREDICTED: Oreochromis niloticus retinoic acid receptor RXR-gamma-B-like, transcript variant 1 (LOC100706800), mRNA	0.0482	0.0177	up	-0.4176	down	-2.6233	down	-0.4352	down	-2.6410	down	-2.2058	down
MPF_LOC100701989.1.2	XM_003442568.1 PREDICTED: Oreochromis niloticus protein FAM100Blike (LOC100701989), mRNA	0.0482	-0.0910	down	0.6610	up	0.4692	up	0.7521	up	0.5602	up	-0.1919	down

MPF_LOC101468487.1.1	XM_004575286.1 PREDICTED: Maylandia zebra elongation of very long chain fatty acids protein 6like (LOC101468487), mRNA	0.0482	-0.0829	down	0.1188	up	0.7581	up	0.2017	up	0.8410	up	0.6393	up
MPF_LOC101066985.1.1	XP_003978412.1 PREDICTED: FH1/FH2 domain-containing protein 3like [Takifugu rubripes]	0.0482	-0.0706	down	-0.1880	down	0.6160	up	-0.1174	down	0.6866	up	0.8039	up
MPF_LOC100689854.1.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0.0482	-0.0140	down	0.2957	up	1.0574	up	0.3096	up	1.0714	up	0.7618	up
MPF_LOC101478678.2.2	XM_004551725.1 PREDICTED: Maylandia zebra transmembrane protein 150A-like (LOC101478678), mRNA	0.0482	0.5022	up	0.1734	up	1.4990	up	-0.3288	down	0.9968	up	1.3256	up
MPF_LOC100693393.1.1	XP_003459043.1 PREDICTED: beta-1,3galactosyltransferase 1-like [Oreochromis niloticus]	0.0482	-0.1152	down	-0.0065	down	0.5563	up	0.1086	up	0.6715	up	0.5628	up
MPF_LOC100708030.1.1	XP_003457772.1 PREDICTED: bone morphogenetic protein 15-like [Oreochromis niloticus]	0.0483	-0.1667	down	0.3050	up	0.9286	up	0.4718	up	1.0953	up	0.6235	up
MPF_LOC101482642.1.1	XM_004539979.1 PREDICTED: Maylandia zebra coiled-coil domaincontaining protein 177-like (LOC101482642), transcript variant X1, mRNA	0.0483	-0.0857	down	0.8426	up	0.9882	up	0.9283	up	1.0739	up	0.1456	up
MPF_contig_025941		0.0483	0.3880	up	0.5301	up	1.3687	up	0.1420	up	0.9807	up	0.8386	up

MPF_LOC101484489.6.10	XM_004548851.1 PREDICTED: Maylandia zebra 14-3-3 protein beta/alpha-A-like (LOC101484489), mRNA	0.0483	-0.0487	down	-0.6697	down	-0.9944	down	-0.6210	down	-0.9457	down	-0.3247	down
MPF_IF6.2.2	[BBH] IF6_DANRE (sp|Q6ZM19) Eukaryotic translation initiation factor 6 OS=Danio rerio GN=eif6 PE=2 SV=1	0.0483	-0.0002	down	0.2074	up	0.5707	up	0.2076	up	0.5709	up	0.3633	up
MPF_LOC100704027.1.1	XM_003457466.1 PREDICTED: Oreochromis niloticus apoptosis-inducing factor 2-like (LOC100704027), mRNA	0.0483	0.2937	up	1.1642	up	1.0593	up	0.8705	up	0.7655	up	-0.1049	down
MPF_contig_041304	XM_004561971.1 PREDICTED: Maylandia zebra run domain Beclin-1 interacting and cystein-rich containing protein-like (LOC101483120), transcript variant X2, mRNA	0.0483	0.0319	up	0.3520	up	1.0303	up	0.3202	up	0.9984	up	0.6783	up
MPF_LOC100692880.1.1	XP_003443649.1 PREDICTED: beta,betacarotene 15,15'monooxygenase-like [Oreochromis niloticus]	0.0483	-0.1200	down	0.1257	up	1.1651	up	0.2457	up	1.2851	up	1.0394	up
MPF_LOC101469738.1.2	XM_004551780.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase MSL2-like (LOC101469738), mRNA	0.0483	-0.0936	down	0.0653	up	1.0319	up	0.1589	up	1.1255	up	0.9666	up
MPF_LOC101475466.2.2	XM_004559920.1 PREDICTED: Maylandia zebra carbohydrate sulfotransferase 11-like (LOC101475466), mRNA	0.0483	0.0967	up	0.2541	up	0.5730	up	0.1574	up	0.4763	up	0.3188	up

MPF_LOC100618396.1.2	XP_003340812.1 PREDICTED: zinc finger protein 420-like [Monodelphis domestica]	0.0483	0.0562	up	0.2694	up	0.9234	up	0.2132	up	0.8672	up	0.6540	up
MPF_LOC101473315.1.1	XM_004572231.1 PREDICTED: Maylandia zebra protein AF1q-like (LOC101473315), transcript variant X2, mRNA	0.0483	0.0201	up	0.0026	up	0.8321	up	-0.0175	down	0.8120	up	0.8295	up
MPF_PRNPRS3.2.10	NM_001013298.1 Danio rerio prion protein, related sequence 3 (prnprs3), mRNA emb|AJ620614.1| Danio rerio mRNA for prion protein 2 (prp2 gene)	0.0483	-0.1811	down	0.1365	up	0.5084	up	0.3176	up	0.6894	up	0.3718	up
MPF_LOC101473952.2.2	XM_004564949.1 PREDICTED: Maylandia zebra transportin-3-like (LOC101473952), mRNA	0.0483	-0.0130	down	-0.0260	down	0.6897	up	-0.0131	down	0.7026	up	0.7157	up
MPF_LOC101065219.1.3	XM_003969289.1 PREDICTED: Takifugu rubripes protein S100-A1-like (LOC101065219), mRNA	0.0483	0.0641	up	-1.0936	down	-3.0014	down	-1.1577	down	-3.0655	down	-1.9078	down
MPF_LOC101163797.1.1	XM_004086537.1 PREDICTED: Oryzias latipes TBC1 domain family member 2A-like (LOC101163797), mRNA	0.0483	-0.0818	down	0.1968	up	0.6086	up	0.2786	up	0.6904	up	0.4118	up
MPF_contig_029328	XM_004570819.1 PREDICTED: Maylandia zebra oxysterol-binding protein-related protein 5-like (LOC101472907), transcript variant X2, mRNA	0.0484	0.2259	up	0.1648	up	1.0814	up	-0.0611	down	0.8555	up	0.9166	up

MPF_LOC101479743.1.1	XM_004559840.1 PREDICTED: Maylandia zebra zinc finger protein 93like (LOC101479743), mRNA	0.0484	0.2012	up	0.2815	up	1.2130	up	0.0803	up	1.0118	up	0.9315	up
MPF_contig_020618		0.0485	0.0287	up	0.2482	up	0.7052	up	0.2195	up	0.6765	up	0.4570	up
MPF_LOC101067754.3.3	XM_003961265.1 PREDICTED: Takifugu rubripes NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subuni 4like (LOC101067754), mRNA	0.0485	-0.0444	down	-2.0100	down	-2.4892	down	-1.9656	down	-2.4448	down	-0.4793	down
MPF_LOC100706240.1.1	XM_003455173.1 PREDICTED: Oreochromis niloticus pre-mRNA-splicing factor SLU7-like (LOC100706240), mRNA	0.0485	-0.2195	down	0.1206	up	0.7846	up	0.3401	up	1.0042	up	0.6641	up
MPF_contig_042600	XM_004567440.1 PREDICTED: Maylandia zebra myb/SANT-like DNAbinding domain-containing protein 2-like (LOC101484373), transcript variant X1, mRNA	0.0485	0.0099	up	-0.2821	down	0.9916	up	-0.2920	down	0.9817	up	1.2738	up
MPF_LOC101465421.2.2	XM_004543074.1 PREDICTED: Maylandia zebra transcription factor 12like (LOC101465421), transcript variant X4, mRNA	0.0485	-0.0170	down	0.4447	up	0.8601	up	0.4616	up	0.8771	up	0.4154	up
MPF_contig_027341		0.0485	-0.0465	down	0.4140	up	2.0740	up	0.4605	up	2.1206	up	1.6600	up
MPF_LOC101482091.1.1	XM_004568619.1 PREDICTED: Maylandia zebra retinoid-inducible serine carboxypeptidase-like (LOC101482091), mRNA	0.0485	-0.0918	down	-0.0223	down	0.6065	up	0.0695	up	0.6984	up	0.6289	up

MPF_contig_019245		0.0485	0.1003	up	0.3564	up	0.7039	up	0.2562	up	0.6036	up	0.3474	up
MPF_LOC101477304.1.1	XM_004560480.1 PREDICTED: Maylandia zebra nuclear pore complex protein Nup88-like (LOC101477304), mRNA	0.0485	-0.0670	down	0.0772	up	0.6573	up	0.1442	up	0.7243	up	0.5801	up
MPF_contig_044005		0.0485	-0.6966	down	-0.9410	down	-2.9635	down	-0.2444	down	-2.2669	down	-2.0225	down
MPF_contig_043890		0.0485	0.0081	up	-0.7774	down	-2.1453	down	-0.7856	down	-2.1534	down	-1.3678	down
MPF_contig_012069	XM_004552661.1 PREDICTED: Maylandia zebra neuropilin-2-like (LOC101479614), transcript variant X1, mRNA	0.0485	0.2050	up	-0.5585	down	-1.0866	down	-0.7635	down	-1.2916	down	-0.5281	down
MPF_LOC101478538.1.2	XM_004541269.1 PREDICTED: Maylandia zebra tripartite motifcontaining protein 46-like (LOC101478538), mRNA	0.0485	-0.0102	down	0.2717	up	0.8612	up	0.2819	up	0.8714	up	0.5895	up
MPF_NEMVEDRAFT_V1G47783.1.1	XP_001618475.1 hypothetical protein NEMVEDRAFT_v1g47783 [Nematostella vectensis]	0.0485	-0.1106	down	0.2904	up	2.1854	up	0.4010	up	2.2960	up	1.8950	up
MPF_contig_009677		0.0485	0.0584	up	-0.4358	down	-2.0235	down	-0.4942	down	-2.0818	down	-1.5877	down
MPF_contig_016368		0.0485	-0.1763	down	0.0454	up	0.7504	up	0.2218	up	0.9267	up	0.7049	up
MPF_LOC100693775.1.1	XM_003443191.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693775 (LOC100693775), mRNA	0.0485	0.5879	up	0.0551	up	1.3314	up	-0.5328	down	0.7435	up	1.2764	up

MPF_LOC101478122.1.2	XM_004552476.1 PREDICTED: Maylandia zebra SH3 and multiple ankyrin repeat domains protein 1-like (LOC101478122), mRNA	0.0485	-0.2244	down	-0.0964	down	0.6482	up	0.1280	up	0.8726	up	0.7445	up
MPF_LOC101468869.1.1	XM_004549331.1 PREDICTED: Maylandia zebra U6 snRNA-associated Sm-like protein LSm6-like (LOC101468869), transcript variant X3, mRNA	0.0485	-0.0954	down	0.1696	up	0.3762	up	0.2650	up	0.4715	up	0.2066	up
MPF_contig_043515		0.0485	-0.9803	down	0.0587	up	-1.6830	down	1.0390	up	-0.7027	down	-1.7417	down
MPF_KLC1.1.1	NP_001075428.1 kinesin light chain 1 isoform 1H [Mus musculus]	0.0485	0.0212	up	0.2051	up	0.5435	up	0.1840	up	0.5224	up	0.3384	up
MPF_LOC100693187.1.1	XP_003453770.1 PREDICTED: leucine-rich repeat and WD repeatcontaining protein 1-like [Oreochromis niloticus]	0.0485	-0.0076	down	-0.0038	down	1.0931	up	0.0038	up	1.1007	up	1.0969	up
MPF_LOC101486124.3.4	XM_004575749.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12-like (LOC101486124), mRNA	0.0485	0.2470	up	-0.2943	down	-2.0699	down	-0.5413	down	-2.3169	down	-1.7757	down
MPF_LOC101475312.1.1	XM_004568156.1 PREDICTED: Maylandia zebra uncharacterized LOC101475312 (LOC101475312), transcript variant X6, mRNA	0.0485	0.1774	up	0.3723	up	0.7111	up	0.1949	up	0.5337	up	0.3388	up

MPF_LOC101483057.2.3	XM_004543628.1 PREDICTED: Maylandia zebra UPF0692 protein C19orf54 homolog (LOC101483057), transcript variant X5, mRNA	0.0485	0.1380	up	0.6125	up	0.5446	up	0.4745	up	0.4066	up	-0.0679	down
MPF_RBBP5.1.1	XP_003447710.1 PREDICTED: retinoblastomabinding protein 5 [Oreochromis niloticus]	0.0485	0.8458	up	0.7068	up	1.4077	up	-0.1390	down	0.5619	up	0.7009	up
MPF_LOC101470874.1.1	XM_004567206.1 PREDICTED: Maylandia zebra abl interactor 1-like (LOC101470874), transcript variant X3, mRNA	0.0485	0.8545	up	0.1245	up	0.5361	up	-0.7300	down	-0.3184	down	0.4116	up
MPF_LOC101480518.1.1	XM_004538169.1 PREDICTED: Maylandia zebra TBC1 domain family member 10A-like (LOC101480518), mRNA	0.0485	-0.1547	down	-0.0518	down	0.4102	up	0.1028	up	0.5648	up	0.4620	up
MPF_LOC101482211.2.2	XM_004547151.1 PREDICTED: Maylandia zebra intracellular hyaluronanbinding protein 4-like (LOC101482211), mRNA	0.0485	0.3006	up	0.3515	up	0.7584	up	0.0509	up	0.4578	up	0.4068	up
MPF_LOC101471367.2.5	XM_004573481.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase CBL-like (LOC101471367), mRNA	0.0485	0.0392	up	-0.0121	down	0.8915	up	-0.0513	down	0.8523	up	0.9037	up
MPF_LOC100695994.31.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0.0485	-0.1206	down	0.1414	up	0.9426	up	0.2620	up	1.0632	up	0.8012	up

MPF_LOC100697615.4.4	XM_003448955.1 PREDICTED: Oreochromis niloticus eukaryotic translation initiation factor 3 subunit K-like (LOC100697615), mRNA	0.0485	0.1342	up	0.3953	up	-0.7224	down	0.2612	up	-0.8566	down	-1.1178	down
MPF_contig_039068		0.0485	0.0146	up	0.0189	up	0.6035	up	0.0043	up	0.5889	up	0.5846	up
MPF_LOC101163960.1.1	XM_004066861.1 PREDICTED: Oryzias latipes cellular retinoic acid-binding protein 1-like (LOC101163960), mRNA	0.0485	0.0882	up	0.4433	up	1.1711	up	0.3551	up	1.0829	up	0.7278	up
MPF_SI_CH211278P9.4.1.1	XP_001336197.4 PREDICTED: NACHT, LRR and PYD domains-containing protein 12 [Danio rerio]	0.0485	0.0189	up	0.1413	up	0.6452	up	0.1224	up	0.6263	up	0.5039	up
MPF_UIF.1.1	UIF_SALSA (sp|B5X3V2) UAP56-interacting factor OS=Salmo salar GN=fyttd1 PE=2 SV=1	0.0485	-0.1223	down	0.2113	up	0.7168	up	0.3336	up	0.8392	up	0.5056	up
MPF_contig_031056	XM_003444094.1 PREDICTED: Oreochromis niloticus ribonuclease UK114like, transcript variant 1 (LOC100710570), mRNA	0.0485	0.0978	up	0.3755	up	0.7128	up	0.2777	up	0.6150	up	0.3373	up
MPF_LOC101482429.1.1	XM_004574980.1 PREDICTED: Maylandia zebra post-GPI attachment to proteins factor 3-like (LOC101482429), mRNA	0.0485	0.0473	up	0.3592	up	1.2473	up	0.3119	up	1.2000	up	0.8881	up
MPF_contig_000216		0.0485	-0.0297	down	0.4509	up	0.9407	up	0.4806	up	0.9704	up	0.4898	up

MPF_LOC101471351.2.2	XM_004571326.1 PREDICTED: Maylandia zebra T-cell activation inhibitor, mitochondrial-like (LOC101471351), transcript variant X4, mRNA	0.0485	0.0524	up	0.3180	up	0.7622	up	0.2656	up	0.7098	up	0.4442	up
MPF_LOC101478874.1.1	XM_004555333.1 PREDICTED: Maylandia zebra uncharacterized LOC101478874 (LOC101478874), transcript variant X1, mRNA	0.0485	-0.1514	down	-0.2948	down	0.6499	up	-0.1434	down	0.8013	up	0.9447	up
MPF_LOC101470485.3.3	XM_004545890.1 PREDICTED: Maylandia zebra uncharacterized LOC101470485 (LOC101470485), mRNA	0.0485	0.0757	up	0.2365	up	0.8722	up	0.1607	up	0.7964	up	0.6357	up
MPF_LOC101479781.1.3	XM_004568703.1 PREDICTED: Maylandia zebra mesoderm development candidate 1-like (LOC101479781), mRNA	0.0485	-0.0680	down	0.1611	up	0.7214	up	0.2291	up	0.7894	up	0.5603	up
MPF_contig_004686		0.0485	-0.1649	down	0.1084	up	0.5657	up	0.2733	up	0.7307	up	0.4573	up
MPF_contig_046594		0.0485	0.0868	up	0.1803	up	0.7629	up	0.0935	up	0.6761	up	0.5826	up
MPF_LOC101481584.1.1	XM_004540453.1 PREDICTED: Maylandia zebra WD repeat-containing protein 25-like (LOC101481584), mRNA	0.0485	-0.0274	down	0.3413	up	1.1569	up	0.3687	up	1.1843	up	0.8155	up

MPF_LOC101471180.4.4	XM_004551222.1 PREDICTED: Maylandia zebra cell adhesion molecule 1-like (LOC101471180), transcript variant X5, mRNA	0.0485	0.4206	up	0.2834	up	1.0001	up	-0.1373	down	0.5795	up	0.7167	up
MPF_LOC101479341.3.9	XM_004575727.1 PREDICTED: Maylandia zebra high affinity immunoglobulin epsilon receptor subunit alpha-like (LOC101479341), partial mRNA	0.0485	0.0577	up	-0.2709	down	0.7957	up	-0.3286	down	0.7380	up	1.0666	up
MPF_LOC101487432.3.3	XM_004569624.1 PREDICTED: Maylandia zebra cdc42 effector protein 3-like (LOC101487432), transcript variant X4, mRNA	0.0485	-0.0504	down	0.1922	up	0.5045	up	0.2427	up	0.5549	up	0.3122	up
MPF_contig_014448		0.0485	0.1246	up	0.2326	up	0.6046	up	0.1080	up	0.4800	up	0.3721	up
MPF_LOC100696688.1.1	XM_003439694.1 PREDICTED: Oreochromis niloticus tight junction protein ZO-3-like (LOC100696688), mRNA	0.0486	-0.1454	down	0.0904	up	1.0717	up	0.2358	up	1.2170	up	0.9813	up
MPF_LOC100694793.1.1	XM_003452016.1 PREDICTED: Oreochromis niloticus mTERF domaincontaining protein 3, mitochondrial-like (LOC100694793), mRNA	0.0486	-0.0902	down	0.1054	up	0.6374	up	0.1957	up	0.7277	up	0.5320	up
MPF_COX17.4.4	COX17_PIG (sp|P81045) Cytochrome c oxidase copper chaperone OS=Sus scrofa GN=COX17 PE=1 SV=1	0.0486	-0.1070	down	0.0019	up	0.7186	up	0.1089	up	0.8256	up	0.7167	up
MPF_contig_003959		0.0486	-0.0539	down	0.0472	up	0.6993	up	0.1011	up	0.7532	up	0.6521	up

MPF_LOC100691323.1.1	XP_003438713.1 PREDICTED: tripartite motifcontaining protein 69-like isoform 1 [Oreochromis niloticus]	0.0486	0.0633	up	0.2911	up	0.7522	up	0.2278	up	0.6890	up	0.4612	up
MPF_LOC101067973.1.1	XM_003978066.1 PREDICTED: Takifugu rubripes tRNA modification GTPase GTPBP3, mitochondrial-like (LOC101067973), mRNA	0.0486	-0.0200	down	0.0090	up	0.6502	up	0.0290	up	0.6702	up	0.6412	up
MPF_LOC101479508.1.1	XM_004545378.1 PREDICTED: Maylandia zebra leucine-rich repeats and immunoglobulin-like domains protein 1-like (LOC101479508), mRNA	0.0486	0.0513	up	-0.0209	down	0.5949	up	-0.0722	down	0.5436	up	0.6158	up
MPF_LOC100703948.1.1	XM_003439297.1 PREDICTED: Oreochromis niloticus membrane-bound transcription factor site-2 protease-like, transcript variant 1 (LOC100703948), mRNA	0.0486	0.4039	up	0.1969	up	1.1843	up	-0.2070	down	0.7804	up	0.9874	up
MPF_LOC101472667.1.1	XM_004559535.1 PREDICTED: Maylandia zebra PDZ domaincontaining protein GIPC1-like (LOC101472667), transcript variant X1, mRNA	0.0486	0.0492	up	0.3544	up	1.0878	up	0.3052	up	1.0387	up	0.7335	up
MPF_LOC446087.1.1	XM_003963804.1 PREDICTED: Takifugu rubripes nicotinic acetylcholine receptor alpha 1a subunit (LOC446087), mRNA	0.0486	-0.1571	down	0.0112	up	0.8761	up	0.1682	up	1.0331	up	0.8649	up

MPF_contig_047950	XR_191716.1 PREDICTED: Maylandia zebra girdin-like (LOC101485337), transcript variant X7, misc_RNA	0.0486	0.1378	up	0.2558	up	0.9797	up	0.1180	up	0.8419	up	0.7239	up
MPF_LOC100704968.1.1	XP_003447950.1 PREDICTED: ATPdependent RNA helicase DDX39A-like [Oreochromis niloticus]	0.0486	-0.1231	down	0.1410	up	0.7118	up	0.2640	up	0.8349	up	0.5709	up
MPF_contig_023146		0.0486	-0.0477	down	0.4039	up	0.7769	up	0.4516	up	0.8247	up	0.3731	up
MPF_LOC100704848.1.1	XM_003438716.1 PREDICTED: Oreochromis niloticus leucine carboxyl methyltransferase 1-like (LOC100704848), mRNA	0.0486	-0.0402	down	0.3019	up	1.2253	up	0.3421	up	1.2655	up	0.9234	up
MPF_LOC101482903.1.2	XM_004550060.1 PREDICTED: Maylandia zebra superoxide dismutase [Cu-Zn]-like (LOC101482903), mRNA	0.0486	0.0531	up	0.0952	up	0.4207	up	0.0421	up	0.3676	up	0.3255	up
MPF_LOC101486796.1.2	XM_004553614.1 PREDICTED: Maylandia zebra elongation of very long chain fatty acids protein 6like (LOC101486796), mRNA	0.0487	0.3094	up	0.2024	up	0.8086	up	-0.1070	down	0.4991	up	0.6062	up
MPF_RL7A.2.2	[BBH] RL7A_TAKRU (sp|O57592) 60S ribosomal protein L7a OS=Takifugu rubripes GN=rpl7a PE=3 SV=3	0.0487	-0.0385	down	-0.5048	down	-1.9501	down	-0.4663	down	-1.9116	down	-1.4453	down
MPF_LOC101487848.1.1	XM_004552880.1 PREDICTED: Maylandia zebra leucine-rich repeatcontaining protein 8C-like	0.0487	-0.1166	down	0.2715	up	0.7667	up	0.3881	up	0.8833	up	0.4952	up

	(LOC101487848), mRNA													
MPF_LOC100694703.1.1	XP_003450648.1 PREDICTED: prenylated Rab acceptor protein 1-like [Oreochromis niloticus]	0.0487	-0.1746	down	0.1489	up	0.6068	up	0.3235	up	0.7815	up	0.4579	up
MPF_LOC101168764.1.1	XP_004084726.1 PREDICTED: insulin receptorlike [Oryzias latipes]	0.0487	-0.1771	down	0.2214	up	1.2058	up	0.3985	up	1.3830	up	0.9844	up
MPF_LOC101481962.1.2	XM_004559755.1 PREDICTED: Maylandia zebra striatin-like (LOC101481962), transcript variant X2, mRNA	0.0487	-0.0629	down	0.0453	up	-0.8670	down	0.1081	up	-0.8041	down	-0.9122	down
MPF_LOC101467619.1.4	XM_004561184.1 PREDICTED: Maylandia zebra ubiquitin thioesterase ZRANB1-like (LOC101467619), mRNA	0.0487	-0.0148	down	-0.0687	down	-1.2467	down	-0.0538	down	-1.2319	down	-1.1780	down
MPF_BGLU_2G04620.1.1	YP_002908152.1 putative membrane-anchored cell surface protein [Burkholderia glumae BGR1]	0.0487	-0.1497	down	0.1520	up	0.7976	up	0.3017	up	0.9473	up	0.6456	up
MPF_NIN.1.1	XM_003442973.1 PREDICTED: Oreochromis niloticus ninein (GSK3B interacting protein) (NIN), mRNA	0.0487	-0.2122	down	0.3523	up	0.1966	up	0.5645	up	0.4088	up	-0.1558	down
MPF_LOC101481552.25.41	XM_004575656.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101481552), mRNA	0.0487	0.1030	up	0.1246	up	-0.8502	down	0.0216	up	-0.9532	down	-0.9748	down

MPF_RTTN.1.1	XM_003443574.1 PREDICTED: Oreochromis niloticus rotatin (RTTN), mRNA	0.0487	-0.0178	down	0.2251	up	1.0618	up	0.2430	up	1.0797	up	0.8367	up
MPF_LOC100703670.1.1	XP_003437761.1 PREDICTED: LOW QUALITY PROTEIN: phosphorylase b kinase regulatory subunit beta-like [Oreochromis niloticus]	0.0487	0.0193	up	0.6506	up	1.1290	up	0.6314	up	1.1098	up	0.4784	up
MPF_LOC101469216.4.4	XM_004539562.1 PREDICTED: Maylandia zebra nuclear factor of activated T-cells, cytoplasmic 3-like (LOC101469216), transcript variant X2, mRNA	0.0487	0.1035	up	0.3190	up	1.0995	up	0.2155	up	0.9961	up	0.7805	up
MPF_contig_035256		0.0487	0.2062	up	0.3937	up	1.0355	up	0.1875	up	0.8294	up	0.6419	up
MPF_LOC101163609.3.3	XP_004079323.1 PREDICTED: uncharacterized protein LOC101163609 [Oryzias latipes]	0.0488	-0.1169	down	0.6913	up	0.5780	up	0.8082	up	0.6950	up	-0.1132	down
MPF_LOC101468652.1.1	XM_004547381.1 PREDICTED: Maylandia zebra POU domain, class 4, transcription factor 2-like (LOC101468652), mRNA	0.0488	0.0086	up	0.2050	up	-0.8202	down	0.1964	up	-0.8288	down	-1.0252	down
MPF_LOC101486284.1.3	XM_004546431.1 PREDICTED: Maylandia zebra transmembrane protein 189-like (LOC101486284), mRNA	0.0488	-0.1679	down	0.0005	up	1.2832	up	0.1684	up	1.4511	up	1.2826	up

MPF_LOC101472565.1.2	XM_004557605.1 PREDICTED: Maylandia zebra MMS19 nucleotide excision repair protein homolog (LOC101472565), mRNA	0.0488	-0.0037	down	0.1830	up	0.7381	up	0.1867	up	0.7417	up	0.5551	up
MPF_LOC100700286.1.1	XP_003447688.1 PREDICTED: protocadherin1-like [Oreochromis niloticus]	0.0488	-0.5248	down	-0.3609	down	0.8305	up	0.1640	up	1.3553	up	1.1914	up
MPF_contig_020945	XM_004542601.1 PREDICTED: Maylandia zebra muscleblind-like protein 1-like (LOC101483053), transcript variant X16, mRNA	0.0488	0.1064	up	-1.3712	down	-3.3838	down	-1.4776	down	-3.4901	down	-2.0126	down
MPF_LOC100708416.1.1	XP_003441462.1 PREDICTED: tubulin polyglutamylase complex subunit 2-like [Oreochromis niloticus]	0.0488	0.4675	up	0.1291	up	0.9730	up	-0.3384	down	0.5055	up	0.8439	up
MPF_LOC100617860.1.1	XP_003340874.1 PREDICTED: zinc finger protein 420-like [Monodelphis domestica]	0.0488	-0.0119	down	0.1396	up	0.8622	up	0.1515	up	0.8741	up	0.7226	up
MPF_LOC101472770.2.6	XM_004562212.1 PREDICTED: Maylandia zebra WAS/WASL-interacting protein family member 2-like (LOC101472770), transcript variant X3, mRNA	0.0488	-0.0414	down	0.4044	up	1.1663	up	0.4458	up	1.2077	up	0.7619	up
MPF_LOC101464072.1.1	XM_004562979.1 PREDICTED: Maylandia zebra heme oxygenase-like (LOC101464072), mRNA	0.0488	-0.0459	down	-0.1183	down	0.8211	up	-0.0724	down	0.8669	up	0.9394	up
MPF_LOC101468563.1.2	XM_004572588.1 PREDICTED: Maylandia zebra alkaline nuclease-like (LOC101468563), transcript variant X6, mRNA	0.0488	-0.4242	down	-0.4291	down	-2.0325	down	-0.0049	down	-1.6083	down	-1.6034	down

MPF_LOC100709062.2.2	XP_003445395.1 PREDICTED: ATP-binding cassette sub-family A member 12-like [Oreochromis niloticus]	0.0488	-0.2789	down	-0.1023	down	0.3770	up	0.1766	up	0.6559	up	0.4793	up
MPF_LOC101477603.1.4	XM_004564201.1 PREDICTED: Maylandia zebra mast/stem cell growth factor receptor kita-like (LOC101477603), transcript variant X1, mRNA	0.0488	-0.1804	down	0.0640	up	1.0465	up	0.2444	up	1.2269	up	0.9825	up
MPF_contig_048210	XM_004539039.1 PREDICTED: Maylandia zebra tuberin-like (LOC101468908), transcript variant X4, mRNA	0.0488	0.1260	up	0.4117	up	0.8901	up	0.2858	up	0.7641	up	0.4784	up
MPF_LOC101468648.3.4	XM_004570179.1 PREDICTED: Maylandia zebra ceramide synthase 1like (LOC101468648), mRNA	0.0489	0.2059	up	0.1387	up	0.9779	up	-0.0672	down	0.7720	up	0.8392	up
MPF_ZN271.1.19	ZN271_HUMAN (sp|Q14591) Zinc finger protein 271 OS=Homo sapiens GN=ZNF271 PE=2 SV=4	0.0489	0.1200	up	0.3158	up	1.0411	up	0.1958	up	0.9211	up	0.7253	up
MPF_LOC101480875.1.1	XM_004574330.1 PREDICTED: Maylandia zebra proline-, glutamic acid- and leucine-rich protein 1-like (LOC101480875), transcript variant X2, mRNA	0.0489	0.4635	up	0.3670	up	0.6808	up	-0.0965	down	0.2173	up	0.3138	up
MPF_contig_037490		0.0490	-0.2183	down	0.2068	up	1.5130	up	0.4251	up	1.7312	up	1.3061	up
MPF_LOC101470369.1.1	XM_004543573.1 PREDICTED: Maylandia zebra structural maintenance of chromosomes protein 4like (LOC101470369), transcript variant X1, mRNA	0.0490	-0.0624	down	0.1099	up	0.7655	up	0.1723	up	0.8279	up	0.6556	up

MPF_LOC101465123.1.1	XM_004541125.1 PREDICTED: Maylandia zebra actin filamentassociated protein 1-like 1like (LOC101465123), transcript variant X3, mRNA	0.0490	0.0498	up	-0.0907	down	0.7423	up	-0.1406	down	0.6925	up	0.8331	up
MPF_contig_002742	XM_004546428.1 PREDICTED: Maylandia zebra kelch-like protein 12like (LOC101485336), transcript variant X2, mRNA	0.0491	0.1174	up	0.2886	up	0.8838	up	0.1712	up	0.7664	up	0.5951	up
MPF_LOC101465780.2.3	XM_004560720.1 PREDICTED: Maylandia zebra voltage-dependent calcium channel gamma-3 subunit-like (LOC101465780), transcript variant X2, mRNA	0.0491	-0.1033	down	0.0196	up	0.5729	up	0.1230	up	0.6762	up	0.5532	up
MPF_LOC100701403.2.2	XM_003454667.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100701403 (LOC100701403), mRNA	0.0491	-0.0529	down	0.0598	up	0.5239	up	0.1128	up	0.5768	up	0.4641	up
MPF_LOC101069688.1.1	XM_003973598.1 PREDICTED: Takifugu rubripes uncharacterized LOC101069688 (LOC101069688), mRNA	0.0491	0.0129	up	0.9158	up	1.0973	up	0.9029	up	1.0844	up	0.1815	up
MPF_contig_015308		0.0491	0.1245	up	0.1116	up	0.5419	up	-0.0129	down	0.4174	up	0.4303	up
MPF_MYO5A.1.1	MYO5A_CHICK (sp|Q02440) Unconventional myosin-Va OS=Gallus gallus GN=MYO5A PE=1 SV=1	0.0491	-0.1732	down	-0.0782	down	1.0826	up	0.0950	up	1.2557	up	1.1608	up

MPF_LOC101475224.2.2	XM_004569937.1 PREDICTED: Maylandia zebra gephyrin-like (LOC101475224), mRNA	0.0492	0.1524	up	0.3520	up	0.7243	up	0.1996	up	0.5719	up	0.3723	up
MPF_LOC101465607.3.4	XM_004543463.1 PREDICTED: Maylandia zebra mitogen-activated protein kinase 6-like (LOC101465607), transcript variant X3, mRNA	0.0492	-0.0530	down	0.1429	up	0.6385	up	0.1959	up	0.6915	up	0.4956	up
MPF_LOC101468265.1.1	XM_004566722.1 PREDICTED: Maylandia zebra iron-sulfur cluster cochaperone protein HscB, mitochondrial-like (LOC101468265), mRNA	0.0492	-0.0295	down	0.4393	up	0.8575	up	0.4689	up	0.8870	up	0.4182	up
MPF_LOC101160373.1.1	XP_004083232.1 PREDICTED: DNA damageregulated autophagy modulator protein 1-like [Oryzias latipes]	0.0492	0.0878	up	-1.0545	down	-2.1845	down	-1.1423	down	-2.2722	down	-1.1299	down
MPF_LOC100694722.1.1	XP_003456565.1 PREDICTED: aftiphilin-like [Oreochromis niloticus]	0.0492	-0.0423	down	0.0483	up	0.9063	up	0.0906	up	0.9486	up	0.8581	up
MPF_contig_015598		0.0492	0.2434	up	0.6382	up	0.5084	up	0.3948	up	0.2650	up	-0.1298	down
MPF_AGFG1.2.7	XM_003441725.1 PREDICTED: Oreochromis niloticus ArfGAP with FG repeats 1 (AGFG1), mRNA	0.0493	-0.1413	down	0.6093	up	1.6529	up	0.7506	up	1.7942	up	1.0436	up
MPF_LOC100699446.1.1	XP_003459443.1 PREDICTED: hypothetical protein LOC100699446 [Oreochromis niloticus]	0.0493	0.0426	up	0.1065	up	0.5214	up	0.0639	up	0.4788	up	0.4149	up

MPF_LOC100704612.1.2	XM_003446652.1 PREDICTED: Oreochromis niloticus interactor protein for cytohesin exchange factors 1like (LOC100704612), mRNA	0.0493	-0.1045	down	0.0519	up	0.4995	up	0.1564	up	0.6040	up	0.4476	up
MPF_contig_028512	XM_004569132.1 PREDICTED: Maylandia zebra solute carrier family 45 member 3-like (LOC101474184), transcript variant X6, mRNA	0.0493	0.0550	up	0.1361	up	0.6840	up	0.0811	up	0.6289	up	0.5478	up
MPF_CD276.6.9	CD276_XENLA (sp|Q68EV1) CD276 antigen homolog OS=Xenopus laevis GN=cd276 PE=2 SV=1	0.0493	-0.4080	down	-1.0944	down	-2.4567	down	-0.6864	down	-2.0487	down	-1.3623	down
MPF_LOC100693817.1.1	XM_003454059.1 PREDICTED: Oreochromis niloticus methionine synthaselike (LOC100693817), mRNA	0.0493	-0.1906	down	-0.0195	down	0.7528	up	0.1710	up	0.9434	up	0.7724	up
MPF_ACHA4.1.1	ACHA4_CHICK (sp|P09482) Neuronal acetylcholine receptor subunit alpha-4 OS=Gallus gallus GN=CHRNA4 PE=1 SV=1	0.0493	-0.1403	down	0.2049	up	0.8468	up	0.3452	up	0.9871	up	0.6419	up
MPF_SUCO.1.1	XM_681409.5 PREDICTED: Danio rerio si:ch211-184m19.1 (si:ch211-184m19.1), mRNA	0.0493	0.0734	up	0.4510	up	0.9429	up	0.3776	up	0.8695	up	0.4919	up
		0.0494	-1.0853	down	-0.5436	down	0.9049	up	0.5416	up	1.9902	up	1.4486	up
MPF_contig_046797		0.0494	0.1889	up	0.1693	up	1.1947	up	-0.0197	down	1.0058	up	1.0254	up

MPF_LOC101464906.1.1	XM_004558151.1 PREDICTED: Maylandia zebra leucine-rich repeat and fibronectin type III domaincontaining protein 1-like (LOC101464906), mRNA	0.0494	-0.3921	down	-0.1035	down	1.0424	up	0.2886	up	1.4345	up	1.1459	up
MPF_LY9.3.3	LY9_HUMAN (sp|Q9HBG7) Tlymphocyte surface antigen Ly-9 OS=Homo sapiens GN=LY9 PE=1 SV=3	0.0494	-0.8371	down	-1.1349	down	-2.9944	down	-0.2978	down	-2.1572	down	-1.8594	down
MPF_LOC101478371.1.2	XM_004568698.1 PREDICTED: Maylandia zebra ankyrin repeat and SOCS box protein 7-like (LOC101478371), mRNA	0.0494	-0.1600	down	0.1365	up	0.9676	up	0.2965	up	1.1276	up	0.8311	up
MPF_LOC101157961.1.1	XP_004075439.1 PREDICTED: 39S ribosomal protein L28, mitochondriallike [Oryzias latipes]	0.0494	0.0055	up	0.0281	up	0.7248	up	0.0225	up	0.7193	up	0.6968	up
MPF_LOC101480673.1.3	XM_004573523.1 PREDICTED: Maylandia zebra protein SMG7-like (LOC101480673), transcript variant X3, mRNA	0.0494	-0.3146	down	0.2621	up	0.9449	up	0.5767	up	1.2595	up	0.6828	up
MPF_LOC101476386.2.2	XM_004567780.1 PREDICTED: Maylandia zebra CUGBP Elav-like family member 2-like (LOC101476386), transcript variant X2, mRNA	0.0494	0.0231	up	0.2983	up	0.6318	up	0.2752	up	0.6087	up	0.3335	up
MPF_contig_006073		0.0494	-0.0951	down	0.1989	up	0.7964	up	0.2941	up	0.8916	up	0.5975	up
MPF_LOC100689949.1.1	XP_003452304.1 PREDICTED: ELMO domain-containing protein 2-like [Oreochromis niloticus]	0.0494	-0.0792	down	-0.1834	down	0.6562	up	-0.1041	down	0.7354	up	0.8396	up

MPF_LOC100534399.1.2	XM_003449684.1 PREDICTED: Oreochromis niloticus annexin A5 (LOC100534399), mRNA	0.0494	-0.0149	down	0.2684	up	0.5567	up	0.2833	up	0.5716	up	0.2883	up
MPF_LOC101484883.1.1	XM_004554888.1 PREDICTED: Maylandia zebra nuclear receptor 2C2associated protein-like (LOC101484883), mRNA	0.0494	-0.0994	down	0.1356	up	0.6539	up	0.2349	up	0.7533	up	0.5183	up
MPF_RS17.4.23	RS17_ICTPU (sp|Q90YQ6) 40S ribosomal protein S17 OS=Ictalurus punctatus GN=rps17 PE=2 SV=3	0.0494	0.1883	up	0.1145	up	0.9463	up	-0.0738	down	0.7580	up	0.8318	up
MPF_LOC101484836.1.1	XM_004543050.1 PREDICTED: Maylandia zebra transcriptional repressor CTCF-like (LOC101484836), mRNA	0.0494	-0.2110	down	0.0705	up	0.8135	up	0.2815	up	1.0245	up	0.7430	up
MPF_LOC100700133.1.1	XP_003454629.1 PREDICTED: alpha-enolaselike [Oreochromis niloticus]	0.0494	0.0472	up	0.2455	up	0.5943	up	0.1983	up	0.5470	up	0.3487	up
MPF_STK38.1.1	XP_003454311.1 PREDICTED: serine/threonine-protein kinase 38 [Oreochromis niloticus]	0.0494	0.0335	up	0.1521	up	0.9062	up	0.1186	up	0.8727	up	0.7542	up
MPF_CCNB1.1.1	[BBH] CCNB1_ORYJA (sp|Q9DGA0) G2/mitoticspecific cyclin-B1 OS=Oryzias javanicus GN=ccnb1 PE=2 SV=2	0.0494	-0.2023	down	0.2231	up	0.5685	up	0.4254	up	0.7708	up	0.3454	up
MPF_LOC100701449.1.1	XP_003444192.1 PREDICTED: shugoshin-like	0.0494	-0.1113	down	0.2460	up	0.8185	up	0.3573	up	0.9299	up	0.5726	up

	1-like [Oreochromis niloticus]													
MPF_LOC100696546.1.1	XP_003450322.1 PREDICTED: autophagy protein 5-like [Oreochromis niloticus]	0.0494	0.9921	up	0.7414	up	1.4581	up	-0.2507	down	0.4659	up	0.7166	up
MPF_HMGA1B.6.6	NM_001077276.1 Danio rerio high mobility group AT-hook 1b (hmga1b), mRNA	0.0494	-0.0540	down	0.2157	up	0.5767	up	0.2697	up	0.6307	up	0.3610	up
MPF_LOC101469584.1.2	XM_004559799.1 PREDICTED: Maylandia zebra serum response factorlike (LOC101469584), mRNA	0.0494	0.1760	up	0.2096	up	1.0524	up	0.0336	up	0.8764	up	0.8428	up
MPF_contig_038033		0.0494	-0.0694	down	0.0203	up	0.5371	up	0.0897	up	0.6066	up	0.5169	up
MPF_LOC100695307.2.3	XP_003448165.1 PREDICTED: enoyl-CoA hydratase domain-containing protein 3, mitochondrial-like [Oreochromis niloticus]	0.0494	-0.2122	down	0.1635	up	0.9555	up	0.3757	up	1.1677	up	0.7920	up
MPF_contig_036878		0.0494	-0.8655	down	-0.6199	down	-2.0652	down	0.2456	up	-1.1997	down	-1.4453	down
MPF_LOC101468827.1.1	XM_004538856.1 PREDICTED: Maylandia zebra sodium channel and clathrin linker 1-like (LOC101468827), transcript variant X2, mRNA	0.0494	-0.0947	down	0.0913	up	0.7604	up	0.1859	up	0.8550	up	0.6691	up
MPF_LOC101162825.1.1	XP_004067316.1 PREDICTED: telomeric repeat-binding factor 2-like [Oryzias latipes]	0.0494	0.1411	up	0.3577	up	0.8675	up	0.2166	up	0.7264	up	0.5098	up
MPF_LOC100691087.1.2	XM_003445024.1 PREDICTED: Oreochromis niloticus putative homeodomain transcription factor 2-like	0.0495	-0.0088	down	0.0145	up	0.7834	up	0.0233	up	0.7922	up	0.7688	up

	(LOC100691087), mRNA													
MPF_LOC101464449.1.1	XM_004541024.1 PREDICTED: Maylandia zebra neuropeptide Y receptor type 2-like (LOC101464449), mRNA	0.0495	0.1766	up	0.5359	up	0.9225	up	0.3593	up	0.7459	up	0.3866	up
MPF_GPX1.2.3	NM_001124525.1 Oncorhynchus mykiss glutathione peroxidase 1 (gpx1), mRNA gb|AY622862.1| Oncorhynchus mykiss glutathione peroxidase type 2 mRNA, complete cds	0.0495	0.1250	up	-0.4321	down	-2.1664	down	-0.5571	down	-2.2914	down	-1.7343	down
MPF_contig_016000	XM_004075770.1 PREDICTED: Oryzias latipes arf-GAP domain and FG repeat-containing protein 1like, transcript variant 1 (LOC101155131), mRNA	0.0495	0.0310	up	0.1080	up	0.8066	up	0.0769	up	0.7756	up	0.6986	up
MPF_LOC100708241.2.3	XM_003441332.1 PREDICTED: Oreochromis niloticus calcium-binding and coiled-coil domain-containing protein 1-like (LOC100708241), mRNA	0.0495	0.1286	up	-0.1317	down	1.3530	up	-0.2603	down	1.2244	up	1.4847	up
MPF_LOC101476857.2.3	XM_004566214.1 PREDICTED: Maylandia zebra 5'-nucleotidase domaincontaining protein 1-like (LOC101476857), mRNA	0.0495	-0.0090	down	0.1586	up	0.5532	up	0.1675	up	0.5622	up	0.3947	up

MPF_contig_038189		0.0495	0.1162	up	0.2806	up	0.8337	up	0.1644	up	0.7175	up	0.5531	up
MPF_LOC100706842.1.1	XP_003451266.1 PREDICTED: ragulator complex protein LAMTOR2like [Oreochromis niloticus]	0.0495	-0.0471	down	0.2103	up	0.6781	up	0.2575	up	0.7252	up	0.4677	up
MPF_contig_035629		0.0495	-0.0485	down	0.0531	up	0.5153	up	0.1016	up	0.5638	up	0.4621	up
MPF_CFAH.8.15	CFAH_BOVIN (sp|Q28085) Complement factor H OS=Bos taurus GN=CFH PE=1 SV=3	0.0495	0.4638	up	-1.1506	down	-3.3531	down	-1.6144	down	-3.8169	down	-2.2025	down
MPF_LOC101480346.4.4	XM_004567337.1 PREDICTED: Maylandia zebra myotubularin-related protein 3-like (LOC101480346), transcript variant X4, mRNA	0.0495	0.1109	up	0.4940	up	0.8130	up	0.3831	up	0.7021	up	0.3190	up
MPF_contig_010480		0.0495	-0.0348	down	0.0235	up	0.6044	up	0.0583	up	0.6392	up	0.5809	up
MPF_LOC101482397.1.3	XM_004570856.1 PREDICTED: Maylandia zebra glycoprotein gp2-like (LOC101482397), mRNA	0.0495	-0.2623	down	-2.1468	down	-3.9305	down	-1.8844	down	-3.6682	down	-1.7837	down
MPF_LOC101470120.1.1	XM_004575698.1 PREDICTED: Maylandia zebra UPF0489 protein C5orf22 homolog (LOC101470120), transcript variant X1, mRNA	0.0495	-0.2682	down	0.2517	up	0.6708	up	0.5200	up	0.9390	up	0.4191	up
MPF_LOC101481410.2.2	XM_004542393.1 PREDICTED: Maylandia zebra mediator of RNA polymerase II transcription subunit 26-like (LOC101481410), mRNA	0.0495	0.0885	up	0.2513	up	1.1144	up	0.1629	up	1.0259	up	0.8630	up

MPF_LOC101467796.9.9	XM_004554825.1 PREDICTED: Maylandia zebra nesprin-2-like (LOC101467796), mRNA	0.0495	-0.1953	down	-0.5003	down	-2.1332	down	-0.3051	down	-1.9379	down	-1.6329	down
MPF_LOC100690119.4.18	XP_003448733.1 PREDICTED: zinc finger protein 16-like [Oreochromis niloticus]	0.0495	0.0679	up	0.3005	up	1.3435	up	0.2326	up	1.2756	up	1.0430	up
MPF_LOC101485768.1.2	XM_004538921.1 PREDICTED: Maylandia zebra meiosis arrest female protein 1 homolog (LOC101485768), transcript variant X7, mRNA	0.0495	-0.1503	down	-0.0985	down	1.1342	up	0.0518	up	1.2845	up	1.2327	up
MPF_LOC101481785.1.1	XM_004564503.1 PREDICTED: Maylandia zebra phosphatidylinositol 4phosphate 3-kinase C2 domain-containing subunit alpha-like (LOC101481785), transcript variant X1, mRNA	0.0495	0.1117	up	0.3138	up	0.8170	up	0.2021	up	0.7053	up	0.5032	up
MPF_LOC100703063.1.1	XM_003444398.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100703063 (LOC100703063), mRNA	0.0495	0.2069	up	0.4303	up	0.8332	up	0.2234	up	0.6263	up	0.4029	up
MPF_LOC101469523.1.1	XM_004567198.1 PREDICTED: Maylandia zebra ATP-dependent zinc metalloprotease YME1L1-like (LOC101469523), transcript variant X1, mRNA	0.0495	-0.2372	down	0.1479	up	0.7462	up	0.3851	up	0.9834	up	0.5983	up
MPF_contig_039806		0.0495	-0.0196	down	0.2138	up	1.2898	up	0.2334	up	1.3094	up	1.0760	up
MPF_contig_028598		0.0495	-0.1988	down	0.2803	up	-0.5253	down	0.4791	up	-0.3265	down	-0.8056	down

MPF_LOC100690548.1.1	XM_003444688.1 PREDICTED: Oreochromis niloticus wolframin-like (LOC100690548), mRNA	0.0495	0.0217	up	-0.2278	down	0.9599	up	-0.2496	down	0.9382	up	1.1877	up
MPF_LOC100707878.1.1	XM_003442005.1 PREDICTED: Oreochromis niloticus putative all-transretinol 13,14-reductase-like (LOC100707878), mRNA	0.0496	-0.2093	down	0.2772	up	0.7737	up	0.4864	up	0.9829	up	0.4965	up
MPF_LOC100695797.1.1	XP_003459798.1 PREDICTED: CAAX prenyl protease 2-like [Oreochromis niloticus]	0.0497	-0.0045	down	0.2013	up	0.6552	up	0.2058	up	0.6597	up	0.4539	up
MPF_contig_028836		0.0497	-0.1147	down	0.2052	up	0.6787	up	0.3199	up	0.7934	up	0.4735	up
MPF_LOC100694797.2.2	XM_003453170.1 PREDICTED: Oreochromis niloticus nucleoprotein TPRlike (LOC100694797), mRNA	0.0497	-0.0901	down	0.1496	up	0.8714	up	0.2397	up	0.9615	up	0.7218	up
MPF_TMCO1.1.1	[BBH] TMCO1_RAT (sp|Q5I0H4) Transmembrane and coiled-coil domains protein 1 OS=Rattus norvegicus GN=Tmco1 PE=2 SV=1	0.0497	-0.1963	down	0.4108	up	0.5929	up	0.6071	up	0.7892	up	0.1821	up
MPF_LOC100710203.2.2	XP_003438952.1 PREDICTED: gametocyte-specific factor 1-like [Oreochromis niloticus]	0.0497	0.3095	up	0.3339	up	0.9800	up	0.0244	up	0.6705	up	0.6461	up

MPF_contig_028214	XM_004556613.1 PREDICTED: Maylandia zebra calcium/calmodulindependent protein kinase type II subunit gamma-like (LOC101474026), transcript variant X10, mRNA	0.0497	-0.0811	down	0.1136	up	0.9339	up	0.1947	up	1.0150	up	0.8203	up
MPF_TYSY.1.1	NP_001134715.1 Thymidylate synthase [Salmo salar]	0.0497	0.4773	up	0.7607	up	1.2034	up	0.2834	up	0.7261	up	0.4427	up
MPF_LOC101480115.2.2	XM_004555427.1 PREDICTED: Maylandia zebra pituitary tumortransforming gene 1 proteininteracting protein-like (LOC101480115), mRNA	0.0497	0.1709	up	0.0826	up	-1.4949	down	-0.0884	down	-1.6658	down	-1.5775	down
MPF_LOC101483139.1.3	XM_004565243.1 PREDICTED: Maylandia zebra protein FAM13C-like (LOC101483139), transcript variant X2, mRNA	0.0497	-0.0071	down	0.1404	up	0.4270	up	0.1476	up	0.4341	up	0.2866	up
MPF_LOC101487243.1.3	XM_004570967.1 PREDICTED: Maylandia zebra pleckstrin homology domain-containing family M member 2-like (LOC101487243), transcript variant X2, mRNA	0.0497	-0.6429	down	-0.4136	down	-1.7460	down	0.2293	up	-1.1031	down	-1.3323	down
MPF_LOC101470017.4.5	XM_004574645.1 PREDICTED: Maylandia zebra putative oxidoreductase GLYR1-like (LOC101470017), transcript variant X5, mRNA	0.0497	0.0578	up	0.1479	up	1.0804	up	0.0901	up	1.0225	up	0.9324	up
MPF_LOC101483648.1.1	XM_004547634.1 PREDICTED: Maylandia zebra protein RTF2 homolog (LOC101483648), mRNA	0.0497	0.0872	up	0.6120	up	1.0584	up	0.5248	up	0.9713	up	0.4464	up

MPF_T2AG.2.2	[BBH] T2AG_PAROL (sp|Q9IA78) Transcription initiation factor IIA subunit 2 OS=Paralichthys olivaceus GN=gtf2a2 PE=3 SV=1	0.0497	0.2096	up	0.6300	up	1.2309	up	0.4204	up	1.0214	up	0.6010	up

MPF_LOC101472522.2.2	XM_004547397.1 PREDICTED: Maylandia zebra nucleolar protein 8-like (LOC101472522), mRNA	0.0497	-0.1652	down	-0.1193	down	0.9019	up	0.0459	up	1.0672	up	1.0212	up
MPF_LOC101466731.1.2	XM_004553632.1 PREDICTED: Maylandia zebra glutamate receptor 2like (LOC101466731), transcript variant X2, mRNA	0.0497	-0.1685	down	-0.5449	down	-2.6739	down	-0.3764	down	-2.5054	down	-2.1290	down
MPF_RL18A.11.14	RL18A_DANRE (sp|Q7ZWJ4) 60S ribosomal protein L18a OS=Danio rerio GN=rpl18a PE=2 SV=1	0.0497	-0.0619	down	-0.5986	down	-1.6180	down	-0.5367	down	-1.5561	down	-1.0193	down
MPF_LOC101469087.3.3	XM_004575459.1 PREDICTED: Maylandia zebra chondroitin sulfate synthase 2-like (LOC101469087), mRNA	0.0498	-0.0993	down	0.2171	up	0.8603	up	0.3164	up	0.9597	up	0.6432	up
MPF_LOC100707856.1.1	XP_003458866.1 PREDICTED: transforming growth factor beta-2-like [Oreochromis niloticus]	0.0498	-0.0419	down	-0.0410	down	-0.9863	down	0.0008	up	-0.9444	down	-0.9452	down
MPF_LOC101487618.1.1	XM_004545480.1 PREDICTED: Maylandia zebra polyribonucleotide 5'hydroxyl-kinase Clp1-like (LOC101487618), transcript variant X2, mRNA	0.0498	-0.0084	down	0.1336	up	0.7475	up	0.1419	up	0.7559	up	0.6140	up

MPF_contig_043444	WP_003975841.1 predicted protein [Streptomyces lividans]	0.0498	0.0963	up	0.3425	up	0.6607	up	0.2462	up	0.5644	up	0.3182	up
MPF_LOC101482535.1.1	XM_004555438.1 PREDICTED: Maylandia zebra transformer-2 protein homolog beta-like (LOC101482535), transcript variant X3, mRNA	0.0498	-0.1336	down	-0.1024	down	0.6820	up	0.0312	up	0.8156	up	0.7844	up
MPF_LOC101487220.1.1	XM_004566606.1 PREDICTED: Maylandia zebra NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial-like (LOC101487220), mRNA	0.0498	-0.1543	down	-0.3684	down	-1.8861	down	-0.2141	down	-1.7318	down	-1.5177	down
MPF_LOC101485716.2.12	XM_004572825.1 PREDICTED: Maylandia zebra multivesicular body subunit 12B-like (LOC101485716), mRNA	0.0498	0.2082	up	0.4109	up	-0.2686	down	0.2027	up	-0.4768	down	-0.6795	down
MPF_LOC100536482.1.1	XP_003198573.1 PREDICTED: zinc finger protein 271-like [Danio rerio]	0.0498	0.0470	up	0.0394	up	1.0540	up	-0.0075	down	1.0070	up	1.0146	up
MPF_LOC101074047.1.1	XP_003966670.1 PREDICTED: histone-lysine N-methyltransferase SETDB2like [Takifugu rubripes]	0.0498	-0.1358	down	0.4166	up	0.5359	up	0.5524	up	0.6717	up	0.1193	up
MPF_contig_045371		0.0498	-0.0742	down	0.1337	up	0.9452	up	0.2079	up	1.0194	up	0.8115	up
MPF_LOC101467621.4.8	XR_190852.1 PREDICTED: Maylandia zebra uncharacterized LOC101467621 (LOC101467621), misc_RNA	0.0498	0.0766	up	-0.0500	down	-1.2606	down	-0.1266	down	-1.3372	down	-1.2106	down

MPF_LOC100701392.1.1	XM_003452212.1 PREDICTED: Oreochromis niloticus protein phosphatase 1K, mitochondrial-like (LOC100701392), mRNA	0.0499	-0.4290	down	-1.4534	down	-2.3419	down	-1.0244	down	-1.9129	down	-0.8885	down
MPF_LOC101483006.1.2	XR_191193.1 PREDICTED: Maylandia zebra unconventional myosin-XVIlike (LOC101483006), transcript variant X4, misc_RNA	0.0499	-0.0112	down	0.0494	up	0.7352	up	0.0606	up	0.7464	up	0.6858	up
MPF_LOC101471902.1.5	XM_004538867.1 PREDICTED: Maylandia zebra phosphatidylinositol 4kinase type 2-beta-like (LOC101471902), mRNA	0.0499	-0.1229	down	0.1365	up	0.6786	up	0.2595	up	0.8016	up	0.5421	up
MPF_RH42.1.1	RH42_ARATH (sp|Q8H0U8) DEAD-box ATP-dependent RNA helicase 42 OS=Arabidopsis thaliana GN=RH42 PE=1 SV=2	0.0499	-0.1692	down	-0.1071	down	-1.2607	down	0.0620	up	-1.0915	down	-1.1536	down
MPF_contig_044644		0.0499	-0.2406	down	-0.1914	down	0.6417	up	0.0492	up	0.8823	up	0.8331	up
MPF_LOC101469612.1.1	XM_004567946.1 PREDICTED: Maylandia zebra mediator of RNA polymerase II transcription subunit 14-like (LOC101469612), transcript variant X3, mRNA	0.0499	-0.2031	down	0.1174	up	0.8138	up	0.3205	up	1.0169	up	0.6964	up
MPF_THOC1.1.1	XM_003437855.1 PREDICTED: Oreochromis niloticus THO complex 1 (THOC1), mRNA	0.0499	-0.0538	down	-0.2310	down	1.0438	up	-0.1772	down	1.0976	up	1.2748	up

MPF_LOC101470529.1.3	XM_004558267.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 16A-like (LOC101470529), mRNA	0.0500	-0.2529	down	0.3966	up	-1.7708	down	0.6495	up	-1.5180	down

MPF_LOC101470529.1.3	XM_004558267.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 16A-like (LOC101470529), mRNA	0.0500	-0.2529	down	0.3966	up	-1.7708	down	0.6495	up	-1.5180	down	-2.1674	down

MPF_LOC101478974.1.1	XM_004554043.1 PREDICTED: Maylandia zebra lethal(3)malignant brain tumor-like protein 1-like (LOC101478974), transcript variant X2, mRNA	0.0500	-0.2770	down	-0.3581	down	0.8722	up	-0.0811	down	1.1492	up	1.2303	up
MPF_LOC101464652.2.3	XM_004541953.1 PREDICTED: Maylandia zebra translocation protein SEC63 homolog (LOC101464652), mRNA	0.0500	0.0180	up	0.0363	up	0.5592	up	0.0184	up	0.5412	up	0.5228	up
MPF_LOC101064338.1.1	XM_003970413.1 PREDICTED: Takifugu rubripes putative monooxygenase p33MONOXlike (LOC101064338), mRNA	0.0500	0.2293	up	0.2160	up	0.7484	up	-0.0133	down	0.5190	up	0.5323	up

4. Supplementary table 6

Group IV

GeneName	**Description**	**p (Corr)**	**p**	**Regulation ([I] vs [II])**	**Regulation ([I] vs [III])**	**Regulation ([I] vs [IV])**	**Regulation ([II] vs [III])**	**Regulation ([II] vs [IV])**	**Regulation ([III] vs [IV])**
MPF_LOC101481552.13.41	XM_004575656.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101481552), mRNA	0,0308	0,0020	down	up	up	up	up	up

MPF_LOC100705728.7.17	XM_003459563.1 PREDICTED: Oreochromis niloticus zinc finger protein RFP-like (LOC100705728), mRNA	0,0064	0,0000	down	up	up	up	up	up
MPF_contig_010078	NA	0,0403	0,0043	down	down	up	up	up	up
MPF_LOC101468090.2.6	XM_004576234.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 1like (LOC101468090), partial mRNA	0,0160	0,0003	down	down	down	up	down	down
MPF_contig_010111	NA	0,0340	0,0026	down	down	down	down	down	down
MPF_SGS4.2.10	SGS4_DROME (sp|Q00725) Salivary glue protein Sgs-4 OS=Drosophila melanogaster GN=Sgs4 PE=2 SV=1	0,0136	0,0001	down	down	down	up	down	down
MPF_LOC100699783.1.1	XP_003456177.1 PREDICTED: myosin-XIX-like [Oreochromis niloticus]	0,0374	0,0035	up	up	up	up	up	up
MPF_contig_010158	NA	0,0242	0,0009	down	down	down	up	down	down
MPF_contig_010163	NA	0,0182	0,0004	up	up	up	down	up	up
MPF_LOC101466605.1.2	XM_004571129.1 PREDICTED: Maylandia zebra signal recognition particle subunit SRP72-like (LOC101466605), mRNA	0,0335	0,0025	down	down	up	up	up	up
MPF_contig_010205	NA	0,0430	0,0051	down	up	up	up	up	up
MPF_LOC101484776.1.1	XM_004550365.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF14-like (LOC101484776), transcript variant X5, mRNA	0,0307	0,0019	down	down	up	up	up	up
MPF_contig_010346	NA	0,0253	0,0011	down	down	up	up	up	up
MPF_contig_010356	NA	0,0450	0,0056	down	down	up	down	up	up
MPF_LOC101472431.1.6	XM_004550961.1 PREDICTED: Maylandia zebra cytochrome P450 4B1-like (LOC101472431), transcript variant X1, mRNA	0,0219	0,0006	down	down	down	up	down	down
MPF_LOC101472025.2.3	XM_004546739.1 PREDICTED: Maylandia zebra zinc finger protein 652-like (LOC101472025), mRNA	0,0357	0,0030	up	up	up	up	up	up
MPF_LOC101479923.1.2	XM_004538167.1 PREDICTED: Maylandia zebra spidroin-2-like (LOC101479923), mRNA	0,0253	0,0011	down	up	up	up	up	up
MPF_LOC101482897.1.9	XM_004572716.1 PREDICTED: Maylandia zebra elongation factor 1-alpha-like (LOC101482897), mRNA	0,0248	0,0010	up	up	down	down	down	down
MPF_IF4G.1.1	IF4G_SCHPO (sp|Q10475) Eukaryotic translation initiation factor 4 gamma OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tif471 PE=1 SV=1	0,0160	0,0003	up	up	down	down	down	down
MPF_LOC101468998.1.1	XM_004556785.1 PREDICTED: Maylandia zebra sclerostin-like (LOC101468998), transcript variant X2, mRNA	0,0227	0,0007	down	up	up	up	up	up
MPF_contig_010460	NA	0,0361	0,0031	up	down	up	down	up	up
MPF_contig_010480	NA	0,0495	0,0075	down	up	up	up	up	up
MPF_contig_001047	XM_004559756.1 PREDICTED: Maylandia zebra vitrin-like (LOC101482458), transcript variant X1, mRNA	0,0288	0,0016	down	down	up	up	up	up
MPF_LOC101479500.1.2	XM_004544158.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 34-like (LOC101479500), transcript variant X2, mRNA	0,0309	0,0020	up	up	up	down	up	up

MPF_LOC101480238.1.1	XM_004539697.1 PREDICTED: Maylandia zebra adenylate cyclase type 2-like (LOC101480238), transcript variant X2, mRNA	0,0153	0,0002	down	up	up	up	up	up
MPF_LOC100693088.1.1	XM_003449441.1 PREDICTED: Oreochromis niloticus neoverrucotoxin subunit alpha-like (LOC100693088), mRNA	0,0371	0,0034	down	down	up	down	up	up
MPF_LOC101463996.1.2	XM_004569096.1 PREDICTED: Maylandia zebra zinc finger protein 850-like (LOC101463996), mRNA	0,0304	0,0019	down	up	up	up	up	up
MPF_LOC101158204.1.2	XM_004072523.1 PREDICTED: Oryzias latipes TBC1 domain family member 10A-like (LOC101158204), mRNA	0,0387	0,0038	down	up	up	up	up	up
MPF_LOC100535419.1.1	XP_003200110.1 PREDICTED: transposon TX1 uncharacterized 149 kDa protein-like [Danio rerio]	0,0171	0,0003	up	down	down	down	down	down
MPF_LOC100690853.1.1	XP_003450715.1 PREDICTED: zinc finger protein 574-like [Oreochromis niloticus]	0,0392	0,0040	up	up	up	up	up	up
MPF_LOC101484172.1.1	XM_004563596.1 PREDICTED: Maylandia zebra centrosome and spindle pole-associated protein 1-like (LOC101484172), transcript variant X3, mRNA	0,0169	0,0003	down	down	up	up	up	up
MPF_MIR29B-2.1.1	NR_030037.1 Danio rerio microRNA 29b-2 (mir29b-2), microRNA	0,0256	0,0011	down	up	up	up	up	up
MPF_contig_010734	NA	0,0224	0,0007	up	down	up	down	up	up
MPF_LOC101463600.1.1	XM_004544939.1 PREDICTED: Maylandia zebra class E basic helix-loop-helix protein 40-like (LOC101463600), mRNA	0,0444	0,0054	down	down	down	down	down	down
MPF_contig_010802	NA	0,0287	0,0016	down	up	up	up	up	up
MPF_LOC101482235.1.2	XM_004552859.1 PREDICTED: Maylandia zebra cysteine protease ATG4B-like (LOC101482235), mRNA	0,0158	0,0002	down	up	up	up	up	up

MPF_KRA43.1.2	KRA43_HUMAN (sp|Q9BYR4) Keratin-associated protein 4-3 OS=Homo sapiens GN=KRTAP4-3 PE=2 SV=2	0,0060	0,0000	down	down	down	down	down	down
MPF_PSV.1.1	PSV_DICDI (sp|P08798) Prespore vesicle protein OS=Dictyostelium discoideum GN=psvA PE=2 SV=3	0,0171	0,0003	down	down	down	up	down	down
MPF_LOC101473906.1.3	XM_004549447.1 PREDICTED: Maylandia zebra max dimerization protein 4-like (LOC101473906), mRNA	0,0400	0,0041	up	up	up	up	up	up
MPF_ZNF32.1.1	ZNF32_MOUSE (sp|Q80V23) Zinc finger protein 32 OS=Mus musculus GN=Znf32 PE=2 SV=1	0,0344	0,0027	down	up	up	up	up	up
MPF_LOC101469812.1.2	XM_004571140.1 PREDICTED: Maylandia zebra polycomb group RING finger protein 3-like (LOC101469812), mRNA	0,0308	0,0020	up	up	up	up	up	up
MPF_LOC101472031.1.3	XM_004571147.1 PREDICTED: Maylandia zebra exosome complex component RRP40-like (LOC101472031), mRNA	0,0345	0,0027	down	up	up	up	up	up
MPF_LOC100709019.1.2	XM_003458034.1 PREDICTED: Oreochromis niloticus ATP synthase subunit g, mitochondrial-like (LOC100709019), mRNA	0,0406	0,0044	up	up	up	up	up	up
MPF_LRP2.2.4	LRP2_HUMAN (sp|P98164) Low-density lipoprotein receptor-related protein 2 OS=Homo sapiens GN=LRP2 PE=1 SV=3	0,0459	0,0059	down	down	up	down	up	up
MPF_LOC101467469.1.1	XM_004573106.1 PREDICTED: Maylandia zebra ras-related protein R-Ras-like (LOC101467469), transcript variant X2, mRNA	0,0202	0,0005	down	up	up	up	up	up

MPF_LOC101474833.1.3	XM_004570025.1 PREDICTED: Maylandia zebra bcl-2-like protein 11-like (LOC101474833), mRNA	0,0215	0,0006	up	down	down	down	down	down
MPF_LOC100691946.1.4	XM_003456019.1 PREDICTED: Oreochromis niloticus serine incorporator 1-like (LOC100691946), mRNA	0,0130	0,0001	up	up	up	down	up	up
MPF_LOC101468451.1.1	XM_004567195.1 PREDICTED: Maylandia zebra WW domain-containing adapter protein with coiledcoil-like (LOC101468451), transcript variant X2, mRNA	0,0080	0,0000	up	up	up	down	up	up
MPF_LOC101487555.1.1	XM_004575183.1 PREDICTED: Maylandia zebra actin-related protein 2/3 complex subunit 2-like (LOC101487555), mRNA	0,0400	0,0042	down	down	up	down	up	up
MPF_RH42.1.1	RH42_ARATH (sp|Q8H0U8) DEAD-box ATP-dependent RNA helicase 42 OS=Arabidopsis thaliana GN=RH42 PE=1 SV=2	0,0499	0,0077	down	down	down	up	down	down
MPF_contig_011239	XM_004562318.1 PREDICTED: Maylandia zebra TOM1-like protein 2-like (LOC101476649), transcript variant X2, mRNA	0,0193	0,0005	down	up	up	up	up	up
MPF_LOC101475776.1.7	XM_004539154.1 PREDICTED: Maylandia zebra ATP synthase subunit d, mitochondrial-like (LOC101475776), transcript variant X2, mRNA	0,0379	0,0036	down	down	up	up	up	up
MPF_LOC101171771.1.2	XM_004077345.1 PREDICTED: Oryzias latipes uncharacterized LOC101171771 (LOC101171771), mRNA	0,0171	0,0003	up	up	down	down	down	down
MPF_LOC101487290.1.1	XM_004559498.1 PREDICTED: Maylandia zebra meteorin-like protein-like (LOC101487290), mRNA	0,0290	0,0017	up	up	up	up	up	up
MPF_LOC101471171.1.1	XM_004549062.1 PREDICTED: Maylandia zebra dolichol-phosphate mannosyltransferase subunit 3-like (LOC101471171), mRNA	0,0270	0,0013	up	up	up	up	up	up
MPF_LOC101465889.2.3	XM_004563621.1 PREDICTED: Maylandia zebra rho guanine nucleotide exchange factor 37-like (LOC101465889), transcript variant X5, mRNA	0,0422	0,0049	down	up	up	up	up	up
MPF_contig_011356	XM_004540345.1 PREDICTED: Maylandia zebra phospholipase DDHD1-like (LOC101479185), transcript variant X1, mRNA	0,0277	0,0014	down	down	up	up	up	up
MPF_CYYR1.1.19	NM_212882.1 Danio rerio cysteine and tyrosine-rich protein 1 (cyyr1), mRNA gb|BC066606.1| Danio rerio cysteine and tyrosine-rich protein 1, mRNA (cDNA clone MGC:77252 IMAGE:6963826), complete cds	0,0177	0,0004	up	up	up	up	up	up
MPF_LOC101074307.1.1	XM_003975871.1 PREDICTED: Takifugu rubripes Golgi reassembly-stacking protein 2-like (LOC101074307), mRNA	0,0280	0,0015	up	up	up	up	up	up
MPF_LOC101466590.1.1	XM_004569012.1 PREDICTED: Maylandia zebra partner and localizer of BRCA2-like (LOC101466590), transcript variant X5, mRNA	0,0160	0,0003	down	down	down	down	down	down
MPF_LOC100691511.1.1	XM_003460361.1 PREDICTED: Oreochromis niloticus transmembrane and ubiquitin-like domaincontaining protein 1-like (LOC100691511), partial mRNA	0,0155	0,0002	down	down	up	up	up	up
MPF_contig_011517	NA	0,0247	0,0010	down	up	up	up	up	up
MPF_RTBS.5.36	RTBS_DROME (sp|Q95SX7) Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1	0,0242	0,0009	down	down	up	up	up	up
MPF_contig_011614	XM_004547127.1 PREDICTED: Maylandia zebra RING finger protein 165-like (LOC101475525), transcript variant X2, mRNA	0,0270	0,0013	up	up	up	down	up	up
MPF_LOC101477400.1.4	XM_004538536.1 PREDICTED: Maylandia zebra cyclin-G2-like (LOC101477400), mRNA	0,0318	0,0021	up	up	up	up	up	up

MPF_LOC101475562.1.1	XM_004576257.1 PREDICTED: Maylandia zebra protein dpy-30 homolog (LOC101475562), transcript variant X2, mRNA	0,0332	0,0024	up	up	up	up	up	up

MPF_RAMP3.1.1	RAMP3_HUMAN (sp|O60896) Receptor activity-modifying protein 3 OS=Homo sapiens GN=RAMP3 PE=2 SV=1	0,0147	0,0002	down	up	up	up	up	up
MPF_RS17.4.23	RS17_ICTPU (sp|Q90YQ6) 40S ribosomal protein S17 OS=Ictalurus punctatus GN=rps17 PE=2 SV=3	0,0494	0,0074	up	up	up	down	up	up
MPF_LOC101162274.1.1	XR_177692.1 PREDICTED: Oryzias latipes uncharacterized LOC101162274 (LOC101162274), misc_RNA	0,0401	0,0042	down	down	up	up	up	up
MPF_RTBS.7.36	RTBS_DROME (sp|Q95SX7) Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1	0,0127	0,0001	down	up	up	up	up	up
MPF_LOC100708352.1.2	XM_003447254.1 PREDICTED: Oreochromis niloticus sodium/hydrogen exchanger 3-like (LOC100708352), mRNA	0,0160	0,0003	down	up	up	up	up	up
MPF_SPCS.1.3	SPCS_DANRE (sp|Q803A7) O-phosphoseryl-tRNA(Sec) selenium transferase OS=Danio rerio GN=sepsecs PE=2 SV=1	0,0228	0,0008	down	up	up	up	up	up
MPF_LOC101484239.1.1	XM_004551175.1 PREDICTED: Maylandia zebra protein EMSY-like (LOC101484239), transcript variant X1, mRNA	0,0419	0,0048	down	up	up	up	up	up
MPF_contig_011890	NA	0,0388	0,0039	down	down	up	up	up	up
MPF_contig_011891	NA	0,0354	0,0029	down	down	up	down	up	up
MPF_LOC101467030.1.1	XM_004563996.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 31-like (LOC101467030), mRNA	0,0308	0,0020	down	down	down	down	down	down
MPF_LOC100692543.1.3	XM_003449439.1 PREDICTED: Oreochromis niloticus microfibril-associated glycoprotein 4-like (LOC100692543), mRNA	0,0171	0,0003	up	down	down	down	down	down
MPF_LOC100699178.1.1	XM_003438369.1 PREDICTED: Oreochromis niloticus inositol 1,4,5-triphosphate receptor-interacting protein-like (LOC100699178), mRNA	0,0293	0,0017	up	down	down	down	down	down
MPF_U5S1.1.1	[BBH] U5S1_MOUSE (sp|O08810) 116 kDa U5 small nuclear ribonucleoprotein component OS=Mus musculus GN=Eftud2 PE=2 SV=1	0,0213	0,0006	down	up	up	up	up	up
MPF_LOC100690233.1.1	XM_003456743.1 PREDICTED: Oreochromis niloticus membrane progestin receptor gamma-B-like, transcript variant 2 (LOC100690233), mRNA	0,0367	0,0033	up	up	up	down	up	up
MPF_LOC100691137.1.1	XM_003455036.1 PREDICTED: Oreochromis niloticus golgin subfamily A member 1-like (LOC100691137), mRNA	0,0450	0,0056	up	up	up	up	up	up
MPF_LOC101466836.2.3	XM_004537932.1 PREDICTED: Maylandia zebra pleckstrin homology-like domain family B member 1like (LOC101466836), mRNA	0,0451	0,0056	up	down	up	down	up	up
MPF_LOC101162776.1.2	XP_004075996.1 PREDICTED: neurofibromin-like [Oryzias latipes]	0,0332	0,0024	down	up	up	up	up	up
MPF_LOC101465372.1.1	XM_004553174.1 PREDICTED: Maylandia zebra zinc finger protein 592-like (LOC101465372), mRNA	0,0479	0,0068	up	down	up	down	up	up

MPF_LOC100696600.1.2	XM_003441455.1 PREDICTED: Oreochromis niloticus actin-related protein 2/3 complex subunit 4-like (LOC100696600), mRNA	0,0160	0,0003	up	up	up	up	up	up
MPF_contig_012354	NA	0,0293	0,0017	down	up	up	up	up	up
MPF_LOC101465317.1.5	XM_004564258.1 PREDICTED: Maylandia zebra ankyrin-2-like (LOC101465317), transcript variant X5, mRNA	0,0283	0,0015	down	down	up	down	up	up
MPF_LOC100710728.2.5	XM_003438906.1 PREDICTED: Oreochromis niloticus CD63 antigen-like (LOC100710728), mRNA	0,0272	0,0014	down	down	up	up	up	up
MPF_LOC101467543.1.1	XM_004567935.1 PREDICTED: Maylandia zebra integrin alpha-4-like (LOC101467543), mRNA	0,0198	0,0005	down	up	down	up	down	down
MPF_LOC100704418.1.1	XM_003445158.1 PREDICTED: Oreochromis niloticus transmembrane 9 superfamily member 2-like (LOC100704418), mRNA	0,0459	0,0059	down	down	up	up	up	up
MPF_LOC101478855.1.1	XM_004550336.1 PREDICTED: Maylandia zebra leucine--tRNA ligase, cytoplasmic-like (LOC101478855), mRNA	0,0454	0,0058	down	up	up	up	up	up
MPF_LOC101469549.1.2	XM_004573028.1 PREDICTED: Maylandia zebra interleukin-1 receptor-like 1-like (LOC101469549), mRNA	0,0150	0,0002	down	down	down	down	down	down
MPF_LOC101487598.1.1	XM_004565176.1 PREDICTED: Maylandia zebra transmembrane protein 158-like (LOC101487598), mRNA	0,0328	0,0023	down	down	up	down	up	up
MPF_COX3.3.3	[BBH] COX3_GADMO (sp|P55777) Cytochrome c oxidase subunit 3 OS=Gadus morhua GN=mt-co3 PE=3 SV=1	0,0419	0,0047	up	up	up	up	up	up
MPF_LOC100693993.1.1	XM_003453809.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693993 (LOC100693993), mRNA	0,0134	0,0001	down	down	down	down	down	down
MPF_LOC101475776.2.7	XM_004539154.1 PREDICTED: Maylandia zebra ATP synthase subunit d, mitochondrial-like (LOC101475776), transcript variant X2, mRNA	0,0208	0,0006	down	up	up	up	up	up
MPF_LOC100700823.1.2	XP_003446356.1 PREDICTED: hypothetical protein LOC100700823 [Oreochromis niloticus]	0,0171	0,0003	down	up	up	up	up	up
MPF_LOC101165910.2.2	XP_004076327.1 PREDICTED: von Willebrand factor A domain-containing protein 7-like [Oryzias latipes]	0,0202	0,0005	up	up	up	up	up	up
MPF_LOC101464595.1.1	XM_004550738.1 PREDICTED: Maylandia zebra uncharacterized LOC101464595 (LOC101464595), mRNA	0,0326	0,0022	up	up	up	up	up	up
MPF_LOC101482643.1.4	XM_004563682.1 PREDICTED: Maylandia zebra importin subunit alpha-7-like (LOC101482643), mRNA	0,0270	0,0013	down	up	up	up	up	up
MPF_LOC101485768.1.2	XM_004538921.1 PREDICTED: Maylandia zebra meiosis arrest female protein 1 homolog (LOC101485768), transcript variant X7, mRNA	0,0495	0,0075	down	down	up	up	up	up
MPF_LOC101477342.1.3	XM_004546475.1 PREDICTED: Maylandia zebra eukaryotic translation elongation factor 1 epsilon-1like (LOC101477342), mRNA	0,0228	0,0008	down	up	up	up	up	up
MPF_LOC101482455.1.1	XM_004559215.1 PREDICTED: Maylandia zebra gap junction gamma-1 protein-like (LOC101482455), mRNA	0,0429	0,0051	down	up	up	up	up	up
MPF_LOC101473955.1.1	XM_004542552.1 PREDICTED: Maylandia zebra WD repeat-containing protein 47-like (LOC101473955), mRNA	0,0222	0,0007	up	up	up	down	up	up

MPF_LOC100488659.3.10	XP_002933173.1 PREDICTED: hypothetical protein LOC100488659 [Xenopus (Silurana) tropicalis]	0,0080	0,0000	down	down	down	down	down	down
MPF_KIT.1.1	[BBH] KIT_TAKRU (sp|Q8AXC6) Mast/stem cell growth factor receptor Kit OS=Takifugu rubripes GN=kit PE=3 SV=1	0,0409	0,0044	up	up	up	up	up	up
MPF_LOC100701568.2.2	XP_003450260.1 PREDICTED: copine-3-like [Oreochromis niloticus]	0,0438	0,0053	down	down	down	up	down	down
MPF_LOC101078876.1.1	XP_003975937.1 PREDICTED: uncharacterized protein LOC101078876 [Takifugu rubripes]	0,0351	0,0028	up	up	up	down	up	up
MPF_LOC101463819.1.1	XM_004549502.1 PREDICTED: Maylandia zebra tetraspanin-5-like (LOC101463819), transcript variant X2, mRNA	0,0171	0,0003	down	down	down	down	down	down
MPF_LOC100708213.1.1	XP_003457845.1 PREDICTED: hypothetical protein LOC100708213 [Oreochromis niloticus]	0,0173	0,0004	down	down	down	down	down	down
MPF_LOC100712299.1.1	XM_003451996.1 PREDICTED: Oreochromis niloticus myoferlin-like (LOC100712299), mRNA	0,0203	0,0005	down	down	down	down	down	down
MPF_LOC101477528.1.1	XM_004568962.1 PREDICTED: Maylandia zebra uncharacterized LOC101477528 (LOC101477528), transcript variant X3, mRNA	0,0231	0,0008	up	up	up	down	up	up
MPF_contig_013080	NA	0,0323	0,0022	down	up	up	up	up	up
MPF_EF1A.5.11	EF1A_ORYLA (sp|Q9YIC0) Elongation factor 1-alpha OS=Oryzias latipes GN=eef1a PE=2 SV=1	0,0445	0,0055	up	up	down	down	down	down
MPF_LOC101477130.1.1	XM_004564031.1 PREDICTED: Maylandia zebra nuclear factor related to kappa-B-binding protein-like (LOC101477130), mRNA	0,0396	0,0041	down	up	up	up	up	up
MPF_contig_013127	XM_004539189.1 PREDICTED: Maylandia zebra ATP-binding cassette sub-family A member 1-like (LOC101484083), transcript variant X1, mRNA	0,0228	0,0008	down	down	down	down	down	down
MPF_contig_013193	XM_004563683.1 PREDICTED: Maylandia zebra KH domain-containing, RNA-binding, signal transduction-associated protein 1-like (LOC101482948), transcript variant X1, mRNA	0,0455	0,0058	down	down	up	up	up	up
MPF_CD68.2.2	NP_001158857.1 Macrosialin precursor [Salmo salar]	0,0388	0,0039	up	down	down	down	down	down
MPF_LOC100697337.2.4	XP_003446015.1 PREDICTED: hypothetical protein LOC100697337 [Oreochromis niloticus]	0,0277	0,0015	down	down	down	down	down	down
MPF_contig_013227	XM_004552675.1 PREDICTED: Maylandia zebra ras-associated and pleckstrin homology domainscontaining protein 1-like (LOC101482814), transcript variant X3, mRNA	0,0169	0,0003	up	down	up	down	up	up
MPF_LOC101479692.1.1	XM_004570130.1 PREDICTED: Maylandia zebra FERM, RhoGEF and pleckstrin domain-containing protein 1-like (LOC101479692), transcript variant X1, mRNA	0,0306	0,0019	down	up	up	up	up	up
MPF_LOC101471553.1.1	XM_004572678.1 PREDICTED: Maylandia zebra protein capicua homolog (LOC101471553), transcript variant X4, mRNA	0,0183	0,0004	down	down	down	down	down	down
MPF_LOC101482088.1.4	XM_004544264.1 PREDICTED: Maylandia zebra ubiquitin-conjugating enzyme E2 D4-like (LOC101482088), mRNA	0,0158	0,0002	down	up	up	up	up	up
MPF_LOC101076641.1.1	XP_003964552.1 PREDICTED: epidermal growth factor receptor kinase substrate 8-like protein 1-like [Takifugu rubripes]	0,0277	0,0014	down	up	up	up	up	up
MPF_contig_013416	XM_004574108.1 PREDICTED: Maylandia zebra alpha-actinin-4-like (LOC101467576), transcript variant X2, mRNA	0,0309	0,0020	down	down	up	down	up	up

MPF_contig_013449	NA	0,0139	0,0001	down	up	up	up	up	up
MPF_LOC100697415.2.3	XP_003444759.1 PREDICTED: neuroblast differentiation-associated protein AHNAK-like [Oreochromis niloticus]	0,0277	0,0015	down	up	up	up	up	up
MPF_LOC101487890.1.1	XM_004542514.1 PREDICTED: Maylandia zebra RING finger protein 126-like (LOC101487890), mRNA	0,0345	0,0027	up	up	up	up	up	up
MPF_LOC101465474.1.1	XM_004554819.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2-like (LOC101465474), mRNA	0,0371	0,0034	up	up	up	up	up	up
MPF_contig_013745	XM_004548188.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 12like (LOC101485157), transcript variant X2, mRNA	0,0150	0,0002	down	up	up	up	up	up
MPF_LOC101486209.1.4	XM_004551098.1 PREDICTED: Maylandia zebra uncharacterized LOC101486209 (LOC101486209), mRNA	0,0178	0,0004	up	down	down	down	down	down
MPF_LOC101484255.1.1	XM_004555723.1 PREDICTED: Maylandia zebra SH2 domain-containing protein 3C-like (LOC101484255), transcript variant X1, mRNA	0,0130	0,0001	down	down	down	down	down	down

MPF_ALDOC.1.1	ALDOC_CARAU (sp|P53448) Fructose-bisphosphate aldolase C OS=Carassius auratus GN=aldoc PE=2 SV=2	0,0367	0,0033	down	up	up	up	up	up
MPF_LOC101464934.2.3	XM_004565357.1 PREDICTED: Maylandia zebra matrix metalloproteinase-14-like (LOC101464934), mRNA	0,0214	0,0006	up	up	down	down	down	down
MPF_LOC100711368.2.3	XM_003442435.1 PREDICTED: Oreochromis niloticus keratin, type I cytoskeletal 13-like (LOC100711368), mRNA	0,0371	0,0034	up	up	up	up	up	up
MPF_LOC100701013.2.2	XM_003447971.1 PREDICTED: Oreochromis niloticus CDGSH iron-sulfur domain-containing protein 3, mitochondrial-like (LOC100701013), mRNA	0,0171	0,0003	down	up	up	up	up	up
MPF_ACTB2.1.2	ACTB2_TAKRU (sp|P53485) Actin, cytoplasmic 2 OS=Takifugu rubripes GN=actbb PE=3 SV=1	0,0269	0,0013	down	down	down	down	down	down
MPF_LOC101488136.1.2	XM_004558958.1 PREDICTED: Maylandia zebra RNA-binding protein 39-like (LOC101488136), mRNA	0,0319	0,0022	up	up	up	up	up	up
MPF_LOC100693211.1.1	XM_003437922.1 PREDICTED: Oreochromis niloticus kinesin-like protein KIF2C-like (LOC100693211), mRNA	0,0453	0,0057	up	up	up	up	up	up
MPF_LOC101464979.2.7	XM_004550563.1 PREDICTED: Maylandia zebra ralBP1-associated Eps domain-containing protein 1like (LOC101464979), transcript variant X4, mRNA	0,0371	0,0035	down	down	up	down	up	up
MPF_EOS1.1.1	XP_004068609.1 PREDICTED: zinc finger protein Eos-like [Oryzias latipes]	0,0286	0,0016	down	up	up	up	up	up
MPF_contig_014026	XM_004549368.1 PREDICTED: Maylandia zebra ras GTPase-activating protein-binding protein 2-like (LOC101479323), transcript variant X1, mRNA	0,0285	0,0016	down	up	up	up	up	up
MPF_LOC101465129.6.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA	0,0123	0,0001	down	down	down	down	down	down
MPF_contig_014071	XM_004574586.1 PREDICTED: Maylandia zebra zinc finger MYND domain-containing protein 11-like (LOC101478959), transcript variant X3, mRNA	0,0213	0,0006	up	up	up	up	up	up
MPF_LOC101480926.1.1	XM_004544359.1 PREDICTED: Maylandia zebra survival motor neuron protein 1-like (LOC101480926), mRNA	0,0149	0,0002	up	up	up	up	up	up

MPF_LOC100691649.1.3	XP_003449900.1 PREDICTED: low molecular weight phosphotyrosine protein phosphatase-like isoform 3 [Oreochromis niloticus] ref|XP_003449901.1| PREDICTED: low molecular weight phosphotyrosine protein phosphatase-like isoform 4 [Oreochromis niloticus]	0,0171	0,0003	up	up	up	up	up	up
MPF_LOC100708209.1.1	XP_003456856.1 PREDICTED: NACHT, LRR and PYD domains-containing protein 3-like [Oreochromis niloticus]	0,0269	0,0013	up	up	up	up	up	up
MPF_LOC101481563.1.1	XM_004556453.1 PREDICTED: Maylandia zebra heat shock 70 kDa protein 1-like (LOC101481563), mRNA	0,0431	0,0051	up	up	up	down	up	up
MPF_contig_014340	XM_004555992.1 PREDICTED: Maylandia zebra protein FAM135A-like (LOC101483692), transcript variant X1, mRNA	0,0374	0,0036	down	up	up	up	up	up
MPF_LOC101156670.1.1	XP_004076053.1 PREDICTED: POU domain class 2-associating factor 1-like [Oryzias latipes]	0,0332	0,0024	down	down	up	up	up	up
MPF_LOC101484306.1.1	XM_004545559.1 PREDICTED: Maylandia zebra integrator complex subunit 5-like (LOC101484306), mRNA	0,0277	0,0015	down	up	up	up	up	up
MPF_LOC101470306.1.1	XM_004574119.1 PREDICTED: Maylandia zebra uncharacterized LOC101470306 (LOC101470306), mRNA	0,0065	0,0000	down	down	down	down	down	down
MPF_LOC100617860.1.1	XP_003340874.1 PREDICTED: zinc finger protein 420-like [Monodelphis domestica]	0,0488	0,0072	down	up	up	up	up	up
MPF_LOC101468583.1.7	XM_004576296.1 PREDICTED: Maylandia zebra uncharacterized LOC101468583 (LOC101468583), mRNA	0,0065	0,0000	down	down	down	down	down	down
MPF_LOC101164889.1.1	XM_004070593.1 PREDICTED: Oryzias latipes putative nuclease HARBI1-like (LOC101164889), mRNA	0,0233	0,0008	down	up	up	up	up	up
MPF_LOC101175132.1.2	XP_004085856.1 PREDICTED: beta-enolase-like isoform 2 [Oryzias latipes]	0,0266	0,0012	down	up	up	up	up	up
MPF_LOC101166970.1.1	XP_004073985.1 PREDICTED: uncharacterized protein LOC101166970 [Oryzias latipes]	0,0160	0,0002	down	down	down	down	down	down
MPF_LOC100706363.1.1	XP_003441373.1 PREDICTED: hypothetical protein LOC100706363 [Oreochromis niloticus]	0,0147	0,0002	down	up	up	up	up	up
MPF_LOC101473946.1.3	XM_004540042.1 PREDICTED: Maylandia zebra protein salvador homolog 1-like (LOC101473946), mRNA	0,0230	0,0008	down	up	up	up	up	up
MPF_contig_014638	NA	0,0262	0,0012	down	up	down	up	down	down
MPF_contig_014649	NA	0,0453	0,0057	down	up	up	up	up	up
MPF_LOC100689854.8.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0,0411	0,0045	down	up	up	up	up	up
MPF_LOC101463698.1.1	XM_004568112.1 PREDICTED: Maylandia zebra maestro heat-like repeat-containing protein family member 1-like (LOC101463698), transcript variant X3, mRNA	0,0194	0,0005	up	up	up	up	up	up
MPF_LOC101468249.1.2	XM_004541040.1 PREDICTED: Maylandia zebra clathrin light chain B-like (LOC101468249), transcript variant X2, mRNA	0,0269	0,0013	down	up	up	up	up	up
MPF_LOC100699885.1.2	XP_003459139.1 PREDICTED: tripartite motif-containing protein 16-like [Oreochromis niloticus]	0,0277	0,0015	down	down	up	down	up	up
MPF_LOC101171771.2.2	XM_004077345.1 PREDICTED: Oryzias latipes uncharacterized LOC101171771 (LOC101171771), mRNA	0,0130	0,0001	down	down	down	down	down	down
MPF_contig_014802	NA	0,0078	0,0000	down	down	down	down	down	down

MPF_contig_014823	NA	0,0178	0,0004	down	down	down	up	down	down
MPF_LOC100712339.2.2	XP_003460124.1 PREDICTED: protein JTB-like [Oreochromis niloticus]	0,0123	0,0001	up	up	up	up	up	up
MPF_BRAFLDRAFT_96790.1	XP_002595816.1 hypothetical protein BRAFLDRAFT_96790 [Branchiostoma floridae]	0,0326	0,0023	up	up	up	up	up	up
MPF_contig_014852	NA	0,0194	0,0005	down	down	down	up	down	down
MPF_contig_014860	NA	0,0453	0,0057	down	up	up	up	up	up
MPF_contig_014890	NA	0,0091	0,0000	down	down	down	up	down	down
MPF_contig_014892	NA	0,0047	0,0000	down	down	down	up	down	down
MPF_contig_014917	NA	0,0205	0,0005	down	down	down	down	down	down
MPF_LOC101475324.3.5	XM_004570832.1 PREDICTED: Maylandia zebra MOB kinase activator 2-like (LOC101475324), transcript variant X4, mRNA	0,0095	0,0000	down	down	down	down	down	down
MPF_contig_014930	XM_004570830.1 PREDICTED: Maylandia zebra MOB kinase activator 2-like (LOC101475324), transcript variant X2, mRNA	0,0150	0,0002	down	up	up	up	up	up
MPF_contig_014940	NA	0,0136	0,0001	down	down	down	down	down	down
MPF_LOC100711510.1.8	XM_003455849.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100711510), mRNA	0,0066	0,0000	down	down	down	down	down	down
MPF_contig_015023	NA	0,0051	0,0000	down	down	down	down	down	down
MPF_LOC100707106.1.1	XP_003451942.1 PREDICTED: recombining binding protein suppressor of hairless-like protein-like [Oreochromis niloticus]	0,0274	0,0014	down	down	up	down	up	up
MPF_LOC101069016.2.2	XM_003977363.1 PREDICTED: Takifugu rubripes synapse-associated protein 1-like (LOC101069016), mRNA	0,0294	0,0017	down	up	up	up	up	up
MPF_contig_015041	NA	0,0460	0,0060	up	up	up	down	up	up
MPF_contig_015096	NA	0,0183	0,0004	down	up	up	up	up	up
MPF_contig_015103	NA	0,0307	0,0019	up	up	up	up	up	up
MPF_LOC100707140.3.4	XP_003458392.1 PREDICTED: hypothetical protein LOC100707140 [Oreochromis niloticus]	0,0198	0,0005	down	down	down	down	down	down
MPF_LOC100707856.1.1	XP_003458866.1 PREDICTED: transforming growth factor beta-2-like [Oreochromis niloticus]	0,0498	0,0076	down	down	down	up	down	down
MPF_contig_015244	NA	0,0333	0,0024	up	up	up	down	up	up
MPF_LOC101475732.4.4	XM_004548444.1 PREDICTED: Maylandia zebra ankyrin repeat and BTB/POZ domain-containing protein BTBD11-A-like (LOC101475732), transcript variant X2, mRNA	0,0467	0,0063	down	down	up	down	up	up
MPF_contig_015308	NA	0,0491	0,0073	up	up	up	down	up	up
MPF_contig_015309	NA	0,0397	0,0041	up	up	up	up	up	up
MPF_contig_015319	NA	0,0371	0,0034	up	up	up	up	up	up

MPF_LOC100701316.1.1	XP_003456261.1 PREDICTED: U3 small nucleolar RNA-associated protein 14 homolog A-like [Oreochromis niloticus]	0,0367	0,0033	up	up	up	up	up	up
MPF_LOC101479727.1.6	XM_004576138.1 PREDICTED: Maylandia zebra uncharacterized LOC101479727 (LOC101479727), mRNA	0,0180	0,0004	up	up	up	up	up	up
MPF_LOC100693543.1.1	XP_003450393.1 PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondriallike [Oreochromis niloticus]	0,0232	0,0008	up	up	up	up	up	up
MPF_contig_015394	NA	0,0190	0,0004	up	up	up	up	up	up
MPF_LOC101466726.1.1	XM_004552330.1 PREDICTED: Maylandia zebra telethonin-like (LOC101466726), mRNA	0,0123	0,0001	down	up	up	up	up	up
MPF_contig_015428	NA	0,0173	0,0003	up	up	up	up	up	up
MPF_LOC100702049.1.1	XP_003458060.1 PREDICTED: major histocompatibility complex class I-related gene protein-like [Oreochromis niloticus]	0,0307	0,0019	up	up	up	up	up	up
MPF_contig_015434	NA	0,0266	0,0012	up	up	up	up	up	up
MPF_contig_015435	NA	0,0129	0,0001	down	down	down	down	down	down
MPF_MYHM2126-2.1.3	XP_003975582.1 PREDICTED: myosin-7 [Takifugu rubripes]	0,0277	0,0014	down	down	down	down	down	down
MPF_contig_015464	NA	0,0039	0,0000	down	down	down	down	down	down
MPF_LOC101168682.3.3	XM_004066371.1 PREDICTED: Oryzias latipes protein S100-B-like, transcript variant 2 (LOC101168682), mRNA	0,0060	0,0000	down	down	down	down	down	down
MPF_contig_015477	NA	0,0231	0,0008	down	down	down	up	down	down
MPF_LOC100700436.1.1	XP_003439415.1 PREDICTED: transcriptional repressor NF-X1-like [Oreochromis niloticus]	0,0243	0,0009	up	up	up	down	up	up
MPF_LOC100690119.8.18	XP_003448733.1 PREDICTED: zinc finger protein 16-like [Oreochromis niloticus]	0,0382	0,0037	up	up	up	up	up	up
MPF_contig_015500	NA	0,0147	0,0002	down	down	down	down	down	down
MPF_LOC101474290.4.6	XM_004573400.1 PREDICTED: Maylandia zebra NHS-like protein 2-like (LOC101474290), transcript variant X4, mRNA	0,0160	0,0003	down	up	up	up	up	up
MPF_contig_015515	NA	0,0171	0,0003	up	up	up	up	up	up
MPF_contig_015519	XM_004555587.1 PREDICTED: Maylandia zebra LIM and senescent cell antigen-like-containing domain protein 1-like (LOC101469398), transcript variant X3, mRNA	0,0472	0,0065	up	up	up	up	up	up
MPF_contig_015520	NA	0,0066	0,0000	down	up	up	up	up	up
MPF_contig_015541	NA	0,0302	0,0018	down	up	up	up	up	up
MPF_LOC100535679.1.1	XP_003198445.1 PREDICTED: zinc finger protein 721-like [Danio rerio]	0,0338	0,0025	down	up	up	up	up	up
MPF_contig_015546	NA	0,0371	0,0034	down	up	up	up	up	up
MPF_contig_015549	NA	0,0270	0,0013	down	down	down	down	down	down

MPF_LOC587493.3.4	XP_792312.2 PREDICTED: uncharacterized protein LOC587493 [Strongylocentrotus purpuratus]	0,0308	0,0020	down	up	up	up	up	up
MPF_contig_015574	NA	0,0224	0,0007	up	up	up	up	up	up
MPF_contig_015580	NA	0,0472	0,0065	up	up	up	up	up	up
MPF_contig_015596	NA	0,0160	0,0003	down	down	down	up	down	down
MPF_LOC101474859.5.21	XM_004575478.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 4like (LOC101474859), transcript variant X2, mRNA	0,0424	0,0049	up	up	down	down	down	down
MPF_LOC101468598.1.2	XM_004559893.1 PREDICTED: Maylandia zebra cyclin-dependent kinase 18-like (LOC101468598), mRNA	0,0356	0,0030	down	up	up	up	up	up
MPF_contig_015699	NA	0,0112	0,0001	down	down	down	down	down	down
MPF_LOC100689854.9.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0,0451	0,0057	up	up	up	up	up	up
MPF_LOC100691115.1.1	XP_003450716.1 PREDICTED: zinc finger protein 574-like [Oreochromis niloticus]	0,0239	0,0009	down	up	up	up	up	up
MPF_contig_015779	NA	0,0474	0,0066	down	up	up	up	up	up
MPF_LOC100711274.1.1	XP_003440891.1 PREDICTED: protein dispatched homolog 1-like [Oreochromis niloticus]	0,0454	0,0058	down	down	up	up	up	up
MPF_contig_015804	NA	0,0450	0,0056	down	up	up	up	up	up
MPF_LOC101467579.1.1	XM_004551299.1 PREDICTED: Maylandia zebra transmembrane protein 182-like (LOC101467579), mRNA	0,0171	0,0003	up	up	up	down	up	up
MPF_LOC101473315.1.1	XM_004572231.1 PREDICTED: Maylandia zebra protein AF1q-like (LOC101473315), transcript variant X2, mRNA	0,0483	0,0070	up	up	up	down	up	up
MPF_LOC101471209.1.3	XM_004561763.1 PREDICTED: Maylandia zebra protein Jade-2-like (LOC101471209), mRNA	0,0134	0,0001	down	up	up	up	up	up
MPF_MLL3.1.1	MLL3_HUMAN (sp|Q8NEZ4) Histone-lysine N-methyltransferase MLL3 OS=Homo sapiens GN=MLL3 PE=1 SV=3	0,0476	0,0067	up	up	up	down	up	up
MPF_contig_016000	XM_004075770.1 PREDICTED: Oryzias latipes arf-GAP domain and FG repeat-containing protein 1like, transcript variant 1 (LOC101155131), mRNA	0,0495	0,0075	up	up	up	up	up	up
MPF_LOC101061889.1.1	XP_003972358.1 PREDICTED: sorbin and SH3 domain-containing protein 2-like [Takifugu rubripes]	0,0234	0,0008	up	up	up	up	up	up
MPF_LOC100695839.1.1	XP_003447752.1 PREDICTED: inositol-pentakisphosphate 2-kinase-like [Oreochromis niloticus]	0,0187	0,0004	up	down	up	down	up	up
MPF_LOC101078388.2.4	XM_003968304.1 PREDICTED: Takifugu rubripes uncharacterized LOC101078388 (LOC101078388), mRNA	0,0319	0,0022	down	down	down	down	down	down
MPF_LOC100710590.1.4	XP_003449469.1 PREDICTED: zinc finger protein 836-like, partial [Oreochromis niloticus]	0,0387	0,0039	up	up	up	up	up	up
MPF_LOC101169293.5.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0,0424	0,0049	down	up	down	up	down	down
MPF_contig_016131	NA	0,0172	0,0003	down	down	down	down	down	down
MPF_LOC100707655.8.19	XM_003454192.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S6-like (LOC100707655), mRNA	0,0145	0,0002	down	down	down	down	down	down

MPF_contig_016136	NA	0,0374	0,0036	down	down	down	down	down	down
MPF_LOC101470738.5.20	XM_004560737.1 PREDICTED: Maylandia zebra actin, cytoplasmic 1-like (LOC101470738), mRNA	0,0123	0,0001	down	down	up	down	up	up
MPF_LOC100694953.1.2	XM_003448201.1 PREDICTED: Oreochromis niloticus troponin T, cardiac muscle isoforms-like (LOC100694953), mRNA	0,0207	0,0005	down	down	up	up	up	up
MPF_LOC101480760.3.13	XM_004547526.1 PREDICTED: Maylandia zebra 40S ribosomal protein S10-like (LOC101480760), transcript variant X2, mRNA	0,0345	0,0027	down	down	up	down	up	up
MPF_ZN121.2.3	ZN121_HUMAN (sp|P58317) Zinc finger protein 121 OS=Homo sapiens GN=ZNF121 PE=2 SV=2	0,0287	0,0016	up	up	up	up	up	up
MPF_contig_016225	XM_004558106.1 PREDICTED: Maylandia zebra phosphatidylinositol-binding clathrin assembly proteinlike (LOC101478138), transcript variant X5, mRNA	0,0224	0,0007	up	up	up	up	up	up
MPF_LOC100700605.10.27	XM_003458555.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100700605), mRNA	0,0171	0,0003	up	down	down	down	down	down
MPF_contig_016274	NA	0,0353	0,0029	down	down	down	down	down	down
MPF_LOC101478322.2.4	XM_004556897.1 PREDICTED: Maylandia zebra capZ-interacting protein-like (LOC101478322), mRNA	0,0171	0,0003	down	up	up	up	up	up
MPF_LOC101486284.1.3	XM_004546431.1 PREDICTED: Maylandia zebra transmembrane protein 189-like (LOC101486284), mRNA	0,0488	0,0072	down	up	up	up	up	up
MPF_LOC100536482.1.1	XP_003198573.1 PREDICTED: zinc finger protein 271-like [Danio rerio]	0,0498	0,0076	up	up	up	down	up	up
MPF_LOC101159641.10.35	XM_004085298.1 PREDICTED: Oryzias latipes tenascin-like (LOC101159641), mRNA	0,0060	0,0000	down	down	down	down	down	down
MPF_LOC101466612.1.2	XM_004549597.1 PREDICTED: Maylandia zebra zinc finger protein 462-like (LOC101466612), transcript variant X1, mRNA	0,0208	0,0006	down	down	down	down	down	down
MPF_LOC101481605.1.1	XM_004544263.1 PREDICTED: Maylandia zebra transcription factor 7-like 1-A-like (LOC101481605), transcript variant X2, mRNA	0,0419	0,0047	up	down	up	down	up	up
MPF_contig_016368	NA	0,0485	0,0071	down	up	up	up	up	up
MPF_contig_016380	NA	0,0108	0,0001	down	up	up	up	up	up
MPF_LOC100695994.1.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0,0472	0,0065	up	up	up	down	up	up
MPF_LOC101473807.1.1	XM_004573575.1 PREDICTED: Maylandia zebra protein C-ets-1-like (LOC101473807), transcript variant X1, mRNA	0,0143	0,0002	down	up	up	up	up	up
MPF_LOC101061679.1.1	XM_003975895.1 PREDICTED: Takifugu rubripes cAMP-responsive element modulator-like (LOC101061679), mRNA	0,0169	0,0003	down	down	down	down	down	down
MPF_contig_016470	NA	0,0438	0,0053	up	up	up	up	up	up
MPF_contig_016490	NA	0,0265	0,0012	down	down	up	down	up	up

MPF_LOC101485878.1.1	XM_004546034.1 PREDICTED: Maylandia zebra poly(rC)-binding protein 4-like (LOC101485878), transcript variant X2, mRNA	0,0326	0,0022	down	down	up	down	up	up
MPF_LOC100701582.1.9	XP_003455288.1 PREDICTED: zinc finger protein 236-like [Oreochromis niloticus]	0,0351	0,0028	up	up	up	up	up	up
MPF_KLHL7.1.1	XP_003444163.1 PREDICTED: kelch-like protein 7 [Oreochromis niloticus]	0,0394	0,0040	down	down	up	up	up	up
MPF_LOC100696802.1.1	XP_003447430.1 PREDICTED: Golgi reassembly-stacking protein 2-like [Oreochromis niloticus]	0,0381	0,0037	down	down	down	up	down	down
MPF_contig_016515	NA	0,0124	0,0001	down	up	up	up	up	up
MPF_LOC101161302.1.1	XP_004068020.1 PREDICTED: very low-density lipoprotein receptor-like [Oryzias latipes]	0,0357	0,0030	up	up	up	down	up	up
MPF_contig_016564	NA	0,0332	0,0023	down	down	up	up	up	up
MPF_LOC100694075.1.1	XM_003449860.1 PREDICTED: Oreochromis niloticus histidine triad nucleotide-binding protein 3-like (LOC100694075), mRNA	0,0464	0,0061	down	up	up	up	up	up
MPF_LOC101487747.1.2	XM_004573537.1 PREDICTED: Maylandia zebra membrane-spanning 4-domains subfamily A member 15-like (LOC101487747), transcript variant X3, mRNA	0,0269	0,0013	up	down	down	down	down	down
MPF_LOC101473558.2.2	XM_004561318.1 PREDICTED: Maylandia zebra transcription factor 7-like 2-like (LOC101473558), transcript variant X13, mRNA	0,0096	0,0000	down	up	up	up	up	up
MPF_LOC100691087.1.2	XM_003445024.1 PREDICTED: Oreochromis niloticus putative homeodomain transcription factor 2-like (LOC100691087), mRNA	0,0495	0,0075	down	up	up	up	up	up
MPF_LOC100697737.1.1	XP_003458594.1 PREDICTED: zinc finger MYM-type protein 4-like [Oreochromis niloticus]	0,0432	0,0052	down	down	up	down	up	up
MPF_LOC101473755.2.3	XM_004564853.1 PREDICTED: Maylandia zebra CCR4-NOT transcription complex subunit 2-like (LOC101473755), transcript variant X2, mRNA	0,0371	0,0035	down	down	up	up	up	up
MPF_VDAC1.1.1	VDAC1_RABIT (sp|Q9TT15) Voltage-dependent anion-selective channel protein 1 OS=Oryctolagus cuniculus GN=VDAC1 PE=2 SV=3	0,0380	0,0037	up	up	up	up	up	up
MPF_contig_016882	NA	0,0169	0,0003	up	down	down	down	down	down
MPF_LOC100695994.3.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0,0304	0,0019	up	up	up	up	up	up
MPF_LOC100702190.2.6	XM_003448143.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L10a-like (LOC100702190), mRNA	0,0200	0,0005	up	up	up	up	up	up
MPF_PDK2.2.4	PDK2_HUMAN (sp|Q15119) [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial OS=Homo sapiens GN=PDK2 PE=1 SV=2	0,0270	0,0013	down	up	up	up	up	up
MPF_LOC101480083.2.3	XM_004548835.1 PREDICTED: Maylandia zebra cytochrome c1, heme protein, mitochondrial-like (LOC101480083), mRNA	0,0253	0,0011	down	down	up	up	up	up
MPF_LOC101467581.1.1	XM_004574714.1 PREDICTED: Maylandia zebra ephrin type-B receptor 4-like (LOC101467581), mRNA	0,0244	0,0010	down	up	up	up	up	up
MPF_LOC101477080.1.1	XM_004549745.1 PREDICTED: Maylandia zebra uncharacterized LOC101477080 (LOC101477080), transcript variant X4, mRNA	0,0411	0,0045	up	down	up	down	up	up
MPF_contig_017040	NA	0,0270	0,0013	down	up	up	up	up	up

MPF_LOC101485466.1.3	XM_004557559.1 PREDICTED: Maylandia zebra trinucleotide repeat-containing gene 6B protein-like (LOC101485466), transcript variant X4, mRNA	0,0411	0,0045	down	up	up	up	up	up
MPF_LOC101471646.1.1	XM_004571230.1 PREDICTED: Maylandia zebra WW domain-binding protein 4-like (LOC101471646), mRNA	0,0471	0,0064	down	up	up	up	up	up
MPF_MK14.1.1	MK14_MOUSE (sp|P47811) Mitogen-activated protein kinase 14 OS=Mus musculus GN=Mapk14 PE=1 SV=3	0,0291	0,0017	up	up	up	up	up	up
MPF_LOC100706126.1.2	XM_003447163.1 PREDICTED: Oreochromis niloticus mediator of RNA polymerase II transcription subunit 30-like (LOC100706126), mRNA	0,0451	0,0057	up	up	up	up	up	up
MPF_contig_017190	NA	0,0150	0,0002	down	down	down	down	down	down
MPF_LOC101481869.3.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA	0,0319	0,0021	down	up	up	up	up	up
MPF_LOC100700438.1.1	XP_003439588.1 PREDICTED: synaptotagmin-1-like [Oreochromis niloticus]	0,0341	0,0026	down	up	up	up	up	up

MPF_LOC101471848.1.1	XM_004573568.1 PREDICTED: Maylandia zebra putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16-like (LOC101471848), transcript variant X1, mRNA	0,0293	0,0017	down	up	up	up	up	up
MPF_LOC101479939.1.1	XM_004563953.1 PREDICTED: Maylandia zebra zinc finger protein 260-like (LOC101479939), mRNA	0,0388	0,0039	down	up	up	up	up	up
MPF_LOC101484122.5.9	XM_004572909.1 PREDICTED: Maylandia zebra eukaryotic translation initiation factor 5A-1-like (LOC101484122), mRNA	0,0394	0,0040	up	up	up	up	up	up
MPF_LOC100690117.1.1	XP_003448481.1 PREDICTED: metastasis suppressor protein 1-like [Oreochromis niloticus]	0,0305	0,0019	down	up	up	up	up	up
MPF_LOC101468502.1.1	XM_004555833.1 PREDICTED: Maylandia zebra copper homeostasis protein cutC homolog (LOC101468502), transcript variant X3, mRNA	0,0278	0,0015	up	up	up	up	up	up
MPF_RAPH1.1.2	XM_003459208.1 PREDICTED: Oreochromis niloticus Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 (RAPH1), mRNA	0,0241	0,0009	down	down	up	down	up	up
MPF_LOC100706818.1.9	XR_134822.1 PREDICTED: Oreochromis niloticus selenoprotein Pa-like (LOC100706818), miscRNA	0,0268	0,0013	down	up	up	up	up	up
MPF_contig_017320	XM_004575932.1 PREDICTED: Maylandia zebra myosin phosphatase Rho-interacting protein-like (LOC101466990), transcript variant X3, mRNA	0,0362	0,0031	down	up	up	up	up	up
MPF_contig_017330	NA	0,0342	0,0026	down	up	up	up	up	up
MPF_TBA1.1.1	TBA1_CHICK (sp|P02552) Tubulin alpha-1 chain (Fragment) OS=Gallus gallus PE=1 SV=1	0,0150	0,0002	up	up	up	up	up	up
MPF_USP24.1.1	XP_003439791.1 PREDICTED: ubiquitin carboxyl-terminal hydrolase 24 [Oreochromis niloticus]	0,0476	0,0067	down	down	up	up	up	up
MPF_LOC100534962.1.1	XP_003201578.1 PREDICTED: oocyte zinc finger protein XlCOF6-like [Danio rerio]	0,0277	0,0015	down	up	up	up	up	up
MPF_contig_017402	XM_004570830.1 PREDICTED: Maylandia zebra MOB kinase activator 2-like (LOC101475324), transcript variant X2, mRNA	0,0212	0,0006	down	down	up	up	up	up
MPF_LOC101472257.1.1	XM_004556797.1 PREDICTED: Maylandia zebra pyruvate dehydrogenase [lipoamide] kinase isozyme 2like (LOC101472257), mRNA	0,0228	0,0008	up	up	up	up	up	up

MPF_LOC101079440.1.1	XM_003966182.1 PREDICTED: Takifugu rubripes protein lifeguard 1-like (LOC101079440), mRNA	0,0371	0,0034	up	up	up	up	up	up
MPF_LOC101477091.1.3	XM_004574318.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101477091), transcript variant X5, mRNA	0,0112	0,0001	up	down	down	down	down	down
MPF_LOC101487772.1.2	XM_004559324.1 PREDICTED: Maylandia zebra alcohol dehydrogenase 1-like (LOC101487772), mRNA	0,0139	0,0001	up	up	up	up	up	up
MPF_contig_017575	NA	0,0198	0,0005	down	down	up	up	up	up
MPF_LOC101169385.1.3	XP_004077303.1 PREDICTED: zinc finger protein 318-like [Oryzias latipes]	0,0267	0,0012	down	up	up	up	up	up
MPF_LOC100707166.2.2	XM_003442172.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100707166 (LOC100707166), mRNA	0,0150	0,0002	up	down	down	down	down	down
MPF_GABPB2B.1.1	NP_001070620.1 GA repeat binding protein, beta 2b [Danio rerio]	0,0302	0,0018	up	up	up	up	up	up
MPF_LOC101467619.1.4	XM_004561184.1 PREDICTED: Maylandia zebra ubiquitin thioesterase ZRANB1-like (LOC101467619), mRNA	0,0487	0,0072	down	down	down	down	down	down
MPF_LOC100693065.5.9	XM_003443772.1 PREDICTED: Oreochromis niloticus NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial-like (LOC100693065), mRNA	0,0354	0,0029	up	up	up	up	up	up
MPF_LOC101470455.1.1	XM_004539752.1 PREDICTED: Maylandia zebra aminopeptidase N-like (LOC101470455), mRNA	0,0213	0,0006	up	down	down	down	down	down
MPF_LOC100705062.1.6	XM_003446407.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100705062 (LOC100705062), mRNA	0,0260	0,0011	up	down	up	down	up	up
MPF_LOC101481038.1.1	XM_004548647.1 PREDICTED: Maylandia zebra cytokine-inducible SH2-containing protein-like (LOC101481038), transcript variant X2, mRNA	0,0160	0,0003	down	up	up	up	up	up
MPF_MLL5.2.3	XP_003452082.1 PREDICTED: histone-lysine N-methyltransferase MLL5 [Oreochromis niloticus]	0,0371	0,0035	down	up	up	up	up	up
MPF_contig_017839	XM_003437559.1 PREDICTED: Oreochromis niloticus cytochrome c oxidase subunit 5A, mitochondriallike, transcript variant 1 (LOC100707142), mRNA	0,0258	0,0011	up	down	up	down	up	up
MPF_LOC100709667.1.5	XM_003438989.1 PREDICTED: Oreochromis niloticus cellular nucleic acid-binding protein-like (LOC100709667), mRNA	0,0346	0,0027	down	down	up	up	up	up
MPF_LOC100706818.3.9	XR_134822.1 PREDICTED: Oreochromis niloticus selenoprotein Pa-like (LOC100706818), miscRNA	0,0293	0,0017	up	up	up	up	up	up
MPF_LOC101470951.1.1	XM_004541051.1 PREDICTED: Maylandia zebra heterogeneous nuclear ribonucleoprotein H-like (LOC101470951), mRNA	0,0438	0,0053	up	up	up	up	up	up
MPF_LOC101467183.1.2	XM_004550296.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101467183), transcript variant X7, mRNA	0,0260	0,0011	down	down	down	down	down	down
MPF_LOC100698172.2.3	XP_003455687.1 PREDICTED: beta-2-microglobulin-like [Oreochromis niloticus]	0,0154	0,0002	down	up	up	up	up	up
MPF_contig_017922	NA	0,0145	0,0002	down	up	up	up	up	up
MPF_LOC101472431.2.6	XM_004550961.1 PREDICTED: Maylandia zebra cytochrome P450 4B1-like (LOC101472431), transcript variant X1, mRNA	0,0295	0,0018	down	down	up	down	up	up

MPF_LOC101474655.1.2	XM_004570828.1 PREDICTED: Maylandia zebra dual specificity protein phosphatase 8-like (LOC101474655), transcript variant X3, mRNA	0,0160	0,0003	down	up	up	up	up	up
MPF_LOC100702052.1.1	XM_003458326.1 PREDICTED: Oreochromis niloticus myosin-XVIIIa-like (LOC100702052), mRNA	0,0217	0,0006	down	up	up	up	up	up
MPF_LOC101073827.1.1	XP_003967391.1 PREDICTED: actin-related protein 6-like [Takifugu rubripes]	0,0315	0,0021	down	up	up	up	up	up
MPF_LOC100700318.1.1	XM_003455569.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L7-like 1-like (LOC100700318), mRNA	0,0217	0,0006	down	up	up	up	up	up
MPF_LOC101469398.1.2	XM_004555590.1 PREDICTED: Maylandia zebra LIM and senescent cell antigen-like-containing domain protein 1-like (LOC101469398), transcript variant X6, mRNA	0,0294	0,0017	up	up	up	up	up	up
MPF_LOC100690119.9.18	XP_003448733.1 PREDICTED: zinc finger protein 16-like [Oreochromis niloticus]	0,0455	0,0058	down	up	up	up	up	up
MPF_LOC101464835.1.1	XM_004566087.1 PREDICTED: Maylandia zebra dickkopf-related protein 3-like (LOC101464835), mRNA	0,0136	0,0001	down	up	up	up	up	up
MPF_LOC100701582.2.9	XP_003455288.1 PREDICTED: zinc finger protein 236-like [Oreochromis niloticus]	0,0354	0,0029	up	down	up	down	up	up
MPF_LOC101466862.1.1	XM_004569189.1 PREDICTED: Maylandia zebra zinc finger protein 40-like (LOC101466862), mRNA	0,0307	0,0019	down	up	up	up	up	up
MPF_NEMVEDRAFT_V1G88	XP_001638721.1 predicted protein [Nematostella vectensis]	0,0277	0,0014	up	up	up	up	up	up
MPF_LOC100694733.1.1	XP_003438312.1 PREDICTED: pleckstrin-like [Oreochromis niloticus]	0,0253	0,0011	down	down	down	down	down	down
MPF_LOC101483918.1.2	XM_004543720.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase SIK2-like (LOC101483918), mRNA	0,0455	0,0058	down	up	up	up	up	up
MPF_contig_018234	NA	0,0260	0,0011	down	up	up	up	up	up
MPF_LOC100708308.2.2	XP_003459094.1 PREDICTED: hypothetical protein LOC100708308 [Oreochromis niloticus]	0,0331	0,0023	up	up	up	up	up	up
MPF_HECTD1.2.4	XM_003451209.1 PREDICTED: Oreochromis niloticus HECT domain containing 1 (HECTD1), mRNA	0,0265	0,0012	down	down	up	up	up	up
MPF_LOC101477442.1.1	XM_004547420.1 PREDICTED: Maylandia zebra GTP-binding protein REM 1-like (LOC101477442), transcript variant X4, mRNA	0,0123	0,0001	down	up	up	up	up	up
MPF_LOC100709926.1.1	XP_003437949.1 PREDICTED: vacuolar protein sorting-associated protein 4B-like [Oreochromis niloticus]	0,0290	0,0017	down	up	up	up	up	up
MPF_contig_018377	XM_004572780.1 PREDICTED: Maylandia zebra unconventional myosin-XVIIIa-like (LOC101474105), transcript variant X1, mRNA	0,0326	0,0022	down	up	up	up	up	up
MPF_LOC100690119.3.18	XP_003448733.1 PREDICTED: zinc finger protein 16-like [Oreochromis niloticus]	0,0337	0,0025	down	up	up	up	up	up
MPF_LOC101485892.5.16	XM_004549780.1 PREDICTED: Maylandia zebra phytanoyl-CoA dioxygenase domain-containing protein 1-like (LOC101485892), mRNA	0,0472	0,0064	down	up	up	up	up	up
MPF_LOC100699885.2.2	XM_003459091.1 PREDICTED: Oreochromis niloticus tripartite motif-containing protein 16-like (LOC100699885), mRNA	0,0160	0,0003	down	down	up	down	up	up
MPF_ZN271.5.19	ZN271_MOUSE (sp|P15620) Zinc finger protein 271 OS=Mus musculus GN=Znf271 PE=2 SV=1	0,0401	0,0042	up	up	up	up	up	up
MPF_contig_018575	NA	0,0060	0,0000	down	down	down	down	down	down

MPF_LOC100700648.1.1	XP_003447359.1 PREDICTED: pyruvate dehydrogenase [lipoamide] kinase isozyme 1-like [Oreochromis niloticus]	0,0305	0,0019	up	up	up	down	up	up
MPF_contig_018608	NA	0,0354	0,0029	down	up	up	up	up	up
MPF_contig_018625	NA	0,0277	0,0014	down	down	up	up	up	up
MPF_LOC101484019.1.1	XM_004545115.1 PREDICTED: Maylandia zebra copine-5-like (LOC101484019), mRNA	0,0112	0,0001	down	down	up	up	up	up
MPF_contig_018702	NA	0,0228	0,0007	up	up	up	down	up	up
MPF_LOC100695994.17.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0,0247	0,0010	down	up	up	up	up	up
MPF_LOC100538336.1.1	XP_003198555.1 PREDICTED: zinc finger protein 729-like [Danio rerio]	0,0472	0,0065	down	up	up	up	up	up
MPF_contig_018804	NA	0,0275	0,0014	up	up	up	up	up	up
MPF_contig_018806	NA	0,0212	0,0006	up	up	up	up	up	up
MPF_LOC101066985.1.1	XP_003978412.1 PREDICTED: FH1/FH2 domain-containing protein 3-like [Takifugu rubripes]	0,0482	0,0069	down	down	up	down	up	up
MPF_LOC100709368.1.1	XP_003455402.1 PREDICTED: large subunit GTPase 1 homolog [Oreochromis niloticus]	0,0171	0,0003	up	up	up	up	up	up
MPF_LOC101480539.1.1	XM_004565871.1 PREDICTED: Maylandia zebra autism susceptibility gene 2 protein-like (LOC101480539), transcript variant X5, mRNA	0,0316	0,0021	down	up	up	up	up	up
MPF_contig_018904	NA	0,0247	0,0010	down	up	up	up	up	up
MPF_contig_018921	NA	0,0278	0,0015	down	down	down	down	down	down
MPF_LOC101475750.1.3	XM_004552928.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase Kist-like (LOC101475750), mRNA	0,0464	0,0061	down	down	up	up	up	up
MPF_LOC101477438.2.2	XM_004545630.1 PREDICTED: Maylandia zebra ligand of Numb protein X 2-like (LOC101477438), transcript variant X3, mRNA	0,0187	0,0004	up	up	up	up	up	up
MPF_LOC101467147.1.5	XM_004566000.1 PREDICTED: Maylandia zebra NEDD8-conjugating enzyme UBE2F-like (LOC101467147), mRNA	0,0243	0,0010	up	up	up	up	up	up
MPF_LOC101468563.1.2	XM_004572588.1 PREDICTED: Maylandia zebra alkaline nuclease-like (LOC101468563), transcript variant X6, mRNA	0,0488	0,0073	down	down	down	down	down	down
MPF_LOC100701421.1.2	XM_003438032.1 PREDICTED: Oreochromis niloticus putative glycerol kinase 5-like (LOC100701421), mRNA	0,0438	0,0053	up	up	up	up	up	up
MPF_LOC569742.1.1	XP_698239.5 PREDICTED: hypothetical protein LOC569742 [Danio rerio]	0,0277	0,0014	down	down	down	up	down	down
MPF_contig_019019	NA	0,0424	0,0049	down	up	up	up	up	up
MPF_contig_019024	XM_004572984.1 PREDICTED: Maylandia zebra A-kinase anchor protein 11-like (LOC101482225), transcript variant X1, mRNA	0,0290	0,0017	down	up	up	up	up	up
MPF_contig_019055	NA	0,0371	0,0034	down	up	up	up	up	up

MPF_contig_019070	NA	0,0333	0,0024	up	up	up	up	up	up
MPF_AHNK.7.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0,0290	0,0017	up	up	up	up	up	up
MPF_ZN583.1.1	ZN583_MOUSE (sp|Q3V080) Zinc finger protein 583 OS=Mus musculus GN=Znf583 PE=2 SV=1	0,0303	0,0019	up	up	up	up	up	up
MPF_LOC101472638.1.2	XM_004574297.1 PREDICTED: Maylandia zebra menin-like (LOC101472638), transcript variant X3, mRNA	0,0352	0,0028	up	up	up	up	up	up
MPF_contig_019120	NA	0,0244	0,0010	down	up	up	up	up	up
MPF_BSL1.1.2	BSL1_TRIVA (sp|Q8MTI2) Putative surface protein bspA-like OS=Trichomonas vaginalis GN=BSPAL1 PE=4 SV=1	0,0326	0,0022	down	up	up	up	up	up
MPF_contig_019188	NA	0,0467	0,0062	down	up	up	up	up	up
MPF_LOC101482403.1.1	XM_004548923.1 PREDICTED: Maylandia zebra proteasome subunit beta type-2-like (LOC101482403), transcript variant X2, mRNA	0,0324	0,0022	up	up	up	down	up	up
MPF_LOC101471734.1.2	XM_004545073.1 PREDICTED: Maylandia zebra dual specificity tyrosine-phosphorylation-regulated kinase 2-like (LOC101471734), transcript variant X3, mRNA	0,0375	0,0036	up	up	up	down	up	up
MPF_contig_001917	NA	0,0247	0,0010	up	up	up	up	up	up
MPF_contig_019251	NA	0,0215	0,0006	up	up	up	up	up	up
MPF_LOC101474655.2.2	XM_004570828.1 PREDICTED: Maylandia zebra dual specificity protein phosphatase 8-like (LOC101474655), transcript variant X3, mRNA	0,0202	0,0005	up	up	up	up	up	up
MPF_contig_019366	NA	0,0403	0,0043	down	up	up	up	up	up
MPF_contig_019367	NA	0,0158	0,0002	down	up	up	up	up	up
MPF_LOC101487136.1.3	XM_004568462.1 PREDICTED: Maylandia zebra probable serine/threonine-protein kinase kinX-like (LOC101487136), mRNA	0,0262	0,0012	down	down	up	up	up	up
MPF_contig_019388	NA	0,0088	0,0000	down	down	down	down	down	down
MPF_FRIL1.1.1	FRIL1_MOUSE (sp|P29391) Ferritin light chain 1 OS=Mus musculus GN=Ftl1 PE=1 SV=2	0,0211	0,0006	down	down	up	down	up	up
MPF_contig_019453	XM_004546174.1 PREDICTED: Maylandia zebra RAF proto-oncogene serine/threonine-protein kinaselike (LOC101470685), transcript variant X1, mRNA	0,0426	0,0050	up	up	up	up	up	up
MPF_LOC101474586.1.5	XM_004553213.1 PREDICTED: Maylandia zebra chromodomain-helicase-DNA-binding protein 2-like (LOC101474586), transcript variant X4, mRNA	0,0472	0,0065	down	down	up	up	up	up
MPF_LOC101485455.1.1	XM_004553256.1 PREDICTED: Maylandia zebra peptidyl-prolyl cis-trans isomerase FKBP4-like (LOC101485455), mRNA	0,0343	0,0026	down	up	up	up	up	up
MPF_contig_019576	NA	0,0077	0,0000	down	up	up	up	up	up
MPF_LOC101475206.2.4	XR_191621.1 PREDICTED: Maylandia zebra uncharacterized LOC101475206 (LOC101475206), transcript variant X2, misc_RNA	0,0310	0,0020	down	up	up	up	up	up

MPF_LOC101175629.2.2	XM_004086349.1 PREDICTED: Oryzias latipes proteasomal ubiquitin receptor ADRM1-like (LOC101175629), mRNA	0,0243	0,0009	up	up	up	up	up	up
MPF_KCC2B.1.1	[BBH] KCC2B_HUMAN (sp|Q13554) Calcium/calmodulin-dependent protein kinase type II subunit beta OS=Homo sapiens GN=CAMK2B PE=1 SV=3	0,0182	0,0004	up	up	up	up	up	up
MPF_contig_019645	NA	0,0247	0,0010	up	up	up	up	up	up
MPF_contig_019661	NA	0,0392	0,0040	up	up	up	up	up	up
MPF_LOC101476796.1.1	XM_004548629.1 PREDICTED: Maylandia zebra vacuolar fusion protein MON1 homolog B-like (LOC101476796), transcript variant X3, mRNA	0,0178	0,0004	up	up	up	up	up	up
MPF_contig_019715	NA	0,0478	0,0068	down	up	up	up	up	up
MPF_LOC101473761.1.1	XM_004565743.1 PREDICTED: Maylandia zebra gamma-aminobutyric acid receptor-associated proteinlike 2-like (LOC101473761), mRNA	0,0130	0,0001	down	up	up	up	up	up
MPF_LOC100694437.1.2	XM_003451931.1 PREDICTED: Oreochromis niloticus NFU1 iron-sulfur cluster scaffold homolog, mitochondrial-like (LOC100694437), mRNA	0,0176	0,0004	down	down	down	up	down	down
MPF_contig_019819	NA	0,0309	0,0020	up	up	up	up	up	up
MPF_contig_019843	NA	0,0305	0,0019	down	down	down	down	down	down
MPF_LOC100705292.1.2	XM_003439058.1 PREDICTED: Oreochromis niloticus kelch-like protein 21-like (LOC100705292), mRNA	0,0159	0,0002	up	up	up	up	up	up
MPF_contig_019861	NA	0,0265	0,0012	down	up	up	up	up	up

MPF_LOC101467621.4.8	XR_190852.1 PREDICTED: Maylandia zebra uncharacterized LOC101467621 (LOC101467621), misc_RNA	0,0498	0,0077	up	down	down	down	down	down
MPF_LOC100692095.1.1	XM_003452823.1 PREDICTED: Oreochromis niloticus aminoacyl tRNA synthase complex-interacting multifunctional protein 2-like (LOC100692095), mRNA	0,0160	0,0003	up	up	up	up	up	up
MPF_LOC101155558.1.1	XM_004082371.1 PREDICTED: Oryzias latipes interferon alpha-inducible protein 27-like protein 2-like (LOC101155558), mRNA	0,0330	0,0023	down	down	down	down	down	down
MPF_LOC101482559.1.1	XM_004563141.1 PREDICTED: Maylandia zebra myopalladin-like (LOC101482559), mRNA	0,0222	0,0007	up	up	up	up	up	up
MPF_contig_019979	NA	0,0277	0,0015	down	down	down	down	down	down
MPF_LOC101487706.1.1	XM_004565535.1 PREDICTED: Maylandia zebra cAMP-responsive element modulator-like (LOC101487706), transcript variant X2, mRNA	0,0147	0,0002	down	down	down	down	down	down
MPF_contig_020041	NA	0,0403	0,0043	down	down	up	up	up	up
MPF_LOC101469816.1.1	XM_004571671.1 PREDICTED: Maylandia zebra hamartin-like (LOC101469816), mRNA	0,0340	0,0026	down	up	up	up	up	up
MPF_ANK3.5.8	ANK3_MOUSE (sp|G5E8K5) Ankyrin-3 OS=Mus musculus GN=Ank3 PE=1 SV=1	0,0367	0,0032	down	up	down	up	down	down
MPF_LOC101468171.1.1	XM_004571311.1 PREDICTED: Maylandia zebra aldehyde dehydrogenase, mitochondrial-like (LOC101468171), transcript variant X2, mRNA	0,0380	0,0037	up	down	up	down	up	up

MPF_contig_020093	NA	0,0329	0,0023	down	up	up	up	up	up
MPF_contig_020110	NA	0,0210	0,0006	down	down	down	down	down	down
MPF_ZO71.3.10	ZO71_XENLA (sp|P18751) Oocyte zinc finger protein XlCOF7.1 (Fragment) OS=Xenopus laevis PE=2 SV=1	0,0267	0,0013	down	up	up	up	up	up
MPF_LOC100696358.1.7	XM_003446291.1 PREDICTED: Oreochromis niloticus heat shock protein HSP 90-beta-like (LOC100696358), mRNA	0,0362	0,0031	down	up	up	up	up	up
MPF_contig_020194	NA	0,0128	0,0001	down	down	down	down	down	down
MPF_LOC101468249.2.2	XM_004541040.1 PREDICTED: Maylandia zebra clathrin light chain B-like (LOC101468249), transcript variant X2, mRNA	0,0270	0,0013	down	up	up	up	up	up
MPF_contig_020221	NA	0,0202	0,0005	down	up	up	up	up	up
MPF_LOC101476003.1.3	XM_004567127.1 PREDICTED: Maylandia zebra plasminogen activator inhibitor 1 RNA-binding proteinlike (LOC101476003), mRNA	0,0478	0,0068	down	up	up	up	up	up
MPF_BLCAP.2.2	[BBH] BLCAP_DANRE (sp|Q9IB61) Bladder cancer-associated protein OS=Danio rerio GN=blcap PE=3 SV=1	0,0371	0,0035	up	up	up	up	up	up
MPF_contig_020368	XM_004550291.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101467183), transcript variant X2, mRNA	0,0208	0,0006	down	down	down	down	down	down
MPF_contig_020382	XM_004548075.1 PREDICTED: Maylandia zebra ras-related protein Rab-5A-like (LOC101476881), transcript variant X1, mRNA	0,0147	0,0002	down	up	up	up	up	up
MPF_LOC100694731.1.1	XP_003438055.1 PREDICTED: potassium voltage-gated channel subfamily V member 2-like [Oreochromis niloticus]	0,0290	0,0016	down	up	up	up	up	up
MPF_LOC101067829.1.1	XM_003962145.1 PREDICTED: Takifugu rubripes G-protein coupled receptor 39-like (LOC101067829), mRNA	0,0283	0,0015	down	down	down	down	down	down
MPF_contig_020534	NA	0,0047	0,0000	up	down	down	down	down	down
MPF_COX7R.2.3	COX7R_BOVIN (sp|Q3T061) Cytochrome c oxidase subunit 7A-related protein, mitochondrial OS=Bos taurus GN=COX7A2L PE=3 SV=1	0,0380	0,0037	down	up	up	up	up	up
MPF_contig_020569	NA	0,0224	0,0007	down	up	up	up	up	up
MPF_LOC101480386.1.1	XM_004574590.1 PREDICTED: Maylandia zebra E3 ubiquitin/ISG15 ligase TRIM25-like (LOC101480386), mRNA	0,0232	0,0008	up	up	up	up	up	up
MPF_contig_020580	NA	0,0047	0,0000	down	down	down	down	down	down
MPF_LOC101467147.3.5	XM_004566000.1 PREDICTED: Maylandia zebra NEDD8-conjugating enzyme UBE2F-like (LOC101467147), mRNA	0,0306	0,0019	down	up	up	up	up	up
MPF_contig_020594	NA	0,0386	0,0038	up	up	up	up	up	up
MPF_LOC100709688.1.1	XM_003443167.1 PREDICTED: Oreochromis niloticus solute carrier family 25 member 38-A-like (LOC100709688), mRNA	0,0335	0,0025	down	up	up	up	up	up
MPF_contig_020638	NA	0,0292	0,0017	up	up	up	down	up	up
MPF_LOC101486063.1.1	XM_004563250.1 PREDICTED: Maylandia zebra highly divergent homeobox-like (LOC101486063), mRNA	0,0169	0,0003	up	up	up	up	up	up

MPF_contig_020724	NA	0,0364	0,0032	down	down	up	down	up	up
MPF_LOC101485143.2.2	XM_004569171.1 PREDICTED: Maylandia zebra UDP-GlcNAc:betaGal beta-1,3-Nacetylglucosaminyltransferase 9-like (LOC101485143), transcript variant X3, mRNA	0,0351	0,0028	up	up	up	up	up	up
MPF_LOC101477737.4.5	XM_004550788.1 PREDICTED: Maylandia zebra complement C1r subcomponent-like (LOC101477737), mRNA	0,0394	0,0040	down	up	up	up	up	up
MPF_LOC101467665.1.2	XM_004545591.1 PREDICTED: Maylandia zebra protein RD3-like (LOC101467665), mRNA	0,0150	0,0002	up	up	up	up	up	up
MPF_SGS4.3.10	SGS4_DROME (sp|Q00725) Salivary glue protein Sgs-4 OS=Drosophila melanogaster GN=Sgs4 PE=2 SV=1	0,0387	0,0038	down	down	up	up	up	up

MPF_LOC101481552.25.41	XM_004575656.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101481552), mRNA	0,0487	0,0072	up	up	down	up	down	down
MPF_contig_020829	NA	0,0419	0,0047	down	down	up	up	up	up
MPF_contig_020856	NA	0,0474	0,0066	down	up	up	up	up	up
MPF_contig_020862	NA	0,0172	0,0003	down	down	down	up	down	down
MPF_LOC100689738.1.1	XP_003443225.1 PREDICTED: major facilitator superfamily domain-containing protein 6-like [Oreochromis niloticus]	0,0173	0,0004	down	up	up	up	up	up
MPF_contig_020884	NA	0,0160	0,0003	up	up	up	up	up	up
MPF_contig_020905	XM_004557861.1 PREDICTED: Maylandia zebra F-box-like/WD repeat-containing protein TBL1X-like (LOC101465000), transcript variant X1, mRNA	0,0243	0,0009	up	up	up	up	up	up
MPF_LOC100691787.1.1	XP_003441155.1 PREDICTED: zinc finger protein 511-like [Oreochromis niloticus]	0,0279	0,0015	up	up	up	down	up	up
MPF_LOC101471367.2.5	XM_004573481.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase CBL-like (LOC101471367), mRNA	0,0485	0,0071	up	down	up	down	up	up
MPF_LOC101466535.2.3	XM_004574367.1 PREDICTED: Maylandia zebra R3H domain-containing protein 4-like (LOC101466535), mRNA	0,0419	0,0048	up	up	up	up	up	up
MPF_LOC101065884.1.2	XM_003965883.1 PREDICTED: Takifugu rubripes 1-acylglycerol-3-phosphate O-acyltransferase ABHD5like (LOC101065884), mRNA	0,0234	0,0008	down	up	up	up	up	up
MPF_contig_020996	NA	0,0359	0,0030	up	up	up	up	up	up
MPF_contig_002093	XM_004561062.1 PREDICTED: Maylandia zebra sentrin-specific protease 6-like (LOC101481863), transcript variant X1, mRNA	0,0182	0,0004	up	up	up	down	up	up
MPF_LOC101484929.1.3	XM_004542976.1 PREDICTED: Maylandia zebra CMP-N-acetylneuraminate-beta-1,4-galactoside alpha2,3-sialyltransferase-like (LOC101484929), mRNA	0,0210	0,0006	up	down	down	down	down	down
MPF_contig_021053	NA	0,0258	0,0011	down	up	up	up	up	up
MPF_LOC101468994.1.1	XM_004555202.1 PREDICTED: Maylandia zebra poly [ADP-ribose] polymerase 2-like (LOC101468994), mRNA	0,0237	0,0009	down	up	up	up	up	up
MPF_contig_021115	NA	0,0367	0,0033	down	down	up	up	up	up

MPF_LOC101169293.6.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0,0055	0,0000	down	down	down	down	down	down
MPF_contig_021167	XM_004541554.1 PREDICTED: Maylandia zebra amyloid-like protein 2-like (LOC101480044), transcript variant X1, mRNA	0,0326	0,0022	down	down	down	down	down	down
MPF_contig_021187	NA	0,0107	0,0001	up	up	up	up	up	up
MPF_LOC100710418.2.4	XM_003450487.1 PREDICTED: Oreochromis niloticus nucleophosmin-like (LOC100710418), mRNA	0,0220	0,0007	up	up	up	up	up	up
MPF_DKC1.2.3	XM_003460212.1 PREDICTED: Oreochromis niloticus dyskeratosis congenita 1, dyskerin (DKC1), mRNA	0,0241	0,0009	down	down	up	up	up	up
MPF_contig_021242	NA	0,0348	0,0027	down	up	up	up	up	up
MPF_LOC101474249.2.3	XM_004540423.1 PREDICTED: Maylandia zebra DNA-binding protein inhibitor ID-3-A-like (LOC101474249), mRNA	0,0094	0,0000	up	up	up	up	up	up
MPF_FA7.2.2	FA7_HUMAN (sp|P08709) Coagulation factor VII OS=Homo sapiens GN=F7 PE=1 SV=1	0,0225	0,0007	down	up	up	up	up	up
MPF_LOC101480733.1.1	XM_004541182.1 PREDICTED: Maylandia zebra TCF3 fusion partner homolog (LOC101480733), transcript variant X1, mRNA	0,0411	0,0045	down	down	up	down	up	up
MPF_LOC100692501.1.2	XM_003459223.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100692501 (LOC100692501), mRNA	0,0153	0,0002	up	down	down	down	down	down
MPF_LOC101482225.2.4	XM_004572985.1 PREDICTED: Maylandia zebra A-kinase anchor protein 11-like (LOC101482225), transcript variant X2, mRNA	0,0243	0,0009	down	up	up	up	up	up
MPF_ESR1.1.1	[BBH] ESR1_PAGMA (sp|O42132) Estrogen receptor OS=Pagrus major GN=esr1 PE=2 SV=1	0,0210	0,0006	up	up	up	up	up	up
MPF_LOC100694852.2.2	XM_003443194.1 PREDICTED: Oreochromis niloticus heme-binding protein 1-like (LOC100694852), mRNA	0,0319	0,0022	down	up	up	up	up	up
MPF_LOC100702463.1.1	XM_003449473.1 PREDICTED: Oreochromis niloticus nucleolar complex protein 3 homolog (LOC100702463), mRNA	0,0089	0,0000	down	up	up	up	up	up
MPF_contig_021432	NA	0,0160	0,0002	down	down	down	down	down	down
MPF_contig_000215	NA	0,0402	0,0042	down	up	up	up	up	up
MPF_LOC100711190.10.17	XM_003443585.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L21-like (LOC100711190), mRNA	0,0332	0,0024	up	up	up	up	up	up
MPF_LOC101487908.1.3	XM_004546898.1 PREDICTED: Maylandia zebra rab effector MyRIP-like (LOC101487908), mRNA	0,0364	0,0032	down	down	up	up	up	up
MPF_IK.1.1	XM_003457013.1 PREDICTED: Oreochromis niloticus IK cytokine, down-regulator of HLA II (IK), mRNA	0,0176	0,0004	up	up	up	up	up	up
MPF_LOC100710653.2.2	XM_003442016.1 PREDICTED: Oreochromis niloticus prohibitin-like (LOC100710653), mRNA	0,0260	0,0011	up	up	up	down	up	up
MPF_LOC101467846.6.11	XM_004567936.1 PREDICTED: Maylandia zebra 60S ribosomal protein L8-like (LOC101467846), mRNA	0,0276	0,0014	up	up	up	up	up	up

MPF_LOC100709648.6.13	XM_003457730.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S4-like (LOC100709648), mRNA	0,0252	0,0010	up	up	up	up	up	up
MPF_LOC101484083.3.3	XM_004539190.1 PREDICTED: Maylandia zebra ATP-binding cassette sub-family A member 1-like (LOC101484083), transcript variant X2, mRNA	0,0213	0,0006	down	down	down	down	down	down
MPF_contig_021708	NA	0,0149	0,0002	down	down	down	down	down	down
MPF_contig_021760	NA	0,0303	0,0019	down	down	down	up	down	down
MPF_contig_021764	NA	0,0277	0,0014	up	up	up	up	up	up
MPF_RT28.3.8	RT28_BOVIN (sp|P82928) 28S ribosomal protein S28, mitochondrial OS=Bos taurus GN=MRPS28 PE=1 SV=2	0,0237	0,0009	down	down	down	up	down	down
MPF_LOC101465998.3.3	XM_004541412.1 PREDICTED: Maylandia zebra serum amyloid P-component-like (LOC101465998), mRNA	0,0332	0,0024	down	up	down	up	down	down
MPF_LOC101161574.6.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0,0078	0,0000	down	down	down	down	down	down
MPF_LOC101477304.1.1	XM_004560480.1 PREDICTED: Maylandia zebra nuclear pore complex protein Nup88-like (LOC101477304), mRNA	0,0485	0,0070	down	up	up	up	up	up
MPF_LOC101154812.1.1	XM_004080807.1 PREDICTED: Oryzias latipes eukaryotic translation initiation factor 5A-1-like, transcript variant 2 (LOC101154812), mRNA	0,0404	0,0043	up	up	up	up	up	up
MPF_contig_021825	NA	0,0277	0,0015	down	down	up	up	up	up
MPF_contig_021826	NA	0,0130	0,0001	down	down	down	down	down	down
MPF_contig_021847	NA	0,0290	0,0017	down	up	up	up	up	up
MPF_LOC100706528.3.6	XM_003439817.1 PREDICTED: Oreochromis niloticus cytochrome b-c1 complex subunit 6, mitochondrial-like (LOC100706528), mRNA	0,0130	0,0001	up	up	up	up	up	up
MPF_contig_021996	NA	0,0064	0,0000	up	up	up	up	up	up
MPF_LOC101483390.1.1	XM_004557184.1 PREDICTED: Maylandia zebra aquaporin-12-like (LOC101483390), mRNA	0,0139	0,0001	down	up	up	up	up	up
MPF_LOC101063002.1.1	XP_003971894.1 PREDICTED: LOW QUALITY PROTEIN: T-cell activation Rho GTPase-activating protein-like [Takifugu rubripes]	0,0143	0,0002	down	down	down	down	down	down
MPF_LOC101466337.6.22	XM_004575687.1 PREDICTED: Maylandia zebra prothymosin alpha-B-like (LOC101466337), mRNA	0,0308	0,0020	up	up	up	up	up	up
MPF_MYO1B.1.2	XP_003443378.1 PREDICTED: myosin-Ib isoform 2 [Oreochromis niloticus]	0,0160	0,0003	up	up	up	up	up	up
MPF_LOC100711254.1.1	XM_003438413.1 PREDICTED: Oreochromis niloticus wings apart-like protein homolog (LOC100711254), mRNA	0,0277	0,0014	down	down	up	down	up	up
MPF_LOC101482306.1.2	XM_004548843.1 PREDICTED: Maylandia zebra phosphoenolpyruvate carboxykinase, cytosolic [GTP]like (LOC101482306), mRNA	0,0319	0,0021	down	up	up	up	up	up
MPF_LOC101073558.1.1	XP_003977072.1 PREDICTED: succinate dehydrogenase [ubiquinone] cytochrome b small subunit B, mitochondrial-like [Takifugu rubripes]	0,0381	0,0037	up	up	up	up	up	up
MPF_LOC101163218.1.1	XP_004083710.1 PREDICTED: integrator complex subunit 9-like [Oryzias latipes]	0,0183	0,0004	down	down	down	down	down	down

MPF_LOC100693225.1.1	XM_003440194.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693225 (LOC100693225), mRNA	0,0266	0,0012	down	up	up	up	up	up
MPF_LOC100695994.18.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0,0351	0,0028	up	up	up	up	up	up
MPF_LOC100693024.1.1	XP_003456072.1 PREDICTED: ubiquitin-conjugating enzyme E2 J1-like isoform 2 [Oreochromis niloticus]	0,0232	0,0008	up	up	up	up	up	up
MPF_LOC100709543.1.1	XP_003454327.1 PREDICTED: cortactin-binding protein 2-like [Oreochromis niloticus]	0,0268	0,0013	up	up	up	up	up	up
MPF_LOC101466337.8.22	XM_004575687.1 PREDICTED: Maylandia zebra prothymosin alpha-B-like (LOC101466337), mRNA	0,0265	0,0012	up	up	up	up	up	up
MPF_LOC101479698.2.3	XM_004547798.1 PREDICTED: Maylandia zebra small integral membrane protein 12-like (LOC101479698), transcript variant X2, mRNA	0,0482	0,0069	up	up	up	up	up	up
MPF_LOC101479635.2.2	XM_004557450.1 PREDICTED: Maylandia zebra 4-hydroxyphenylpyruvate dioxygenase-like (LOC101479635), mRNA	0,0150	0,0002	up	up	up	up	up	up
MPF_G0S2.1.1	[BBH] G0S2_MOUSE (sp|Q61585) G0/G1 switch protein 2 OS=Mus musculus GN=G0s2 PE=2 SV=1	0,0182	0,0004	up	up	up	down	up	up
MPF_contig_002256	NA	0,0406	0,0044	up	up	up	up	up	up
MPF_LOC101483704.1.1	XM_004559123.1 PREDICTED: Maylandia zebra mannose-1-phosphate guanyltransferase beta-like (LOC101483704), mRNA	0,0470	0,0064	down	down	up	up	up	up
MPF_LOC101479305.2.6	XM_004546110.1 PREDICTED: Maylandia zebra cytosolic sulfotransferase 3-like (LOC101479305), transcript variant X2, mRNA	0,0147	0,0002	down	down	down	down	down	down
MPF_LOC101480468.1.1	XM_004547044.1 PREDICTED: Maylandia zebra ras association domain-containing protein 2-like (LOC101480468), mRNA	0,0352	0,0028	down	up	up	up	up	up
MPF_LOC101158190.1.1	XP_004069427.1 PREDICTED: mitochondrial inner membrane protease subunit 2-like [Oryzias latipes]	0,0298	0,0018	down	up	up	up	up	up

MPF_contig_022848	NA	0,0068	0,0000	down	up	up	up	up	up
MPF_LOC100689854.3.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0,0454	0,0058	up	up	up	up	up	up
MPF_LOC101471890.1.1	XM_004559351.1 PREDICTED: Maylandia zebra nuclear GTPase SLIP-GC-like (LOC101471890), mRNA	0,0136	0,0001	down	down	down	down	down	down
MPF_LOC100707353.1.5	XM_003445500.1 PREDICTED: Oreochromis niloticus zinc finger MYM-type protein 4-like (LOC100707353), mRNA	0,0370	0,0033	down	up	up	up	up	up
MPF_LOC101488105.1.1	XM_004550275.1 PREDICTED: Maylandia zebra beta-2 adrenergic receptor-like (LOC101488105), mRNA	0,0224	0,0007	down	down	up	up	up	up
MPF_LOC100705746.1.3	XP_003443116.1 PREDICTED: trafficking protein particle complex subunit 5-like [Oreochromis niloticus]	0,0337	0,0025	up	up	up	up	up	up
MPF_LOC100707676.3.3	XM_003458184.1 PREDICTED: Oreochromis niloticus transcription factor p65-like (LOC100707676), mRNA	0,0213	0,0006	down	down	down	down	down	down
MPF_contig_023161	NA	0,0432	0,0052	down	up	up	up	up	up
MPF_LOC100696809.1.3	XP_003449500.1 PREDICTED: hypothetical protein LOC100696809 [Oreochromis niloticus]	0,0250	0,0010	down	up	up	up	up	up

MPF_LOC101470075.3.5	XM_004567108.1 PREDICTED: Maylandia zebra fragile X mental retardation syndrome-related protein 2-like (LOC101470075), transcript variant X2, mRNA	0,0474	0,0066	down	down	up	down	up	up
MPF_LOC101481065.2.2	XM_004554051.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(s) subunit alphalike (LOC101481065), mRNA	0,0143	0,0002	down	down	up	up	up	up
MPF_LOC100693055.1.1	XM_003440029.1 PREDICTED: Oreochromis niloticus cyclic AMP-dependent transcription factor ATF-6 alpha-like (LOC100693055), mRNA	0,0400	0,0042	up	down	up	down	up	up
MPF_LOC101168245.2.2	XM_004079605.1 PREDICTED: Oryzias latipes ATP-binding cassette sub-family E member 1-like (LOC101168245), mRNA	0,0207	0,0005	up	up	up	up	up	up
MPF_LOC101464652.2.3	XM_004541953.1 PREDICTED: Maylandia zebra translocation protein SEC63 homolog (LOC101464652), mRNA	0,0500	0,0077	up	up	up	up	up	up
MPF_LOC101482276.1.1	XM_004565422.1 PREDICTED: Maylandia zebra chromodomain-helicase-DNA-binding protein 8-like (LOC101482276), mRNA	0,0155	0,0002	up	up	up	down	up	up
MPF_contig_023282	NA	0,0147	0,0002	down	up	up	up	up	up
MPF_LOC101075711.1.1	XM_003977781.1 PREDICTED: Takifugu rubripes ubiquitin carboxyl-terminal hydrolase 32-like (LOC101075711), mRNA	0,0248	0,0010	down	up	up	up	up	up
MPF_LOC101471773.1.3	XM_004553653.1 PREDICTED: Maylandia zebra dihydropteridine reductase-like (LOC101471773), mRNA	0,0182	0,0004	down	up	up	up	up	up
MPF_EIF4A2.1.1	NM_001102893.1 Xenopus (Silurana) tropicalis eukaryotic translation initiation factor 4A2 (eif4a2), mRNA gb|BC135871.1| Xenopus tropicalis hypothetical protein LOC100124955, mRNA (cDNA clone MGC:121826 IMAGE:7637784), complete cds	0,0293	0,0017	down	down	down	up	down	down
MPF_LOC101473512.1.1	XM_004573574.1 PREDICTED: Maylandia zebra retroviral integration site protein Fli-1 homolog (LOC101473512), mRNA	0,0193	0,0005	down	down	down	down	down	down
MPF_contig_023396	NA	0,0452	0,0057	down	up	up	up	up	up
MPF_contig_023403	NA	0,0130	0,0001	down	down	down	down	down	down
MPF_LOC101472640.3.4	XM_004574391.1 PREDICTED: Maylandia zebra microtubule-associated serine/threonine-protein kinase 3-like (LOC101472640), transcript variant X2, mRNA	0,0202	0,0005	down	down	down	down	down	down
MPF_ZNF84.7.14	ZNF84_HUMAN (sp|P51523) Zinc finger protein 84 OS=Homo sapiens GN=ZNF84 PE=1 SV=2	0,0366	0,0032	down	up	up	up	up	up
MPF_contig_023437	NA	0,0229	0,0008	down	down	down	up	down	down
MPF_contig_023467	NA	0,0358	0,0030	down	up	up	up	up	up
MPF_LOC101464811.2.4	XM_004559330.1 PREDICTED: Maylandia zebra methionine aminopeptidase 1-like (LOC101464811), mRNA	0,0248	0,0010	up	up	up	up	up	up
MPF_LOC100702591.1.2	XM_003459100.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100702591), mRNA	0,0110	0,0001	up	up	up	up	up	up
MPF_contig_023491	NA	0,0450	0,0056	up	down	up	down	up	up
MPF_RTBS.12.36	RTBS_DROME (sp|Q95SX7) Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1	0,0080	0,0000	down	down	down	down	down	down

MPF_LOC101481888.1.1	XM_004542490.1 PREDICTED: Maylandia zebra BTB/POZ domain-containing protein 2-like (LOC101481888), mRNA	0,0290	0,0017	down	up	up	up	up	up
MPF_LOC101474859.8.21	XM_004575478.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 4like (LOC101474859), transcript variant X2, mRNA	0,0123	0,0001	down	up	up	up	up	up
MPF_LOC101167561.1.2	XP_004075784.1 PREDICTED: uncharacterized protein LOC101167561 [Oryzias latipes]	0,0304	0,0019	down	up	up	up	up	up
MPF_contig_023516	NA	0,0041	0,0000	down	down	down	down	down	down
MPF_LOC101170497.3.8	XP_004086004.1 PREDICTED: oocyte zinc finger protein XlCOF6-like [Oryzias latipes]	0,0380	0,0037	down	up	up	up	up	up
MPF_contig_023536	NA	0,0458	0,0059	down	up	up	up	up	up
MPF_BM1_14085.2.5	XP_001894282.1 T-cell receptor beta chain ANA 11 [Brugia malayi]	0,0472	0,0064	up	up	up	up	up	up

MPF_LOC101474305.11.20	XM_004575475.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101474305), mRNA	0,0371	0,0035	down	up	down	up	down	down
MPF_LOC100148223.2.2	XP_003201586.1 PREDICTED: zinc finger protein 729-like [Danio rerio]	0,0379	0,0036	up	up	up	up	up	up
MPF_LOC101163553.1.1	XP_004066464.1 PREDICTED: zinc finger protein 658-like [Oryzias latipes]	0,0268	0,0013	up	up	up	up	up	up
MPF_LOC100695994.19.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0,0432	0,0052	up	up	up	up	up	up
MPF_LOC101475700.1.3	XM_004564763.1 PREDICTED: Maylandia zebra phosphate carrier protein, mitochondrial-like (LOC101475700), transcript variant X2, mRNA	0,0239	0,0009	down	down	down	up	down	down
MPF_LOC100703120.2.3	XP_003458215.1 PREDICTED: hypothetical protein LOC100703120 [Oreochromis niloticus]	0,0119	0,0001	down	down	down	up	down	down
MPF_LOC100695994.20.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0,0352	0,0028	up	up	up	up	up	up
MPF_LOC101470101.3.4	XM_004572496.1 PREDICTED: Maylandia zebra collagen alpha-1(XIII) chain-like (LOC101470101), mRNA	0,0222	0,0007	down	up	up	up	up	up
MPF_LOC100692111.1.1	XP_003456389.1 PREDICTED: transmembrane protein 180-like [Oreochromis niloticus]	0,0260	0,0011	down	up	up	up	up	up
MPF_contig_023611	NA	0,0195	0,0005	down	down	down	up	down	down
MPF_contig_023617	NA	0,0473	0,0066	up	up	up	up	up	up
MPF_LOC100705419.1.1	XP_003446703.1 PREDICTED: protein midA homolog, mitochondrial-like [Oreochromis niloticus]	0,0450	0,0056	down	up	up	up	up	up
MPF_LOC100135188.1.5	NP_001107363.1 uncharacterized protein LOC100135188 [Xenopus (Silurana) tropicalis]	0,0054	0,0000	down	down	down	down	down	down
MPF_EIF3K.3.3	EIF3K_DANRE (sp|Q567V6) Eukaryotic translation initiation factor 3 subunit K OS=Danio rerio GN=eif3k PE=2 SV=1	0,0150	0,0002	down	down	down	down	down	down
MPF_contig_023735	NA	0,0160	0,0003	up	up	down	down	down	down
MPF_contig_023741	NA	0,0325	0,0022	down	up	up	up	up	up
MPF_LOC100706878.2.6	XP_003458391.1 PREDICTED: hypothetical protein LOC100706878 [Oreochromis niloticus]	0,0218	0,0006	down	down	down	up	down	down

MPF_contig_023802	NA	0,0369	0,0033	up	up	up	up	up	up
MPF_contig_023804	NA	0,0243	0,0010	down	down	down	down	down	down
MPF_LOC101481821.1.3	XM_004550250.1 PREDICTED: Maylandia zebra DNA-directed RNA polymerase III subunit RPC9-like (LOC101481821), mRNA	0,0304	0,0019	down	down	up	down	up	up
MPF_LOC101476819.3.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0,0188	0,0004	down	down	down	up	down	down
MPF_POPTRDRAFT_794775	XP_002338344.1 predicted protein [Populus trichocarpa]	0,0047	0,0000	up	down	down	down	down	down
MPF_contig_023930	NA	0,0097	0,0000	down	down	down	down	down	down
MPF_LOC100701582.7.9	XP_003455288.1 PREDICTED: zinc finger protein 236-like [Oreochromis niloticus]	0,0469	0,0063	down	up	up	up	up	up
MPF_LOC100696099.1.3	XP_003448423.1 PREDICTED: phosphoenolpyruvate carboxykinase, cytosolic [GTP]-like [Oreochromis niloticus]	0,0246	0,0010	down	up	up	up	up	up
MPF_contig_023946	NA	0,0171	0,0003	down	up	up	up	up	up
MPF_contig_023955	NA	0,0153	0,0002	down	up	up	up	up	up
MPF_LOC100698625.18.22	XM_003456694.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100698625), mRNA	0,0419	0,0047	up	up	up	up	up	up
MPF_contig_023972	NA	0,0123	0,0001	up	up	up	up	up	up
MPF_contig_023989	NA	0,0147	0,0002	down	down	down	down	down	down
MPF_LOC101471689.1.2	XM_004555845.1 PREDICTED: Maylandia zebra peroxisome proliferator-activated receptor gamma coactivator-related protein 1-like (LOC101471689), transcript variant X2, mRNA	0,0418	0,0047	up	down	up	down	up	up
MPF_contig_024013	NA	0,0277	0,0015	down	down	up	down	up	up
MPF_LOC100702478.4.6	XM_003453592.1 PREDICTED: Oreochromis niloticus tripartite motif-containing protein 39-like (LOC100702478), mRNA	0,0148	0,0002	up	up	up	up	up	up
MPF_LOC101485903.1.2	XM_004575263.1 PREDICTED: Maylandia zebra low-density lipoprotein receptor-related protein 10-like (LOC101485903), mRNA	0,0371	0,0035	down	up	up	up	up	up
MPF_contig_024030	NA	0,0176	0,0004	down	down	down	up	down	down
MPF_LOC100700605.16.27	XM_003458555.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100700605), mRNA	0,0338	0,0025	down	down	down	up	down	down
MPF_LOC100710590.3.4	XP_003449469.1 PREDICTED: zinc finger protein 836-like, partial [Oreochromis niloticus]	0,0370	0,0033	up	up	up	up	up	up
MPF_LOC100711656.2.2	XP_003446481.1 PREDICTED: cytosolic endo-beta-N-acetylglucosaminidase-like [Oreochromis niloticus]	0,0224	0,0007	down	down	down	up	down	down
MPF_contig_024077	NA	0,0371	0,0034	down	down	down	down	down	down
MPF_LOC100708750.2.2	XM_003457879.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100708750), mRNA	0,0243	0,0009	down	down	up	down	up	up
MPF_contig_024093	NA	0,0228	0,0008	up	up	up	up	up	up
MPF_contig_024095	NA	0,0268	0,0013	down	up	down	up	down	down

MPF_contig_024116	NA	0,0351	0,0028	down	up	up	up	up	up
MPF_LOC101485716.5.12	XM_004572825.1 PREDICTED: Maylandia zebra multivesicular body subunit 12B-like (LOC101485716), mRNA	0,0065	0,0000	down	down	down	down	down	down
MPF_contig_024216	NA	0,0290	0,0017	up	up	down	up	down	down

MPF_LOC100691365.1.2	XM_003446687.1 PREDICTED: Oreochromis niloticus UPF0463 transmembrane protein C6orf35 homolog (LOC100691365), mRNA	0,0173	0,0003	down	up	up	up	up	up
MPF_LOC100712012.2.3	XP_003446066.1 PREDICTED: neural cell adhesion molecule L1-like [Oreochromis niloticus]	0,0243	0,0009	up	up	up	down	up	up
MPF_LOC101484746.1.1	XM_004544275.1 PREDICTED: Maylandia zebra DNA-directed RNA polymerase III subunit RPC4-like (LOC101484746), mRNA	0,0338	0,0025	up	up	up	down	up	up
MPF_LOC101466474.1.1	XM_004562278.1 PREDICTED: Maylandia zebra inactive rhomboid protein 1-like (LOC101466474), transcript variant X3, mRNA	0,0333	0,0024	down	down	up	down	up	up
MPF_LOC101464072.1.1	XM_004562979.1 PREDICTED: Maylandia zebra heme oxygenase-like (LOC101464072), mRNA	0,0488	0,0073	down	down	up	down	up	up
MPF_LOC101172990.10.36	XM_004073898.1 PREDICTED: Oryzias latipes uncharacterized LOC101172990 (LOC101172990), mRNA	0,0136	0,0001	down	up	up	up	up	up
MPF_CRE_23222.1.2	XP_003089877.1 hypothetical protein CRE_23222 [Caenorhabditis remanei]	0,0311	0,0020	down	down	down	up	down	down
MPF_contig_024387	NA	0,0351	0,0028	up	up	up	down	up	up
MPF_contig_024441	NA	0,0287	0,0016	down	up	up	up	up	up
MPF_contig_024477	NA	0,0432	0,0052	down	up	up	up	up	up
MPF_LOC101484616.1.1	XM_004561445.1 PREDICTED: Maylandia zebra anaphase-promoting complex subunit 15-like (LOC101484616), mRNA	0,0383	0,0038	down	up	up	up	up	up
MPF_NEMVEDRAFT_V1G11	XP_001628905.1 predicted protein [Nematostella vectensis]	0,0346	0,0027	up	down	down	down	down	down
MPF_LOC100692664.1.1	XP_003458729.1 PREDICTED: neutrophil cytosol factor 1-like [Oreochromis niloticus]	0,0371	0,0034	down	down	down	down	down	down
MPF_LOC101475042.1.1	XM_004549634.1 PREDICTED: Maylandia zebra dymeclin-like (LOC101475042), transcript variant X1, mRNA	0,0135	0,0001	up	up	up	up	up	up
MPF_contig_024644	NA	0,0239	0,0009	down	down	up	up	up	up
MPF_EJP617_28390.1.2	YP_005819407.1 hypothetical protein EJP617_28390 [Erwinia sp. Ejp617]	0,0195	0,0005	down	down	up	up	up	up
MPF_LOC101169385.2.3	XP_004077303.1 PREDICTED: zinc finger protein 318-like [Oryzias latipes]	0,0327	0,0023	down	up	up	up	up	up
MPF_contig_024721	NA	0,0107	0,0001	down	down	down	down	down	down
MPF_PHUM_PHUM529360.1	XP_002431439.1 ngd5/osm-6/ift52, putative [Pediculus humanus corporis]	0,0154	0,0002	down	down	down	up	down	down
1MPF_contig_024739	XM_004075770.1 PREDICTED: Oryzias latipes arf-GAP domain and FG repeat-containing protein like, transcript variant 1 (LOC101155131), mRNA	0,0453	0,0057	up	up	up	up	up	up

MPF_LOC101475088.1.1	XM_004563653.1 PREDICTED: Maylandia zebra DNA polymerase sigma-like (LOC101475088), transcript variant X2, mRNA	0,0421	0,0048	down	up	up	up	up	up
MPF_LOC101169532.31.45	XP_004070110.1 PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Oryzias latipes]	0,0315	0,0021	down	up	up	up	up	up
MPF_LOC100705639.1.1	XP_003458308.1 PREDICTED: arachidonate 5-lipoxygenase-activating protein-like isoform 1 [Oreochromis niloticus]	0,0309	0,0020	up	up	up	up	up	up
MPF_BM1_02870.1.1	XP_001892072.1 T-cell receptor beta chain ANA 11 [Brugia malayi]	0,0131	0,0001	down	up	up	up	up	up
MPF_ACVR2AA.1.1	NP_001103748.1 activin receptor type-2A precursor [Danio rerio]	0,0215	0,0006	up	up	up	up	up	up
MPF_contig_025000	XM_003963344.1 PREDICTED: Takifugu rubripes 60S ribosomal protein L32-like, transcript variant 1 (LOC101066639), mRNA	0,0096	0,0000	down	up	up	up	up	up
MPF_LOC101470650.2.2	XM_004540130.1 PREDICTED: Maylandia zebra nesprin-1-like (LOC101470650), transcript variant X2, mRNA	0,0224	0,0007	down	down	down	down	down	down
MPF_contig_025080	NA	0,0208	0,0005	down	up	up	up	up	up
MPF_CD4.1.1	NP_001072091.1 T-cell surface glycoprotein CD4 [Takifugu rubripes]	0,0164	0,0003	up	up	up	up	up	up
MPF_LOC101476442.1.1	XM_004576449.1 PREDICTED: Maylandia zebra uncharacterized LOC101476442 (LOC101476442), mRNA	0,0366	0,0032	down	down	up	up	up	up
MPF_LOC100701988.2.2	XM_003442403.1 PREDICTED: Oreochromis niloticus CD2 antigen cytoplasmic tail-binding protein 2like (LOC100701988), mRNA	0,0438	0,0053	down	up	up	up	up	up
MPF_LOC100710021.1.1	XP_003438623.1 PREDICTED: LOW QUALITY PROTEIN: BAH and coiled-coil domain-containing protein 1-like [Oreochromis niloticus]	0,0265	0,0012	down	down	up	down	up	up
MPF_contig_025134	XM_004548413.1 PREDICTED: Maylandia zebra forkhead box protein M1-like (LOC101468468), transcript variant X1, mRNA	0,0438	0,0053	down	down	up	up	up	up
MPF_LOC100711183.1.2	XM_003441343.1 PREDICTED: Oreochromis niloticus protein timeless homolog (LOC100711183), mRNA	0,0371	0,0034	up	up	up	up	up	up
MPF_LOC100708328.1.1	XM_003441248.1 PREDICTED: Oreochromis niloticus glutamine-rich protein 1-like (LOC100708328), mRNA	0,0354	0,0029	down	up	up	up	up	up
MPF_contig_025238	NA	0,0354	0,0029	up	up	up	up	up	up
MPF_LOC101469930.1.1	XM_004551309.1 PREDICTED: Maylandia zebra inosine-uridine preferring nucleoside hydrolase-like (LOC101469930), transcript variant X2, mRNA	0,0084	0,0000	up	up	up	up	up	up
MPF_LOC100710612.1.1	XM_003454616.1 PREDICTED: Oreochromis niloticus macrophage mannose receptor 1-like (LOC100710612), mRNA	0,0160	0,0002	down	down	down	down	down	down
MPF_IKBKAP.1.1	XM_003443430.1 PREDICTED: Oreochromis niloticus inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein (IKBKAP), mRNA	0,0357	0,0030	up	up	up	up	up	up
MPF_contig_025280	NA	0,0225	0,0007	up	up	up	up	up	up

MPF_contig_025289	XM_004549968.1 PREDICTED: Maylandia zebra baculoviral IAP repeat-containing protein 2-like (LOC101484124), transcript variant X3, mRNA	0,0389	0,0039	up	up	up	up	up	up
MPF_LOC101471219.1.1	XM_004539755.1 PREDICTED: Maylandia zebra A-kinase anchor protein 13-like (LOC101471219), mRNA	0,0345	0,0027	down	up	up	up	up	up
MPF_LOC101486310.2.2	XM_004574350.1 PREDICTED: Maylandia zebra protein FAM49A-like (LOC101486310), transcript variant X3, mRNA	0,0088	0,0000	up	up	up	up	up	up
MPF_LOC101077402.8.11	XP_003965662.1 PREDICTED: uncharacterized protein LOC101077402 [Takifugu rubripes]	0,0169	0,0003	up	up	up	up	up	up
MPF_FHOD3.2.2	XP_003437785.1 PREDICTED: FH1/FH2 domain-containing protein 3 [Oreochromis niloticus]	0,0211	0,0006	up	down	up	down	up	up
MPF_LOC101169190.1.1	XP_004068046.1 PREDICTED: Usher syndrome type-1C protein-binding protein 1-like [Oryzias latipes]	0,0150	0,0002	down	down	down	down	down	down
MPF_LOC101479581.1.3	XM_004543518.1 PREDICTED: Maylandia zebra uncharacterized LOC101479581 (LOC101479581), mRNA	0,0171	0,0003	up	up	up	up	up	up
MPF_LOC100703894.1.1	XP_003447861.1 PREDICTED: rho GTPase-activating protein 11A-like [Oreochromis niloticus]	0,0434	0,0052	down	up	up	up	up	up
MPF_LOC101478567.1.1	XM_004547038.1 PREDICTED: Maylandia zebra claudin-5-like (LOC101478567), mRNA	0,0372	0,0035	down	down	up	up	up	up
MPF_LOC101476415.1.1	XM_004548724.1 PREDICTED: Maylandia zebra prostacyclin synthase-like (LOC101476415), mRNA	0,0320	0,0022	down	up	down	up	down	down
MPF_AT1A1.1.3	AT1A1_OREMO (sp|Q9YH26) Sodium/potassium-transporting ATPase subunit alpha-1 OS=Oreochromis mossambicus GN=atp1a1 PE=2 SV=2	0,0371	0,0034	up	down	up	down	up	up
MPF_LOC100699298.1.1	XP_003446682.1 PREDICTED: galectin-8-like [Oreochromis niloticus]	0,0148	0,0002	down	down	up	down	up	up
MPF_LOC100689746.1.1	XP_003445067.1 PREDICTED: proline-rich protein 5-like [Oreochromis niloticus]	0,0232	0,0008	down	up	up	up	up	up
MPF_contig_025533	XM_004574317.1 PREDICTED: Maylandia zebra EH domain-binding protein 1-like protein 1-like (LOC101477091), transcript variant X4, mRNA	0,0147	0,0002	down	down	down	down	down	down
MPF_contig_025542	NA	0,0367	0,0033	up	down	up	down	up	up
MPF_LOC101469036.1.1	XM_004542267.1 PREDICTED: Maylandia zebra platelet-activating factor acetylhydrolase-like (LOC101469036), transcript variant X1, mRNA	0,0253	0,0011	up	down	down	down	down	down
MPF_LOC101475930.1.1	XM_004549175.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF19A-like (LOC101475930), mRNA	0,0477	0,0067	down	up	up	up	up	up
MPF_LOC101465950.2.3	XM_004573375.1 PREDICTED: Maylandia zebra transcription initiation factor TFIID subunit 1-like (LOC101465950), transcript variant X5, mRNA	0,0418	0,0047	up	up	up	down	up	up
MPF_LOC101475675.1.1	XM_004558632.1 PREDICTED: Maylandia zebra Golgi phosphoprotein 3-like (LOC101475675), mRNA	0,0405	0,0044	down	up	up	up	up	up
MPF_contig_025758	NA	0,0277	0,0014	down	down	up	down	up	up
MPF_LOC101469126.1.1	XM_004562729.1 PREDICTED: Maylandia zebra monocarboxylate transporter 13-like (LOC101469126), transcript variant X5, mRNA	0,0244	0,0010	up	down	down	down	down	down
MPF_LOC101484444.1.1	XM_004563244.1 PREDICTED: Maylandia zebra uncharacterized LOC101484444 (LOC101484444), mRNA	0,0178	0,0004	up	up	up	down	up	up

MPF_LOC101469798.3.3	XM_004544314.1 PREDICTED: Maylandia zebra ubiquitin-like protein 4A-like (LOC101469798), mRNA	0,0265	0,0012 up	up	up	up	up	up
MPF_contig_002574	NA	0,0306	0,0019 down	up	up	up	up	up
MPF_LOC101469266.2.2	XM_004548320.1 PREDICTED: Maylandia zebra SCY1-like protein 2-like (LOC101469266), mRNA	0,0421	0,0049 down	up	up	up	up	up
MPF_contig_002577	NA	0,0398	0,0041 up	up	up	down	up	up
MPF_contig_025884	NA	0,0169	0,0003 down	up	up	up	up	up
MPF_LOC101469584.1.2	XM_004559799.1 PREDICTED: Maylandia zebra serum response factor-like (LOC101469584), mRNA	0,0494	0,0074 up	up	up	up	up	up
MPF_LOC100697348.1.1	XM_003449454.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100697348 (LOC100697348), mRNA	0,0287	0,0016 up	down	down	down	down	down
MPF_LOC101469314.1.1	XR_190849.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 44-like (LOC101469314), transcript variant X3, misc_RNA	0,0169	0,0003 down	up	up	up	up	up
MPF_LOC101478245.1.1	XM_004561422.1 PREDICTED: Maylandia zebra huntingtin-interacting protein 1-like (LOC101478245), transcript variant X3, mRNA	0,0253	0,0011 down	up	up	up	up	up
MPF_LOC101067973.1.1	XM_003978066.1 PREDICTED: Takifugu rubripes tRNA modification GTPase GTPBP3, mitochondriallike (LOC101067973), mRNA	0,0486	0,0072 down	up	up	up	up	up
MPF_LOC101156189.1.1	XM_004076645.1 PREDICTED: Oryzias latipes tetratricopeptide repeat protein 1-like (LOC101156189), mRNA	0,0327	0,0023 down	up	up	up	up	up
MPF_LOC100706983.6.11	XM_003460062.1 PREDICTED: Oreochromis niloticus 28S ribosomal protein S28, mitochondrial-like (LOC100706983), mRNA	0,0073	0,0000 down	down	down	up	down	down
MPF_LOC101479961.1.1	XM_004544000.1 PREDICTED: Maylandia zebra bromodomain and WD repeat-containing protein 1-like (LOC101479961), transcript variant X2, mRNA	0,0460	0,0060 up	down	up	down	up	up
MPF_LOC101484718.1.2	XM_004561625.1 PREDICTED: Maylandia zebra UV radiation resistance-associated gene protein-like (LOC101484718), mRNA	0,0224	0,0007 up	up	up	up	up	up
MPF_LOC100701712.1.1	XM_003441390.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100701712 (LOC100701712), mRNA	0,0107	0,0001 down	down	down	down	down	down
MPF_contig_026006	NA	0,0243	0,0009 up	up	up	up	up	up
MPF_ZGC_110848.1.1	NM_001013329.1 Danio rerio zgc:110848 (zgc:110848), mRNA gb|BC090793.1| Danio rerio zgc:110848, mRNA (cDNA clone MGC:110848 IMAGE:7156048), complete cds	0,0260	0,0011 down	up	up	up	up	up
MPF_LOC101467998.1.1	XM_004574373.1 PREDICTED: Maylandia zebra amyloid beta A4 precursor protein-binding family A member 1-like (LOC101467998), mRNA	0,0143	0,0002 up	up	up	up	up	up
MPF_LOC100697921.1.1	XM_003439274.1 PREDICTED: Oreochromis niloticus uncharacterized protein C8orf59 homolog (LOC100697921), mRNA	0,0467	0,0062 up	up	up	up	up	up
MPF_LOC101474121.9.17	XM_004575391.1 PREDICTED: Maylandia zebra stonustoxin subunit beta-like (LOC101474121), mRNA	0,0374	0,0035 down	up	down	up	down	down

MPF_contig_026192	NA	0,0228	0,0008	down	up	up	up	up	up
MPF_LOC101484929.2.3	XM_004542976.1 PREDICTED: Maylandia zebra CMP-N-acetylneuraminate-beta-1,4-galactoside alpha2,3-sialyltransferase-like (LOC101484929), mRNA	0,0107	0,0001	up	down	down	down	down	down
MPF_contig_026229	XM_004562887.1 PREDICTED: Maylandia zebra ras-related protein Rab-3D-like (LOC101465588), transcript variant X1, mRNA	0,0268	0,0013	up	up	up	up	up	up
MPF_LOC100698606.1.1	XM_003451611.1 PREDICTED: Oreochromis niloticus ceroid-lipofuscinosis neuronal protein 5-like (LOC100698606), mRNA	0,0394	0,0040	down	up	down	up	down	down
MPF_ATF6B.1.1	XM_004073727.1 PREDICTED: Oryzias latipes cyclic AMP-dependent transcription factor ATF-6 betalike (LOC101165322), mRNA	0,0366	0,0032	up	up	up	down	up	up
MPF_LOC101471166.1.1	XM_004547008.1 PREDICTED: Maylandia zebra clathrin heavy chain 1-like (LOC101471166), transcript variant X1, mRNA	0,0363	0,0032	down	down	down	down	down	down
MPF_contig_026354	NA	0,0367	0,0033	down	up	up	up	up	up
MPF_LOC101471935.1.1	XM_004545975.1 PREDICTED: Maylandia zebra transcription factor MafB-like (LOC101471935), mRNA	0,0143	0,0002	down	down	down	down	down	down
MPF_contig_026412	NA	0,0421	0,0048	down	down	up	down	up	up
MPF_LOC100694797.1.2	XP_003453218.1 PREDICTED: nucleoprotein TPR-like [Oreochromis niloticus]	0,0178	0,0004	down	up	up	up	up	up
MPF_LOC100710715.2.3	XM_003458665.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100710715 (LOC100710715), mRNA	0,0269	0,0013	up	up	up	up	up	up
MPF_LOC101466470.1.1	XM_004561464.1 PREDICTED: Maylandia zebra protein FAM43A-like (LOC101466470), mRNA	0,0060	0,0000	down	down	down	down	down	down
MPF_LOC100690727.1.1	XM_003443255.1 PREDICTED: Oreochromis niloticus ribosomal RNA processing protein 1 homolog Blike (LOC100690727), mRNA	0,0041	0,0000	down	down	down	up	down	down
MPF_LOC101463863.1.2	XR_190895.1 PREDICTED: Maylandia zebra palmitoyltransferase ZDHHC7-like (LOC101463863), transcript variant X2, misc_RNA	0,0270	0,0014	down	up	up	up	up	up
MPF_LOC101466337.11.22	XM_004575687.1 PREDICTED: Maylandia zebra prothymosin alpha-B-like (LOC101466337), mRNA	0,0176	0,0004	down	up	up	up	up	up
MPF_LOC100705458.1.1	XP_003457013.1 PREDICTED: syntenin-1-like [Oreochromis niloticus]	0,0407	0,0044	down	down	up	up	up	up
MPF_LOC101469146.1.1	XM_004567105.1 PREDICTED: Maylandia zebra dedicator of cytokinesis protein 11-like (LOC101469146), transcript variant X3, mRNA	0,0395	0,0041	down	down	up	down	up	up
MPF_LOC100699446.1.1	XP_003459443.1 PREDICTED: hypothetical protein LOC100699446 [Oreochromis niloticus]	0,0493	0,0074	up	up	up	up	up	up
MPF_contig_026550	NA	0,0387	0,0038	down	down	down	down	down	down
MPF_LOC101463970.1.1	XM_004540289.1 PREDICTED: Maylandia zebra nardilysin-like (LOC101463970), mRNA	0,0358	0,0030	down	up	up	up	up	up
MPF_ENPP1.1.2	XM_003446358.1 PREDICTED: Oreochromis niloticus ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA	0,0143	0,0002	down	down	down	down	down	down
MPF_contig_026633	XM_004549165.1 PREDICTED: Maylandia zebra neurocalcin-delta B-like (LOC101473406), transcript variant X2, mRNA	0,0306	0,0019	up	up	up	up	up	up

MPF_LOC100709600.1.1	XM_003445263.1 PREDICTED: Oreochromis niloticus zinc-binding protein A33-like (LOC100709600), mRNA	0,0171	0,0003	up	up	up	up	up	up
MPF_LOC100705885.1.1	XM_003453768.1 PREDICTED: Oreochromis niloticus Fc receptor-like protein 3-like (LOC100705885), mRNA	0,0288	0,0016	down	up	up	up	up	up
MPF_LOC101468796.3.3	XM_004575287.1 PREDICTED: Maylandia zebra barrier-to-autointegration factor-like protein-like (LOC101468796), mRNA	0,0401	0,0042	down	up	up	up	up	up
MPF_LOC101463781.1.1	XM_004541855.1 PREDICTED: Maylandia zebra dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial-like (LOC101463781), mRNA	0,0311	0,0020	up	up	up	up	up	up
MPF_LOC101487734.1.2	XM_004571292.1 PREDICTED: Maylandia zebra cytohesin-4-like (LOC101487734), mRNA	0,0187	0,0004	down	down	down	down	down	down
MPF_LOC101470901.5.10	XM_004574121.1 PREDICTED: Maylandia zebra 40S ribosomal protein S3-like (LOC101470901), mRNA	0,0354	0,0029	down	down	up	up	up	up
MPF_contig_026762	NA	0,0248	0,0010	down	down	up	up	up	up
MPF_CO8A1.4.5	CO8A1_RABIT (sp|P14282) Collagen alpha-1(VIII) chain OS=Oryctolagus cuniculus GN=COL8A1 PE=2 SV=1	0,0243	0,0009	up	up	up	up	up	up
MPF_LOC101470873.3.3	XM_004543575.1 PREDICTED: Maylandia zebra importin subunit alpha-4-like (LOC101470873), mRNA	0,0329	0,0023	up	up	up	up	up	up
MPF_LOC101483176.1.1	XM_004548925.1 PREDICTED: Maylandia zebra claspin-like (LOC101483176), transcript variant X1, mRNA	0,0421	0,0049	down	up	up	up	up	up
MPF_contig_026897	NA	0,0464	0,0061	down	up	down	up	down	down
MPF_LOC100708025.2.2	XM_003456564.1 PREDICTED: Oreochromis niloticus cytohesin-4-like (LOC100708025), mRNA	0,0266	0,0012	down	down	down	down	down	down
MPF_GORAB.1.1	GORAB_MOUSE (sp|Q8BRM2) RAB6-interacting golgin OS=Mus musculus GN=Gorab PE=1 SV=1	0,0468	0,0063	down	up	up	up	up	up
MPF_LOC100703013.1.1	XM_003452384.1 PREDICTED: Oreochromis niloticus HAUS augmin-like complex subunit 6-like (LOC100703013), mRNA	0,0474	0,0066	up	up	up	up	up	up
MPF_ZNFX1.2.3	XM_003456110.1 PREDICTED: Oreochromis niloticus zinc finger, NFX1-type containing 1 (ZNFX1), mRNA	0,0353	0,0029	down	down	up	down	up	up
MPF_contig_002690	NA	0,0271	0,0014	up	up	up	up	up	up
MPF_contig_027052	NA	0,0142	0,0001	down	down	down	down	down	down
MPF_LOC101064281.1.1	XP_003976694.1 PREDICTED: uncharacterized protein LOC101064281 [Takifugu rubripes]	0,0309	0,0020	down	up	up	up	up	up
MPF_LOC101468042.2.2	XM_004543565.1 PREDICTED: Maylandia zebra P2Y purinoceptor 13-like (LOC101468042), transcript variant X2, mRNA	0,0334	0,0024	down	down	up	up	up	up
MPF_LOC101483324.1.1	XM_004541004.1 PREDICTED: Maylandia zebra regulator of cell cycle RGCC-like (LOC101483324), mRNA	0,0123	0,0001	up	up	up	up	up	up
MPF_LOC101469089.3.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA	0,0279	0,0015	up	down	down	down	down	down

MPF_LOC101464277.1.1	XM_004543741.1 PREDICTED: Maylandia zebra rho guanine nucleotide exchange factor 12-like (LOC101464277), transcript variant X3, mRNA	0,0232	0,0008	up	up	up	up	up	up
MPF_LOC101483661.2.5	XM_004572907.1 PREDICTED: Maylandia zebra traf2 and NCK-interacting protein kinase-like (LOC101483661), transcript variant X1, mRNA	0,0262	0,0011	down	down	up	up	up	up
MPF_LOC100697044.1.1	XM_003460170.1 PREDICTED: Oreochromis niloticus myc-induced nuclear antigen-like (LOC100697044), mRNA	0,0143	0,0002	up	up	up	up	up	up
MPF_LOC100695046.1.1	XM_003449864.1 PREDICTED: Oreochromis niloticus pleckstrin homology domain-containing family G member 1-like (LOC100695046), mRNA	0,0457	0,0059	up	up	up	up	up	up
MPF_LOC101467152.1.1	XM_004567377.1 PREDICTED: Maylandia zebra glutaredoxin-2, mitochondrial-like (LOC101467152), transcript variant X2, mRNA	0,0131	0,0001	down	up	up	up	up	up
MPF_GABP2.1.1	GABP2_BOVIN (sp|Q0V8G2) GA-binding protein subunit beta-2 OS=Bos taurus GN=GABPB2 PE=2 SV=2	0,0288	0,0016	up	up	up	up	up	up
MPF_LOC101473334.2.2	XM_004553568.1 PREDICTED: Maylandia zebra histone-lysine N-methyltransferase SETD7-like (LOC101473334), mRNA	0,0244	0,0010	down	up	up	up	up	up
MPF_LOC101480083.3.3	XM_004548835.1 PREDICTED: Maylandia zebra cytochrome c1, heme protein, mitochondrial-like (LOC101480083), mRNA	0,0243	0,0009	up	up	up	down	up	up
MPF_LOC101468648.3.4	XM_004570179.1 PREDICTED: Maylandia zebra ceramide synthase 1-like (LOC101468648), mRNA	0,0489	0,0073	up	up	up	down	up	up
MPF_LOC101486367.1.1	XM_004543922.1 PREDICTED: Maylandia zebra transforming growth factor beta regulator 1-like (LOC101486367), transcript variant X1, mRNA	0,0289	0,0016	down	down	up	up	up	up
MPF_contig_027303	NA	0,0103	0,0001	down	up	up	up	up	up
MPF_LOC101486277.2.2	XM_004568460.1 PREDICTED: Maylandia zebra uncharacterized LOC101486277 (LOC101486277), mRNA	0,0225	0,0007	down	down	down	down	down	down
MPF_LOC101477354.1.1	XM_004572334.1 PREDICTED: Maylandia zebra terminal uridylyltransferase 4-like (LOC101477354), mRNA	0,0277	0,0014	down	down	up	down	up	up
MPF_contig_027340	NA	0,0367	0,0033	down	down	down	down	down	down
MPF_LOC101472403.3.3	XM_004569122.1 PREDICTED: Maylandia zebra G1/S-specific cyclin-D2-like (LOC101472403), transcript variant X2, mRNA	0,0258	0,0011	up	up	up	up	up	up
MPF_LOC101464701.1.2	XM_004575190.1 PREDICTED: Maylandia zebra angio-associated migratory cell protein-like (LOC101464701), mRNA	0,0346	0,0027	down	up	up	up	up	up
MPF_contig_027390	NA	0,0319	0,0021	down	up	up	up	up	up
MPF_contig_027404	XM_004568351.1 PREDICTED: Maylandia zebra protein kinase C beta type-like (LOC101478005), transcript variant X1, mRNA	0,0171	0,0003	down	down	down	down	down	down

MPF_CNDH2.1.1	[BBH] CNDH2_DANRE (sp|Q5RH01) Condensin-2 complex subunit H2 OS=Danio rerio GN=ncaph2 PE=2 SV=1	0,0287	0,0016	up	up	up	down	up	up
MPF_LOC101482091.1.1	XM_004568619.1 PREDICTED: Maylandia zebra retinoid-inducible serine carboxypeptidase-like (LOC101482091), mRNA	0,0485	0,0070	down	down	up	up	up	up

MPF_LOC100703241.5.9	XM_003440649.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S29-like (LOC100703241), mRNA	0,0328	0,0023	down	up	up	up	up	up
MPF_NCKAP1L.2.2	XM_003451841.1 PREDICTED: Oreochromis niloticus NCK-associated protein 1-like (NCKAP1L), mRNA	0,0041	0,0000	down	down	down	down	down	down
MPF_CSF12.1.1	[BBH] CSF12_TAKRU (sp|Q8UVR8) Macrophage colony-stimulating factor 1 receptor 2 OS=Takifugu rubripes GN=csf1r2 PE=3 SV=1	0,0171	0,0003	down	up	up	up	up	up
MPF_LOC100690992.1.1	XM_003442702.1 PREDICTED: Oreochromis niloticus Rieske domain-containing protein-like (LOC100690992), mRNA	0,0228	0,0008	down	up	up	up	up	up
MPF_LOC101473623.3.9	XM_004576627.1 PREDICTED: Maylandia zebra ferritin, middle subunit-like (LOC101473623), mRNA	0,0286	0,0016	down	up	up	up	up	up
MPF_LOC101484297.1.2	XM_004567347.1 PREDICTED: Maylandia zebra pyrroline-5-carboxylate reductase 3-like (LOC101484297), mRNA	0,0277	0,0015	down	down	up	up	up	up
MPF_contig_027603	NA	0,0244	0,0010	up	up	up	up	up	up
MPF_LOC101471011.1.2	XM_004555841.1 PREDICTED: Maylandia zebra LIM domain-binding protein 1-like (LOC101471011), transcript variant X1, mRNA	0,0294	0,0017	up	up	up	up	up	up
MPF_contig_027617	NA	0,0226	0,0007	down	down	down	up	down	down
MPF_LOC100700407.1.1	XM_003454414.1 PREDICTED: Oreochromis niloticus IGF-like family receptor 1-like (LOC100700407), mRNA	0,0137	0,0001	down	down	down	down	down	down
MPF_contig_027704	NA	0,0400	0,0042	up	up	up	up	up	up
MPF_RS6.6.11	RS6_PROMA (sp|Q7V9F9) 30S ribosomal protein S6 OS=Prochlorococcus marinus (strain SARG / CCMP1375 / SS120) GN=rpsF PE=3 SV=1	0,0047	0,0000	down	down	down	down	down	down
MPF_SPCS.3.3	[BBH] SPCS_DANRE (sp|Q803A7) O-phosphoseryl-tRNA(Sec) selenium transferase OS=Danio rerio GN=sepsecs PE=2 SV=1	0,0253	0,0011	down	up	up	up	up	up
MPF_LOC100703241.6.9	XM_003440649.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S29-like (LOC100703241), mRNA	0,0381	0,0037	down	up	up	up	up	up
MPF_CD63.1.2	NM_001124496.1 Oncorhynchus mykiss Cd63 antigen (cd63), mRNA gb|AY593998.1| Oncorhynchus mykiss CD63 (CD63) mRNA, complete cds	0,0110	0,0001	down	down	down	down	down	down
MPF_TNR1B.1.1	[BBH] TNR1B_MOUSE (sp|P25119) Tumor necrosis factor receptor superfamily member 1B OS=Mus musculus GN=Tnfrsf1b PE=2 SV=1	0,0047	0,0000	down	down	down	down	down	down
MPF_LOC101472043.8.14	XM_004573789.1 PREDICTED: Maylandia zebra tight junction-associated protein 1-like (LOC101472043), transcript variant X4, mRNA	0,0290	0,0016	down	down	down	up	down	down
MPF_LOC100701834.2.2	XM_003448970.1 PREDICTED: Oreochromis niloticus probable G-protein coupled receptor 171-like (LOC100701834), mRNA	0,0066	0,0000	up	down	down	down	down	down
MPF_contig_027934	NA	0,0226	0,0007	up	up	up	up	up	up
MPF_contig_027940	NA	0,0371	0,0034	down	down	up	down	up	up
MPF_LOC101468902.2.2	XM_004561019.1 PREDICTED: Maylandia zebra thyroid hormone receptor beta-like (LOC101468902), transcript variant X5, mRNA	0,0449	0,0056	down	down	up	up	up	up

MPF_ZG26.1.1	ZG26_XENLA (sp|P18715) Gastrula zinc finger protein XlCGF26.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0,0318	0,0021	up	up	up	up	up	up
MPF_contig_027988	XM_004562927.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase N1-like (LOC101475594), transcript variant X1, mRNA	0,0160	0,0003	down	up	up	up	up	up
MPF_LOC101487908.2.3	XM_004546898.1 PREDICTED: Maylandia zebra rab effector MyRIP-like (LOC101487908), mRNA	0,0419	0,0048	down	up	up	up	up	up
MPF_LOC101466459.21.29	XM_004554283.1 PREDICTED: Maylandia zebra semaphorin-3G-like (LOC101466459), mRNA	0,0334	0,0024	up	up	up	up	up	up
MPF_contig_028027	NA	0,0328	0,0023	down	up	up	up	up	up
MPF_LOC101480587.2.2	XM_004553594.1 PREDICTED: Maylandia zebra fibroblast growth factor receptor-like 1-like (LOC101480587), mRNA	0,0375	0,0036	down	up	up	up	up	up
MPF_BHWA1_01395.1.1	YP_002721575.1 hypothetical protein BHWA1_01395 [Brachyspira hyodysenteriae WA1]	0,0171	0,0003	down	down	down	down	down	down
MPF_LOC100703752.1.1	XP_003456347.1 PREDICTED: glia-derived nexin-like [Oreochromis niloticus]	0,0295	0,0018	down	down	down	up	down	down
MPF_LOC101473877.1.1	XM_004541986.1 PREDICTED: Maylandia zebra cyclin-C-like (LOC101473877), mRNA	0,0256	0,0011	up	up	up	down	up	up
MPF_LOC101478089.1.1	XM_004544632.1 PREDICTED: Maylandia zebra S-adenosylmethionine synthase isoform type-2-like (LOC101478089), mRNA	0,0461	0,0060	down	down	up	up	up	up
MPF_LOC100697193.1.1	XM_003454893.1 PREDICTED: Oreochromis niloticus phosducin-like protein 3-like (LOC100697193), mRNA	0,0286	0,0016	up	up	up	down	up	up
MPF_LOC101162518.1.1	XP_004068643.1 PREDICTED: syndecan-4-like [Oryzias latipes]	0,0208	0,0005	down	down	up	up	up	up
MPF_contig_002810	NA	0,0371	0,0034	down	up	up	up	up	up
MPF_contig_028214	XM_004556613.1 PREDICTED: Maylandia zebra calcium/calmodulin-dependent protein kinase type II subunit gamma-like (LOC101474026), transcript variant X10, mRNA	0,0497	0,0076	down	up	up	up	up	up
MPF_contig_028215	NA	0,0253	0,0011	down	up	up	up	up	up
MPF_SSGZ1_0670.2.2	YP_006074071.1 TPR repeat protein [Streptococcus suis GZ1]	0,0289	0,0016	up	up	up	up	up	up
MPF_LOC101487751.2.3	XM_004574697.1 PREDICTED: Maylandia zebra active regulator of SIRT1-like (LOC101487751), transcript variant X1, mRNA	0,0371	0,0034	up	up	up	down	up	up
MPF_GBG12.1.1	NM_001165215.1 Oncorhynchus mykiss Guanine nucleotide-binding protein GI/GS/GO gamma-12 subunit (gbg12), mRNA gb|BT074358.1| Oncorhynchus mykiss clone omyk-evo-513-041 Guanine nucleotide-binding protein GI/GS/GO gamma-12 subunit precursor putative mRNA, complete cds	0,0169	0,0003	up	up	up	up	up	up
MPF_contig_002825	XM_004549786.1 PREDICTED: Maylandia zebra rap guanine nucleotide exchange factor 1-like (LOC101486972), transcript variant X3, mRNA	0,0471	0,0064	down	up	up	up	up	up
MPF_contig_028400	NA	0,0460	0,0060	down	down	up	up	up	up
MPF_contig_028429	NA	0,0160	0,0002	down	down	down	down	down	down

MPF_COX17.4.4	COX17_PIG (sp|P81045) Cytochrome c oxidase copper chaperone OS=Sus scrofa GN=COX17 PE=1 SV=1	0,0486	0,0072	down	up	up	up	up	up
MPF_contig_028512	XM_004569132.1 PREDICTED: Maylandia zebra solute carrier family 45 member 3-like (LOC101474184), transcript variant X6, mRNA	0,0493	0,0074	up	up	up	up	up	up
MPF_contig_002843	NA	0,0131	0,0001	down	up	up	up	up	up
MPF_Z658B.1.1	Z658B_HUMAN (sp|Q4V348) Zinc finger protein 658B OS=Homo sapiens GN=ZNF658B PE=2 SV=1	0,0354	0,0029	up	up	up	up	up	up
MPF_contig_028611	NA	0,0432	0,0052	down	up	up	up	up	up
MPF_LOC101464848.5.5	XM_004545232.1 PREDICTED: Maylandia zebra bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]-like (LOC101464848), transcript variant X2, mRNA	0,0352	0,0028	down	down	down	up	down	down
MPF_TNFAIP8L2A.1.2	NM_001045301.1 Danio rerio tumor necrosis factor, alpha-induced protein 8, like 2a (tnfaip8l2a), mRNA gb|BC117652.1| Danio rerio zgc:136816, mRNA (cDNA clone MGC:136816 IMAGE:7258718), complete cds	0,0308	0,0020	up	up	up	up	up	up
MPF_contig_028664	NA	0,0231	0,0008	up	down	down	down	down	down
MPF_contig_028671	NA	0,0310	0,0020	down	down	up	down	up	up
MPF_XFIN.1.1	XFIN_XENLA (sp|P08045) Zinc finger protein Xfin OS=Xenopus laevis PE=1 SV=1	0,0256	0,0011	up	up	up	up	up	up
MPF_IF44L.3.4	IF44L_MOUSE (sp|Q9BDB7) Interferon-induced protein 44-like OS=Mus musculus GN=Ifi44l PE=2 SV=2	0,0162	0,0003	up	down	down	down	down	down
MPF_SGS4.8.10	SGS4_DROME (sp|Q00725) Salivary glue protein Sgs-4 OS=Drosophila melanogaster GN=Sgs4 PE=2 SV=1	0,0278	0,0015	down	up	up	up	up	up
MPF_FZD6.6.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440 IMAGE:6971142), complete cds	0,0112	0,0001	down	down	down	down	down	down
MPF_contig_028725	NA	0,0178	0,0004	up	up	up	up	up	up
MPF_LOC100711484.7.8	XM_003448843.1 PREDICTED: Oreochromis niloticus E3 ubiquitin/ISG15 ligase TRIM25-like (LOC100711484), mRNA	0,0123	0,0001	up	up	up	up	up	up
MPF_contig_028735	NA	0,0171	0,0003	down	down	down	up	down	down
MPF_contig_028743	NA	0,0332	0,0024	down	up	up	up	up	up
MPF_LOC101476780.4.7	XM_004544243.1 PREDICTED: Maylandia zebra serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform-like (LOC101476780), mRNA	0,0330	0,0023	down	up	up	up	up	up
MPF_LOC100698625.19.22	XM_003456694.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100698625), mRNA	0,0392	0,0040	up	up	up	up	up	up
MPF_contig_028771	NA	0,0332	0,0024	down	down	down	up	down	down
MPF_LOC101483926.1.2	XM_004546690.1 PREDICTED: Maylandia zebra ubiquitin carboxyl-terminal hydrolase 12-like (LOC101483926), mRNA	0,0287	0,0016	up	up	up	up	up	up
MPF_contig_028794	NA	0,0467	0,0063	down	down	down	up	down	down
MPF_ZN271.9.19	ZN271_MOUSE (sp|P15620) Zinc finger protein 271 OS=Mus musculus GN=Znf271 PE=2 SV=1	0,0368	0,0033	up	up	up	up	up	up

MPF_contig_028818	NA	0,0054	0,0000	down	down	down	down	down	down
MPF_LOC100703657.7.12	XM_003456466.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100703657), mRNA	0,0472	0,0065	down	down	down	up	down	down
MPF_contig_028837	NA	0,0333	0,0024	up	up	up	up	up	up
MPF_ZNF79.1.3	ZNF79_HUMAN (sp|Q15937) Zinc finger protein 79 OS=Homo sapiens GN=ZNF79 PE=1 SV=2	0,0356	0,0030	up	up	up	up	up	up
MPF_PPIA.1.6	PPIA_BLAGE (sp|P54985) Peptidyl-prolyl cis-trans isomerase OS=Blattella germanica GN=CYPA PE=2 SV=1	0,0438	0,0053	up	down	up	down	up	up
MPF_contig_028860	NA	0,0080	0,0000	down	down	down	down	down	down

MPF_SGS4.9.10	SGS4_DROME (sp|Q00725) Salivary glue protein Sgs-4 OS=Drosophila melanogaster GN=Sgs4 PE=2 SV=1	0,0293	0,0017	down	up	up	up	up	up
MPF_contig_028908	NA	0,0150	0,0002	up	up	up	up	up	up
MPF_contig_028924	NA	0,0326	0,0022	up	up	up	up	up	up
MPF_LOC101465407.2.4	XM_004540009.1 PREDICTED: Maylandia zebra transmembrane protein 87A-like (LOC101465407), mRNA	0,0333	0,0024	up	up	up	up	up	up
MPF_IFIT5.6.9	NM_001142188.1 Xenopus (Silurana) tropicalis interferon-induced protein with tetratricopeptide repeats 5 (ifit5), mRNA gb|BC168560.1| Xenopus tropicalis cDNA clone MGC:184922 IMAGE:7678513, complete cds	0,0308	0,0020	up	up	up	up	up	up
MPF_contig_028953	NA	0,0303	0,0019	down	up	up	up	up	up
MPF_contig_028954	NA	0,0193	0,0005	down	up	up	up	up	up
MPF_LOC101465228.1.1	XM_004565359.1 PREDICTED: Maylandia zebra sal-like protein 2-like (LOC101465228), transcript variant X2, mRNA	0,0286	0,0016	down	up	up	up	up	up
MPF_LOC101477850.7.10	XM_004575562.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12like (LOC101477850), mRNA	0,0152	0,0002	down	up	up	up	up	up
MPF_LOC101474972.2.4	XM_004576316.1 PREDICTED: Maylandia zebra zinc finger protein 771-like (LOC101474972), partial mRNA	0,0267	0,0012	up	up	up	up	up	up
MPF_LOC101487307.4.5	XM_004564717.1 PREDICTED: Maylandia zebra ankyrin repeat domain-containing protein 6-like (LOC101487307), transcript variant X4, mRNA	0,0041	0,0000	down	down	down	down	down	down
MPF_contig_028990	NA	0,0358	0,0030	down	down	down	down	down	down
MPF_contig_029011	NA	0,0318	0,0021	up	up	up	down	up	up
MPF_contig_029012	NA	0,0252	0,0010	down	down	down	down	down	down
MPF_LOC101474972.3.4	XM_004576316.1 PREDICTED: Maylandia zebra zinc finger protein 771-like (LOC101474972), partial mRNA	0,0454	0,0058	down	up	up	up	up	up
MPF_contig_029034	NA	0,0371	0,0035	up	up	up	up	up	up

MPF_contig_029035	NA	0,0293	0,0017	down	down	down	down	down	down
MPF_LOC101480883.1.1	XM_004553334.1 PREDICTED: Maylandia zebra choline kinase alpha-like (LOC101480883), mRNA	0,0269	0,0013	up	up	up	up	up	up
MPF_contig_029060	NA	0,0343	0,0026	up	up	up	down	up	up
MPF_contig_029062	NA	0,0344	0,0026	down	down	up	up	up	up
MPF_LOC101464712.2.5	XM_004554817.1 PREDICTED: Maylandia zebra interferon alpha-inducible protein 27-like protein 2Blike (LOC101464712), transcript variant X2, mRNA	0,0256	0,0011	up	down	down	down	down	down
MPF_contig_000291	NA	0,0410	0,0045	up	up	up	up	up	up
MPF_CR2.1.1	CR2_MOUSE (sp|P19070) Complement receptor type 2 OS=Mus musculus GN=Cr2 PE=2 SV=1	0,0127	0,0001	down	down	down	down	down	down
MPF_LOC101480436.4.4	XM_004564408.1 PREDICTED: Maylandia zebra cbp/p300-interacting transactivator 3-like (LOC101480436), mRNA	0,0047	0,0000	down	down	down	down	down	down
MPF_LOC100708241.2.3	XM_003441332.1 PREDICTED: Oreochromis niloticus calcium-binding and coiled-coil domaincontaining protein 1-like (LOC100708241), mRNA	0,0495	0,0075	up	down	up	down	up	up
MPF_LOC101464726.1.4	XM_004561458.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase TRIP12-like (LOC101464726), mRNA	0,0288	0,0016	up	up	up	up	up	up
MPF_contig_029231	NA	0,0319	0,0021	down	down	down	down	down	down
MPF_LOC101465276.5.8	XM_004553799.1 PREDICTED: Maylandia zebra MAP kinase-interacting serine/threonine-protein kinase 2-like (LOC101465276), mRNA	0,0467	0,0062	down	up	up	up	up	up
MPF_contig_029262	NA	0,0265	0,0012	down	down	down	down	down	down
MPF_LOC101469667.2.2	XM_004557497.1 PREDICTED: Maylandia zebra V-set and transmembrane domain-containing protein 4like (LOC101469667), mRNA	0,0304	0,0019	down	up	up	up	up	up
MPF_LOC101485691.1.3	XM_004568633.1 PREDICTED: Maylandia zebra homeobox protein Hox-B4a-like (LOC101485691), mRNA	0,0270	0,0013	down	down	up	down	up	up
MPF_contig_029328	XM_004570819.1 PREDICTED: Maylandia zebra oxysterol-binding protein-related protein 5-like (LOC101472907), transcript variant X2, mRNA	0,0484	0,0070	up	up	up	down	up	up
MPF_LOC101487074.1.1	XM_004574997.1 PREDICTED: Maylandia zebra cGMP-specific 3',5'-cyclic phosphodiesterase-like (LOC101487074), transcript variant X3, mRNA	0,0211	0,0006	down	down	down	up	down	down
MPF_contig_029430	NA	0,0477	0,0067	down	down	up	up	up	up
MPF_LOC101486817.1.1	XM_004561164.1 PREDICTED: Maylandia zebra potassium channel subfamily K member 1-like (LOC101486817), mRNA	0,0466	0,0062	down	up	up	up	up	up
MPF_LOC100696688.1.1	XM_003439694.1 PREDICTED: Oreochromis niloticus tight junction protein ZO-3-like (LOC100696688), mRNA	0,0486	0,0071	down	up	up	up	up	up
MPF_contig_029562	XM_004575516.1 PREDICTED: Maylandia zebra protein FAM222B-like (LOC101485279), transcript variant X1, mRNA	0,0281	0,0015	down	up	up	up	up	up

MPF_LOC100695382.1.1	XM_003443115.1 PREDICTED: Oreochromis niloticus galectin-2-like (LOC100695382), mRNA	0,0357	0,0030	up	down	up	down	up	up
MPF_contig_029572	XM_004564782.1 PREDICTED: Maylandia zebra arrestin domain-containing protein 2-like (LOC101479940), transcript variant X3, mRNA	0,0358	0,0030	up	down	down	down	down	down
MPF_LOC101483152.2.3	XM_004544173.1 PREDICTED: Maylandia zebra GTPase-activating protein and VPS9 domaincontaining protein 1-like (LOC101483152), mRNA	0,0237	0,0009	down	up	up	up	up	up
MPF_LOC101474833.3.3	XM_004570025.1 PREDICTED: Maylandia zebra bcl-2-like protein 11-like (LOC101474833), mRNA	0,0277	0,0015	up	down	down	down	down	down
MPF_contig_029610	NA	0,0172	0,0003	down	down	down	up	down	down
MPF_ROBO2.1.2	ROBO2_HUMAN (sp|Q9HCK4) Roundabout homolog 2 OS=Homo sapiens GN=ROBO2 PE=1 SV=2	0,0169	0,0003	up	up	up	up	up	up
MPF_contig_029673	NA	0,0424	0,0049	up	down	down	down	down	down
MPF_LOC101465253.1.1	XM_004548778.1 PREDICTED: Maylandia zebra 2',5'-phosphodiesterase 12-like (LOC101465253), transcript variant X1, mRNA	0,0354	0,0029	up	up	up	down	up	up
MPF_LOC100691095.1.2	XM_003446686.1 PREDICTED: Oreochromis niloticus AT-rich interactive domain-containing protein 1Blike (LOC100691095), mRNA	0,0266	0,0012	up	up	up	up	up	up
MPF_RNF220.1.3	XM_003456173.1 PREDICTED: Oreochromis niloticus ring finger protein 220 (RNF220), mRNA	0,0453	0,0057	down	down	up	down	up	up
MPF_TOR1A.1.1	TOR1A_MOUSE (sp|Q9ER39) Torsin-1A OS=Mus musculus GN=Tor1a PE=1 SV=1	0,0411	0,0045	down	down	down	down	down	down
MPF_LOC100706800.1.1	XM_003439818.1 PREDICTED: Oreochromis niloticus retinoic acid receptor RXR-gamma-B-like, transcript variant 1 (LOC100706800), mRNA	0,0482	0,0069	up	down	down	down	down	down
MPF_contig_029831	NA	0,0176	0,0004	down	down	down	down	down	down
MPF_LOC101157468.1.1	XM_004074359.1 PREDICTED: Oryzias latipes uncharacterized LOC101157468 (LOC101157468), mRNA	0,0455	0,0058	down	up	up	up	up	up
MPF_LOC101470017.4.5	XM_004574645.1 PREDICTED: Maylandia zebra putative oxidoreductase GLYR1-like (LOC101470017), transcript variant X5, mRNA	0,0497	0,0076	up	up	up	up	up	up
MPF_contig_029996	NA	0,0321	0,0022	up	up	up	up	up	up
MPF_LOC100697391.1.1	XP_003460149.1 PREDICTED: cystine/glutamate transporter-like [Oreochromis niloticus]	0,0144	0,0002	down	up	up	up	up	up
MPF_LOC101469738.1.2	XM_004551780.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase MSL2-like (LOC101469738), mRNA	0,0483	0,0070	down	up	up	up	up	up
MPF_LOC101474552.1.1	XM_004568338.1 PREDICTED: Maylandia zebra BRCA1-associated ATM activator 1-like (LOC101474552), mRNA	0,0337	0,0025	up	down	up	down	up	up
MPF_LOC101064336.1.1	XP_003970294.1 PREDICTED: leucine-rich repeat neuronal protein 4-like [Takifugu rubripes]	0,0262	0,0012	up	down	up	down	up	up
MPF_LOC100709275.1.1	XM_003454278.1 PREDICTED: Oreochromis niloticus regulator of telomere elongation helicase 1-like (LOC100709275), mRNA	0,0407	0,0044	down	up	up	up	up	up
MPF_LOC101478456.1.1	XM_004545288.1 PREDICTED: Maylandia zebra prickle-like protein 2-like (LOC101478456), transcript variant X2, mRNA	0,0458	0,0059	down	up	up	up	up	up

MPF_LOC101476666.1.3	XM_004541357.1 PREDICTED: Maylandia zebra epithelial splicing regulatory protein 1-like (LOC101476666), transcript variant X2, mRNA	0,0304	0,0019 up	down	up	down	up	up
MPF_LOC101472355.1.1	XM_004556700.1 PREDICTED: Maylandia zebra peripheral myelin protein 22-like (LOC101472355), mRNA	0,0144	0,0002 down	down	down	down	down	down
MPF_LOC101470369.1.1	XM_004543573.1 PREDICTED: Maylandia zebra structural maintenance of chromosomes protein 4-like (LOC101470369), transcript variant X1, mRNA	0,0490	0,0073 down	up	up	up	up	up
MPF_LOC101475646.3.5	XM_004550973.1 PREDICTED: Maylandia zebra metal regulatory transcription factor 1-like (LOC101475646), mRNA	0,0287	0,0016 down	up	up	up	up	up
MPF_LOC101479127.1.1	XM_004548455.1 PREDICTED: Maylandia zebra integrin-alpha FG-GAP repeat-containing protein 2like (LOC101479127), mRNA	0,0213	0,0006 up	up	up	up	up	up
MPF_LOC100691060.1.1	XP_003439383.1 PREDICTED: hypothetical protein LOC100691060 [Oreochromis niloticus]	0,0373	0,0035 down	down	up	down	up	up
MPF_LOC101466332.2.2	XM_004574102.1 PREDICTED: Maylandia zebra heterogeneous nuclear ribonucleoprotein L-like (LOC101466332), mRNA	0,0101	0,0001 down	up	up	up	up	up
MPF_LOC101465139.2.2	XM_004544582.1 PREDICTED: Maylandia zebra WSC domain-containing protein 2-like (LOC101465139), transcript variant X2, mRNA	0,0449	0,0056 up	up	up	up	up	up
MPF_LOC101481543.7.7	XM_004550249.1 PREDICTED: Maylandia zebra zinc finger BED domain-containing protein 1-like (LOC101481543), mRNA	0,0154	0,0002 down	down	down	down	down	down
MPF_LOC101473667.1.2	XM_004568855.1 PREDICTED: Maylandia zebra stress response protein nst1-like (LOC101473667), mRNA	0,0293	0,0017 down	up	up	up	up	up
MPF_LOC101476996.1.1	XM_004575053.1 PREDICTED: Maylandia zebra outer dense fiber protein 2-like (LOC101476996), transcript variant X4, mRNA	0,0329	0,0023 down	up	up	up	up	up
MPF_LOC101465123.1.1	XM_004541125.1 PREDICTED: Maylandia zebra actin filament-associated protein 1-like 1-like (LOC101465123), transcript variant X3, mRNA	0,0490	0,0073 up	down	up	down	up	up
MPF_contig_030509	XM_004568369.1 PREDICTED: Maylandia zebra arfaptin-1-like (LOC101482665), transcript variant X2, mRNA	0,0311	0,0020 down	up	up	up	up	up
MPF_LOC101469018.2.2	XM_004563092.1 PREDICTED: Maylandia zebra arginine and glutamate-rich protein 1-B-like (LOC101469018), transcript variant X2, mRNA	0,0150	0,0002 down	up	up	up	up	up
MPF_COG8.1.1	XM_003437743.1 PREDICTED: Oreochromis niloticus component of oligomeric golgi complex 8 (COG8), mRNA	0,0267	0,0012 up	up	up	down	up	up
MPF_LOC100690548.1.1	XM_003444688.1 PREDICTED: Oreochromis niloticus wolframin-like (LOC100690548), mRNA	0,0495	0,0075 up	down	up	down	up	up
MPF_LOC101487917.3.6	XM_004572192.1 PREDICTED: Maylandia zebra PERQ amino acid-rich with GYF domain-containing protein 1-like (LOC101487917), mRNA	0,0143	0,0002 up	up	up	down	up	up
MPF_LOC101486555.1.1	XM_004564613.1 PREDICTED: Maylandia zebra junctophilin-3-like (LOC101486555), mRNA	0,0380	0,0037 down	down	up	down	up	up
MPF_LOC100700496.3.3	XM_003453022.1 PREDICTED: Oreochromis niloticus probable ribonuclease ZC3H12D-like (LOC100700496), mRNA	0,0219	0,0007 down	down	down	down	down	down

MPF_PSD12.1.1	PSD12_BOVIN (sp|Q2KJ25) 26S proteasome non-ATPase regulatory subunit 12 OS=Bos taurus GN=PSMD12 PE=2 SV=3	0,0293	0,0017	down	up	up	up	up	up
MPF_LOC101471828.1.2	XM_004545262.1 PREDICTED: Maylandia zebra receptor-type tyrosine-protein phosphatase alpha-like (LOC101471828), transcript variant X2, mRNA	0,0410	0,0045	up	down	up	down	up	up
MPF_LOC100704190.2.2	XR_134884.1 PREDICTED: Oreochromis niloticus complement C4-like (LOC100704190), miscRNA	0,0150	0,0002	down	down	down	down	down	down
MPF_LOC100710689.1.1	XM_003452076.1 PREDICTED: Oreochromis niloticus GPN-loop GTPase 2-like (LOC100710689), mRNA	0,0455	0,0058	up	up	up	up	up	up
MPF_contig_000307	NA	0,0450	0,0056	up	up	up	up	up	up
MPF_LOC100690432.1.1	XM_003439085.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100690432 (LOC100690432), mRNA	0,0126	0,0001	down	down	down	down	down	down
MPF_LOC101476385.1.1	XM_004567688.1 PREDICTED: Maylandia zebra secretory carrier-associated membrane protein 5-like (LOC101476385), transcript variant X2, mRNA	0,0160	0,0002	down	up	up	up	up	up
MPF_contig_030785	NA	0,0354	0,0029	down	up	up	up	up	up
MPF_LOC101064289.1.1	XM_003978509.1 PREDICTED: Takifugu rubripes ketohexokinase-like (LOC101064289), mRNA	0,0285	0,0016	down	down	up	down	up	up
MPF_LOC101475774.1.1	XM_004538970.1 PREDICTED: Maylandia zebra stromal membrane-associated protein 1-like (LOC101475774), mRNA	0,0446	0,0055	down	up	up	up	up	up
MPF_LOC101477684.2.4	XM_004539594.1 PREDICTED: Maylandia zebra small EDRK-rich factor 2-like (LOC101477684), mRNA	0,0252	0,0010	up	up	up	up	up	up
MPF_LOC101484675.2.2	XM_004549119.1 PREDICTED: Maylandia zebra hepatoma-derived growth factor-like (LOC101484675), transcript variant X2, mRNA	0,0144	0,0002	down	up	up	up	up	up
MPF_contig_030877	NA	0,0287	0,0016	down	up	up	up	up	up
MPF_LOC100700215.1.1	XM_003451785.1 PREDICTED: Oreochromis niloticus E3 ubiquitin-protein ligase synoviolin-like (LOC100700215), mRNA	0,0311	0,0020	down	down	up	up	up	up
MPF_LOC100693621.3.4	XM_003448445.1 PREDICTED: Oreochromis niloticus medium-chain specific acyl-CoA dehydrogenase, mitochondrial-like (LOC100693621), mRNA	0,0451	0,0057	down	down	up	down	up	up
MPF_AP2MB.1.1	[BBH] AP2MB_DANRE (sp|Q7ZW98) AP-2 complex subunit mu-B OS=Danio rerio GN=ap2m1b PE=2 SV=1	0,0474	0,0066	up	up	up	up	up	up
MPF_contig_030933	NA	0,0354	0,0029	up	up	up	up	up	up
MPF_LOC101480666.2.2	XM_004572977.1 PREDICTED: Maylandia zebra regulator of cell cycle RGCC-like (LOC101480666), mRNA	0,0232	0,0008	down	up	up	up	up	up
MPF_contig_003091	NA	0,0385	0,0038	down	up	up	up	up	up
MPF_contig_031009	XM_004546030.1 PREDICTED: Maylandia zebra dystroglycan-like (LOC101485248), transcript variant X1, mRNA	0,0479	0,0068	up	down	up	down	up	up
MPF_LOC101480115.2.2	XM_004555427.1 PREDICTED: Maylandia zebra pituitary tumor-transforming gene 1 protein-interacting protein-like (LOC101480115), mRNA	0,0497	0,0076	up	up	down	down	down	down
MPF_contig_031014	XM_004549212.1 PREDICTED: Maylandia zebra zinc finger and BTB domain-containing protein 10-like (LOC101485347), transcript variant X1, mRNA	0,0437	0,0053	down	down	up	up	up	up

MPF_contig_031055	XM_004564782.1 PREDICTED: Maylandia zebra arrestin domain-containing protein 2-like (LOC101479940), transcript variant X3, mRNA	0,0463	0,0061	up	down	down	down	down	down
MPF_LOC100711455.1.1	XM_003441344.1 PREDICTED: Oreochromis niloticus melanocyte protein PMEL-like (LOC100711455), mRNA	0,0244	0,0010	down	down	up	down	up	up
MPF_LOC101485782.1.1	XM_004542236.1 PREDICTED: Maylandia zebra SNW domain-containing protein 1-like (LOC101485782), mRNA	0,0482	0,0069	up	down	up	down	up	up
MPF_LOC101156534.2.3	XR_177556.1 PREDICTED: Oryzias latipes synaptotagmin-1-like (LOC101156534), misc_RNA	0,0224	0,0007	down	down	up	down	up	up

MPF_LOC101465052.1.1	XM_004568916.1 PREDICTED: Maylandia zebra V-set and transmembrane domain-containing protein 2A-like (LOC101465052), mRNA	0,0126	0,0001	down	up	up	up	up	up
MPF_LOC101473149.5.5	XM_004560655.1 PREDICTED: Maylandia zebra V-type proton ATPase 16 kDa proteolipid subunit-like (LOC101473149), mRNA	0,0080	0,0000	down	up	up	up	up	up
MPF_LOC101477684.3.4	XM_004539594.1 PREDICTED: Maylandia zebra small EDRK-rich factor 2-like (LOC101477684), mRNA	0,0204	0,0005	up	up	up	up	up	up
MPF_contig_031251	NA	0,0262	0,0012	up	up	up	up	up	up
MPF_LOC101482669.1.1	XM_004545112.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein-like 3-like (LOC101482669), mRNA	0,0275	0,0014	down	up	up	up	up	up
MPF_LOC101472935.1.1	XM_004576185.1 PREDICTED: Maylandia zebra prestin-like (LOC101472935), mRNA	0,0359	0,0030	down	up	up	up	up	up
MPF_LOC101484055.3.4	XM_004553153.1 PREDICTED: Maylandia zebra tropomyosin alpha-1 chain-like (LOC101484055), transcript variant X3, mRNA	0,0224	0,0007	down	up	up	up	up	up
MPF_LOC101475522.1.1	XM_004546567.1 PREDICTED: Maylandia zebra 5-oxoprolinase-like (LOC101475522), transcript variant X3, mRNA	0,0383	0,0038	up	up	up	down	up	up
MPF_LOC101466833.2.2	XM_004560812.1 PREDICTED: Maylandia zebra sugar phosphate exchanger 3-like (LOC101466833), mRNA	0,0341	0,0026	up	up	up	up	up	up
MPF_LOC101464139.1.1	XM_004553987.1 PREDICTED: Maylandia zebra protein SOGA1-like (LOC101464139), transcript variant X1, mRNA	0,0183	0,0004	down	down	up	down	up	up
MPF_NEMVEDRAFT_V1G47	XP_001618475.1 hypothetical protein NEMVEDRAFT_v1g47783 [Nematostella vectensis]	0,0485	0,0070	down	up	up	up	up	up
MPF_contig_031602	NA	0,0277	0,0014	up	up	up	up	up	up
MPF_LOC101169293.7.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0,0302	0,0018	down	up	down	up	down	down
MPF_contig_031648	NA	0,0403	0,0043	down	up	up	up	up	up
MPF_LOC101469336.3.3	XM_004566007.1 PREDICTED: Maylandia zebra ras-related protein M-Ras-like (LOC101469336), mRNA	0,0367	0,0033	down	down	down	down	down	down
MPF_LOC101480294.1.1	XM_004551160.1 PREDICTED: Maylandia zebra probable E3 ubiquitin-protein ligase DTX2-like (LOC101480294), transcript variant X2, mRNA	0,0375	0,0036	down	up	up	up	up	up
MPF_LOC101170487.4.4	XM_004085086.1 PREDICTED: Oryzias latipes low-density lipoprotein receptor 2-like (LOC101170487), mRNA	0,0123	0,0001	up	down	down	down	down	down

MPF_LOC101466459.1.29	XM_004554283.1 PREDICTED: Maylandia zebra semaphorin-3G-like (LOC101466459), mRNA	0,0407	0,0044	down	up	up	up	up	up
MPF_LOC101482130.4.7	XM_004574887.1 PREDICTED: Maylandia zebra low affinity immunoglobulin gamma Fc region receptor II-b-like (LOC101482130), mRNA	0,0371	0,0035	down	down	up	down	up	up
MPF_CP2K1.1.1	CP2K1_ONCMY (sp|Q92090) Cytochrome P450 2K1 OS=Oncorhynchus mykiss GN=cyp2k1 PE=2 SV=1	0,0319	0,0021	down	up	up	up	up	up
MPF_LOC100704036.1.1	XM_003459031.1 PREDICTED: Oreochromis niloticus ADP-ribosylation factor-related protein 1-like (LOC100704036), mRNA	0,0265	0,0012	down	up	up	up	up	up
MPF_contig_031900	NA	0,0168	0,0003	up	up	down	down	down	down
MPF_contig_031909	XM_004555771.1 PREDICTED: Maylandia zebra metal transporter CNNM4-like (LOC101472255), transcript variant X2, mRNA	0,0290	0,0017	down	up	up	up	up	up
MPF_LOC100693585.1.1	XM_003439014.1 PREDICTED: Oreochromis niloticus ceramide synthase 5-like (LOC100693585), mRNA	0,0209	0,0006	up	up	up	down	up	up
MPF_LOC101477513.1.1	XM_004565497.1 PREDICTED: Maylandia zebra syntaphilin-like (LOC101477513), transcript variant X3, mRNA	0,0319	0,0021	down	up	up	up	up	up
MPF_contig_000319	NA	0,0272	0,0014	down	up	up	up	up	up
MPF_PRR21.2.3	PRR21_HUMAN (sp|Q8WXC7) Putative proline-rich protein 21 OS=Homo sapiens GN=PRR21 PE=5 SV=1	0,0293	0,0017	up	up	up	up	up	up
MPF_LOC100711421.1.1	XM_003456495.1 PREDICTED: Oreochromis niloticus 3-oxo-5-alpha-steroid 4-dehydrogenase 2-like (LOC100711421), mRNA	0,0270	0,0013	up	up	up	up	up	up
MPF_LOC101477137.2.2	XM_004542098.1 PREDICTED: Maylandia zebra peptidyl-prolyl cis-trans isomerase FKBP3-like (LOC101477137), mRNA	0,0243	0,0010	down	up	up	up	up	up
MPF_contig_031996	NA	0,0119	0,0001	up	down	down	down	down	down
MPF_LOC101485840.1.2	XM_004561077.1 PREDICTED: Maylandia zebra uncharacterized LOC101485840 (LOC101485840), mRNA	0,0235	0,0008	down	down	up	down	up	up
MPF_LOC100691235.2.2	XP_003438556.1 PREDICTED: integrin beta-4-like [Oreochromis niloticus]	0,0371	0,0034	down	down	up	down	up	up
MPF_contig_032061	NA	0,0243	0,0009	down	up	down	up	down	down
MPF_LOC100692880.1.1	XP_003443649.1 PREDICTED: beta,beta-carotene 15,15'-monooxygenase-like [Oreochromis niloticus]	0,0483	0,0070	down	up	up	up	up	up
MPF_contig_032148	NA	0,0210	0,0006	up	up	up	up	up	up
MPF_contig_003206	NA	0,0213	0,0006	up	up	up	up	up	up

MPF_LOC101476629.1.1	XM_004554227.1 PREDICTED: Maylandia zebra SPRY domain-containing SOCS box protein 1-like (LOC101476629), mRNA	0,0457	0,0059	down	up	up	up	up	up
MPF_LOC100535356.1.1	XP_003199172.1 PREDICTED: gastrula zinc finger protein XlCGF57.1-like [Danio rerio]	0,0371	0,0034	down	down	down	down	down	down
MPF_LOC100695417.1.1	XP_003451815.1 PREDICTED: caspase-3-like [Oreochromis niloticus]	0,0387	0,0039	down	down	up	down	up	up

MPF_TSP_02148.1.1	XP_003377890.1 7 transmembrane receptor [Trichinella spiralis]	0,0144	0,0002	down	down	down	down	down	down
MPF_LOC101480702.3.4	XM_004557634.1 PREDICTED: Maylandia zebra mitogen-activated protein kinase 8B-like (LOC101480702), mRNA	0,0134	0,0001	down	down	down	down	down	down
MPF_contig_032225	NA	0,0332	0,0024	down	down	down	down	down	down
MPF_contig_032239	NA	0,0182	0,0004	down	down	down	down	down	down
MPF_LOC100709350.3.3	XP_003449297.1 PREDICTED: cryptochrome-2-like [Oreochromis niloticus]	0,0287	0,0016	down	up	up	up	up	up
MPF_LOC101467550.1.2	XM_004568834.1 PREDICTED: Maylandia zebra cyclin-dependent kinase 17-like (LOC101467550), transcript variant X2, mRNA	0,0367	0,0032	up	up	up	up	up	up
MPF_contig_032259	NA	0,0088	0,0000	up	down	down	down	down	down
MPF_NEMVEDRAFT_V1G98	XP_001635459.1 predicted protein [Nematostella vectensis]	0,0253	0,0011	down	down	up	up	up	up
MPF_LOC100692165.1.1	XP_003445661.1 PREDICTED: lysine-specific demethylase 2B-like [Oreochromis niloticus]	0,0266	0,0012	down	down	up	down	up	up
MPF_LOC100699407.1.3	XM_003451114.1 PREDICTED: Oreochromis niloticus stress-associated endoplasmic reticulum protein 1-like (LOC100699407), mRNA	0,0237	0,0009	down	down	up	down	up	up
MPF_FZD6.7.11	NM_200561.2 Danio rerio frizzled homolog 6 (Drosophila) (fzd6), mRNA gb|BC065361.1| Danio rerio zgc:65879, mRNA (cDNA clone MGC:77440 IMAGE:6971142), complete cds	0,0295	0,0018	down	down	down	down	down	down
MPF_LOC100705554.1.1	XR_134753.1 PREDICTED: Oreochromis niloticus monocarboxylate transporter 12-B-like (LOC100705554), miscRNA	0,0371	0,0035	down	down	up	up	up	up
1MPF_LOC101464301.1.2	XM_004571738.1 PREDICTED: Maylandia zebra PH domain leucine-rich repeat protein phosphatase like (LOC101464301), mRNA	0,0467	0,0062	up	down	up	down	up	up
MPF_contig_032370	NA	0,0354	0,0029	up	up	up	down	up	up
MPF_contig_032375	NA	0,0425	0,0050	down	up	up	up	up	up
MPF_contig_032377	NA	0,0343	0,0026	down	up	up	up	up	up
MPF_contig_032379	NA	0,0314	0,0021	up	down	down	down	down	down
MPF_LOC100709791.1.1	XP_003448471.1 PREDICTED: tripartite motif-containing protein 16-like [Oreochromis niloticus]	0,0171	0,0003	down	down	up	down	up	up
MPF_LOC100707046.10.12	XM_003454686.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100707046), mRNA	0,0148	0,0002	down	down	up	up	up	up
MPF_contig_032441	NA	0,0467	0,0063	down	down	down	up	down	down
MPF_contig_032442	NA	0,0228	0,0008	down	down	down	down	down	down
MPF_LOC100693362.6.13	XP_003450310.1 PREDICTED: fucolectin-1-like [Oreochromis niloticus]	0,0395	0,0041	down	up	up	up	up	up
MPF_contig_032499	NA	0,0270	0,0013	down	up	up	up	up	up
MPF_contig_032524	NA	0,0190	0,0004	down	up	down	up	down	down
MPF_contig_032527	NA	0,0160	0,0002	up	down	up	down	up	up

MPF_LOC100699367.1.1	XM_003441300.1 PREDICTED: Oreochromis niloticus receptor tyrosine-protein kinase erbB-3-like (LOC100699367), mRNA	0,0480	0,0068	down	up	down	up	down	down
MPF_contig_032559	NA	0,0356	0,0030	down	up	up	up	up	up
MPF_contig_032594	NA	0,0415	0,0046	down	up	up	up	up	up
MPF_LOC101487307.5.5	XM_004564717.1 PREDICTED: Maylandia zebra ankyrin repeat domain-containing protein 6-like (LOC101487307), transcript variant X4, mRNA	0,0388	0,0039	down	down	down	down	down	down
MPF_LOC100708533.1.1	XM_003447172.1 PREDICTED: Oreochromis niloticus annexin A2-like (LOC100708533), mRNA	0,0041	0,0000	down	down	down	up	down	down
MPF_LOC101486578.1.2	XM_004546432.1 PREDICTED: Maylandia zebra solute carrier family 52, riboflavin transporter, member 3-A-like (LOC101486578), mRNA	0,0403	0,0043	down	down	up	up	up	up
MPF_LOC101480093.8.8	XM_004574589.1 PREDICTED: Maylandia zebra tripartite motif-containing protein 16-like (LOC101480093), mRNA	0,0143	0,0002	up	up	up	up	up	up
MPF_contig_032639	NA	0,0277	0,0014	up	up	up	up	up	up
MPF_LOC101472043.11.14	XM_004573789.1 PREDICTED: Maylandia zebra tight junction-associated protein 1-like (LOC101472043), transcript variant X4, mRNA	0,0171	0,0003	down	down	down	down	down	down
MPF_LOC101469933.1.1	XM_004575028.1 PREDICTED: Maylandia zebra zinc finger protein 578-like (LOC101469933), transcript variant X2, mRNA	0,0094	0,0000	up	down	up	down	up	up
MPF_LOC101468583.4.7	XM_004576296.1 PREDICTED: Maylandia zebra uncharacterized LOC101468583 (LOC101468583), mRNA	0,0224	0,0007	down	down	down	down	down	down
MPF_contig_032690	NA	0,0270	0,0013	down	up	down	up	down	down
MPF_contig_032693	NA	0,0160	0,0003	up	up	up	up	up	up
MPF_contig_032698	NA	0,0418	0,0047	up	up	up	up	up	up
MPF_LOC101467736.7.8	XM_004564634.1 PREDICTED: Maylandia zebra peptidyl-prolyl cis-trans isomerase F, mitochondrial like (LOC101467736), mRNA	0,0371	0,0034	down	up	up	up	up	up
MPF_LOC101464586.2.2	XM_004571741.1 PREDICTED: Maylandia zebra tensin-3-like (LOC101464586), transcript variant X3, mRNA	0,0223	0,0007	down	down	down	down	down	down
MPF_LOC100694557.22.24	XM_003458536.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100694557), mRNA	0,0339	0,0025	down	up	up	up	up	up
MPF_LOC100705728.15.17	XM_003459563.1 PREDICTED: Oreochromis niloticus zinc finger protein RFP-like (LOC100705728), mRNA	0,0379	0,0036	down	up	up	up	up	up
MPF_contig_032770	NA	0,0304	0,0019	down	down	up	down	up	up
MPF_LOC100706211.1.2	XM_003445662.1 PREDICTED: Oreochromis niloticus piwi-like protein 2-like (LOC100706211), mRNA	0,0333	0,0024	down	up	down	up	down	down
MPF_LOC100695519.2.3	XM_003458222.1 PREDICTED: Oreochromis niloticus zinc finger protein 92-like (LOC100695519), mRNA	0,0277	0,0015	up	up	up	up	up	up
MPF_contig_032817	NA	0,0270	0,0013	up	up	up	up	up	up

MPF_CD63.2.2	NM_001124496.1 Oncorhynchus mykiss Cd63 antigen (cd63), mRNA gb|AY593998.1| Oncorhynchus mykiss CD63 (CD63) mRNA, complete cds	0,0397	0,0041	down	down	up	up	up	up
MPF_contig_032831	NA	0,0107	0,0001	down	down	down	down	down	down
MPF_LOC101477850.10.10	XM_004575562.1 PREDICTED: Maylandia zebra NACHT, LRR and PYD domains-containing protein 12like (LOC101477850), mRNA	0,0256	0,0011	down	up	up	up	up	up
MPF_contig_032910	NA	0,0101	0,0001	down	down	down	up	down	down
MPF_LOC101473946.3.3	XM_004540042.1 PREDICTED: Maylandia zebra protein salvador homolog 1-like (LOC101473946), mRNA	0,0333	0,0024	down	down	up	up	up	up
MPF_contig_032974	NA	0,0287	0,0016	down	up	up	up	up	up
MPF_LOC101468989.1.2	XM_004554477.1 PREDICTED: Maylandia zebra fatty acid-binding protein, intestinal-like (LOC101468989), mRNA	0,0338	0,0025	up	down	up	down	up	up
MPF_contig_033110	NA	0,0269	0,0013	up	up	up	up	up	up
MPF_LOC101469611.1.3	XM_004544219.1 PREDICTED: Maylandia zebra nuclear receptor ROR-beta-like (LOC101469611), transcript variant X3, mRNA	0,0419	0,0047	up	up	up	up	up	up
MPF_LOC100700602.2.2	XP_003457975.1 PREDICTED: hypothetical protein LOC100700602 [Oreochromis niloticus]	0,0055	0,0000	up	down	down	down	down	down
MPF_PIGR.3.3	XP_004177171.1 PREDICTED: polymeric immunoglobulin receptor [Taeniopygia guttata]	0,0243	0,0009	down	up	up	up	up	up
MPF_NEMVEDRAFT_V1G15	XP_001618924.1 hypothetical protein NEMVEDRAFT_v1g152920 [Nematostella vectensis]	0,0243	0,0010	up	up	up	down	up	up
MPF_LOC101473402.1.1	XM_004548338.1 PREDICTED: Maylandia zebra protein kinase C and casein kinase substrate in neurons protein 2-like (LOC101473402), transcript variant X3, mRNA	0,0277	0,0015	down	down	down	down	down	down
MPF_contig_003321	NA	0,0294	0,0017	up	down	up	down	up	up
MPF_LOC100695076.5.8	XP_003455918.1 PREDICTED: hypothetical protein LOC100695076 [Oreochromis niloticus]	0,0123	0,0001	down	up	up	up	up	up
MPF_LOC101061900.3.4	XP_003975298.1 PREDICTED: uncharacterized protein LOC101061900 [Takifugu rubripes]	0,0333	0,0024	down	down	up	up	up	up
MPF_LOC100706471.2.2	XP_003445630.1 PREDICTED: drebrin-like protein-like [Oreochromis niloticus]	0,0214	0,0006	down	up	up	up	up	up
MPF_LOC101478533.1.1	XM_004539963.1 PREDICTED: Maylandia zebra tandem C2 domains nuclear protein-like (LOC101478533), mRNA	0,0343	0,0026	down	up	up	up	up	up
MPF_contig_033415	NA	0,0046	0,0000	down	down	down	down	down	down
MPF_contig_033443	NA	0,0347	0,0027	up	up	up	up	up	up
MPF_LOC100690883.1.2	XP_003458178.1 PREDICTED: zinc finger protein 84-like [Oreochromis niloticus]	0,0068	0,0000	up	up	up	up	up	up
MPF_contig_033538	XM_004562711.1 PREDICTED: Maylandia zebra uncharacterized LOC101464922 (LOC101464922), transcript variant X1, mRNA	0,0128	0,0001	down	down	up	up	up	up
MPF_contig_033609	NA	0,0239	0,0009	down	up	up	up	up	up
MPF_contig_033779	XM_004541356.1 PREDICTED: Maylandia zebra epithelial splicing regulatory protein 1-like (LOC101476666), transcript variant X1, mRNA	0,0290	0,0017	up	down	up	down	up	up

MPF_LOC101073138.2.2	XP_003966361.1 PREDICTED: tumor necrosis factor receptor superfamily member 5-like [Takifugu rubripes]	0,0327	0,0023	down	down	up	up	up	up
MPF_contig_033812	NA	0,0080	0,0000	down	up	up	up	up	up
MPF_LOC101485582.2.4	XM_004540190.1 PREDICTED: Maylandia zebra polypyrimidine tract-binding protein 1-like (LOC101485582), mRNA	0,0464	0,0061	up	up	up	up	up	up
MPF_LOC101483528.1.1	XM_004542875.1 PREDICTED: Maylandia zebra epidermal growth factor receptor-like (LOC101483528), mRNA	0,0150	0,0002	up	down	up	down	up	up
MPF_contig_033848	NA	0,0308	0,0020	down	up	up	up	up	up
MPF_LOC100706202.1.1	XM_003443483.1 PREDICTED: Oreochromis niloticus E3 ubiquitin-protein ligase MARCH6-like (LOC100706202), mRNA	0,0474	0,0066	up	up	up	up	up	up
MPF_LOC100711740.1.1	XM_003444597.1 PREDICTED: Oreochromis niloticus UBX domain-containing protein 1-like (LOC100711740), mRNA	0,0380	0,0037	down	down	up	up	up	up
MPF_LOC101483967.1.1	XM_004553054.1 PREDICTED: Maylandia zebra E3 SUMO-protein ligase PIAS1-like (LOC101483967), mRNA	0,0419	0,0048	down	up	up	up	up	up
MPF_LOC101471344.2.2	XM_004570568.1 PREDICTED: Maylandia zebra growth arrest and DNA damage-inducible protein GADD45 alpha-like (LOC101471344), transcript variant X1, mRNA	0,0371	0,0034	down	up	up	up	up	up
MPF_contig_034000	NA	0,0355	0,0029	up	up	up	down	up	up
MPF_LOC101068490.2.3	XP_003971983.1 PREDICTED: C-type lectin domain family 4 member F-like [Takifugu rubripes]	0,0219	0,0006	up	up	up	up	up	up
MPF_LOC100707640.2.2	XP_003451524.1 PREDICTED: hypothetical protein LOC100707640 [Oreochromis niloticus]	0,0126	0,0001	down	down	down	down	down	down
MPF_contig_034121	NA	0,0354	0,0029	down	up	up	up	up	up
MPF_LOC100705244.1.1	XM_003450063.1 PREDICTED: Oreochromis niloticus heme oxygenase 2-like (LOC100705244), mRNA	0,0243	0,0009	down	down	down	down	down	down
MPF_contig_034180	NA	0,0270	0,0013	down	down	down	up	down	down
MPF_contig_034181	NA	0,0228	0,0008	down	down	down	down	down	down
MPF_contig_034209	XM_003198881.1 PREDICTED: Danio rerio retrotransposable element Tf2 155 kDa protein type 1-like (LOC100535308), mRNA	0,0269	0,0013	down	down	down	up	down	down
MPF_LOC100703046.1.1	XM_003439129.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100703046 (LOC100703046), mRNA	0,0476	0,0067	down	up	up	up	up	up
MPF_LOC101479743.1.1	XM_004559840.1 PREDICTED: Maylandia zebra zinc finger protein 93-like (LOC101479743), mRNA	0,0484	0,0070	up	up	up	up	up	up
MPF_LOC100705819.1.1	XP_003438527.1 PREDICTED: hypothetical protein LOC100705819 [Oreochromis niloticus]	0,0315	0,0021	down	down	down	down	down	down
MPF_contig_034320	NA	0,0228	0,0008	down	up	down	up	down	down
MPF_LOC100005864.2.2	XP_001921726.1 PREDICTED: GTPase IMAP family member 8-like [Danio rerio]	0,0127	0,0001	down	down	down	down	down	down

MPF_LOC100691043.5.5	XM_003457742.1 PREDICTED: Oreochromis niloticus NACHT, LRR and PYD domains-containing protein 12-like (LOC100691043), mRNA	0,0172	0,0003	down	down	down	down	down	down
MPF_LOC101482551.1.1	XM_004538177.1 PREDICTED: Maylandia zebra smoothelin-like (LOC101482551), mRNA	0,0237	0,0009	down	down	down	down	down	down
MPF_LOC101480576.2.3	XM_004574067.1 PREDICTED: Maylandia zebra uncharacterized LOC101480576 (LOC101480576), mRNA	0,0333	0,0024	down	down	down	up	down	down
MPF_LOC101486200.2.2	XM_004548856.1 PREDICTED: Maylandia zebra sodium- and chloride-dependent taurine transporterlike (LOC101486200), mRNA	0,0167	0,0003	down	up	up	up	up	up
MPF_LOC100712490.2.2	XM_003454128.1 PREDICTED: Oreochromis niloticus T-complex protein 1 subunit delta-like (LOC100712490), mRNA	0,0275	0,0014	up	up	up	up	up	up
MPF_LOC101473669.3.4	XM_004545518.1 PREDICTED: Maylandia zebra uncharacterized LOC101473669 (LOC101473669), mRNA	0,0150	0,0002	down	up	up	up	up	up
MPF_PRG4.1.4	PRG4_MOUSE (sp|Q9JM99) Proteoglycan 4 OS=Mus musculus GN=Prg4 PE=1 SV=2	0,0189	0,0004	down	up	up	up	up	up
MPF_COX1.5.7	[BBH] COX1_SALSA (sp|Q9ZZM6) Cytochrome c oxidase subunit 1 OS=Salmo salar GN=mt-co1 PE=3 SV=1	0,0301	0,0018	up	up	up	up	up	up
MPF_contig_000345	NA	0,0251	0,0010	up	up	up	up	up	up
MPF_LOC101469870.4.4	XM_004537942.1 PREDICTED: Maylandia zebra A disintegrin and metalloproteinase with thrombospondin motifs 8-like (LOC101469870), mRNA	0,0419	0,0048	up	up	down	down	down	down
MPF_LOC100695229.4.4	XM_003450269.1 PREDICTED: Oreochromis niloticus induced myeloid leukemia cell differentiation protein Mcl-1 homolog (LOC100695229), mRNA	0,0267	0,0012	down	up	up	up	up	up
MPF_LOC101478322.4.4	XM_004556897.1 PREDICTED: Maylandia zebra capZ-interacting protein-like (LOC101478322), mRNA	0,0245	0,0010	down	up	up	up	up	up
MPF_COX2.4.4	[BBH] COX2_GADMO (sp|Q37741) Cytochrome c oxidase subunit 2 OS=Gadus morhua GN=mt-co2 PE=3 SV=1	0,0310	0,0020	up	up	up	down	up	up
MPF_COX1.6.7	COX1_PETMA (sp|Q35536) Cytochrome c oxidase subunit 1 OS=Petromyzon marinus GN=MT-CO1 PE=3 SV=1	0,0405	0,0044	up	up	up	down	up	up
MPF_LOC101466866.1.1	XM_004570172.1 PREDICTED: Maylandia zebra uncharacterized LOC101466866 (LOC101466866), mRNA	0,0171	0,0003	down	up	up	up	up	up
MPF_LOC101070225.1.1	XM_003971715.1 PREDICTED: Takifugu rubripes histidine triad nucleotide-binding protein 3-like (LOC101070225), mRNA	0,0411	0,0045	up	up	up	down	up	up
MPF_LOC101484951.3.3	XM_004546887.1 PREDICTED: Maylandia zebra myosin regulatory light chain 2, smooth muscle minor isoform-like (LOC101484951), mRNA	0,0224	0,0007	down	down	down	down	down	down
MPF_LOC101474346.2.2	XM_004540807.1 PREDICTED: Maylandia zebra protein phosphatase 1 regulatory subunit 14B-like (LOC101474346), mRNA	0,0066	0,0000	down	up	up	up	up	up
MPF_LOC101474972.4.4	XM_004576316.1 PREDICTED: Maylandia zebra zinc finger protein 771-like (LOC101474972), partial mRNA	0,0449	0,0055	up	up	up	up	up	up
MPF_contig_034756	XM_004561310.1 PREDICTED: Maylandia zebra transcription factor 7-like 2-like (LOC101473558), transcript variant X5, mRNA	0,0054	0,0000	down	up	up	up	up	up
MPF_DHR13.1.1	DHR13_BOVIN (sp|Q17QU7) Dehydrogenase/reductase SDR family member 13 OS=Bos taurus GN=DHRS13 PE=2 SV=1	0,0270	0,0013	down	up	up	up	up	up

MPF_contig_034792	NA	0,0041	0,0000	down	down	down	down	down	down
MPF_LOC101483587.1.1	XM_004558848.1 PREDICTED: Maylandia zebra ubiquitin-conjugating enzyme E2 T-like (LOC101483587), transcript variant X2, mRNA	0,0258	0,0011	up	up	up	up	up	up
MPF_LOC101466842.5.5	XM_004540117.1 PREDICTED: Maylandia zebra syntaxin-binding protein 5-like (LOC101466842), transcript variant X5, mRNA	0,0224	0,0007	up	up	up	up	up	up
MPF_ZGC_153740.2.2	NM_001045430.1 Danio rerio zgc:153740 (zgc:153740), mRNA gb|BC122406.1| Danio rerio zgc:153740, mRNA (cDNA clone MGC:153740 IMAGE:8148169), complete cds	0,0251	0,0010	down	up	up	up	up	up
MPF_LOC101485374.1.1	XM_004557191.1 PREDICTED: Maylandia zebra ubiquitin carboxyl-terminal hydrolase 24-like (LOC101485374), transcript variant X2, mRNA	0,0299	0,0018	up	up	up	up	up	up
MPF_contig_034872	NA	0,0400	0,0042	down	down	up	up	up	up
MPF_contig_034874	NA	0,0213	0,0006	up	up	up	up	up	up
MPF_contig_034908	NA	0,0277	0,0015	down	up	up	up	up	up
MPF_contig_034929	NA	0,0468	0,0063	down	down	down	up	down	down
MPF_LOC101474368.1.1	XM_004567962.1 PREDICTED: Maylandia zebra integrin beta-like protein 1-like (LOC101474368), mRNA	0,0171	0,0003	down	up	up	up	up	up
MPF_LOC101482932.1.1	XM_004557736.1 PREDICTED: Maylandia zebra neurabin-1-like (LOC101482932), transcript variant X3, mRNA	0,0413	0,0046	down	up	up	up	up	up
MPF_contig_034973	NA	0,0225	0,0007	down	down	up	down	up	up
MPF_LOC101167302.2.2	XP_004073563.1 PREDICTED: PDZ and LIM domain protein 7-like [Oryzias latipes]	0,0107	0,0001	down	up	up	up	up	up
MPF_contig_035016	NA	0,0371	0,0035	down	up	up	up	up	up
MPF_LOC100699307.1.1	XM_003449296.1 PREDICTED: Oreochromis niloticus serine/threonine-protein kinase SIK3 homolog (LOC100699307), mRNA	0,0388	0,0039	down	up	up	up	up	up
MPF_LOC100694934.2.2	XP_003442506.1 PREDICTED: putative N-acetylglucosamine-6-phosphate deacetylase-like [Oreochromis niloticus]	0,0054	0,0000	down	down	up	up	up	up
MPF_LOC100690746.2.2	XM_003448354.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S23-like (LOC100690746), mRNA	0,0476	0,0067	up	up	up	up	up	up
MPF_contig_035190	NA	0,0239	0,0009	down	up	up	up	up	up
MPF_BTNL2.7.7	BTNL2_MOUSE (sp|O70355) Butyrophilin-like protein 2 OS=Mus musculus GN=Btnl2 PE=2 SV=2	0,0290	0,0017	down	up	up	up	up	up
MPF_contig_035224	XM_004568483.1 PREDICTED: Maylandia zebra copine-3-like (LOC101469901), transcript variant X1, mRNA	0,0460	0,0060	down	down	down	up	down	down
MPF_LOC101468521.1.1	XM_004563278.1 PREDICTED: Maylandia zebra serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform-like (LOC101468521), mRNA	0,0171	0,0003	down	up	up	up	up	up
MPF_contig_035284	NA	0,0266	0,0012	down	up	down	up	down	down

MPF_RL15.5.6	RL15_PARDA (sp|Q7T3N3) 60S ribosomal protein L15 OS=Paramisgurnus dabryanus GN=rpl15 PE=2 SV=3	0,0380	0,0037	down	down	up	down	up	up
MPF_LOC100700732.1.1	XM_003444889.1 PREDICTED: Oreochromis niloticus WAP four-disulfide core domain protein 3-like (LOC100700732), mRNA	0,0248	0,0010	down	down	down	up	down	down
MPF_contig_035389	XM_003441012.1 PREDICTED: Oreochromis niloticus proactivator polypeptide-like, transcript variant 1 (LOC100689911), mRNA	0,0277	0,0014	down	up	up	up	up	up
MPF_LOC101467757.2.2	XM_004546448.1 PREDICTED: Maylandia zebra cytosolic sulfotransferase 3-like (LOC101467757), mRNA	0,0148	0,0002	up	up	up	up	up	up
MPF_contig_035410	XM_004556101.1 PREDICTED: Maylandia zebra transforming acidic coiled-coil-containing protein 2-like (LOC101481661), transcript variant X15, mRNA	0,0389	0,0039	down	up	up	up	up	up
MPF_contig_035424	NA	0,0253	0,0011	down	down	down	up	down	down
MPF_MIR24-5.1.1	NR_048933.1 Danio rerio microRNA mir-24-5 (mir24-5), microRNA	0,0041	0,0000	down	down	down	down	down	down
MPF_LOC101471083.3.3	XM_004575129.1 PREDICTED: Maylandia zebra mucin-2-like (LOC101471083), mRNA	0,0255	0,0011	up	up	up	down	up	up
MPF_contig_035510	NA	0,0173	0,0004	down	down	up	up	up	up
MPF_LOC100711469.1.2	XM_003445853.1 PREDICTED: Oreochromis niloticus beta-synuclein-like (LOC100711469), mRNA	0,0224	0,0007	down	down	up	down	up	up
MPF_LOC101486107.1.1	XM_004550367.1 PREDICTED: Maylandia zebra AF4/FMR2 family member 4-like (LOC101486107), transcript variant X1, mRNA	0,0136	0,0001	down	up	up	up	up	up
MPF_contig_035547	NA	0,0199	0,0005	down	down	down	down	down	down
MPF_HMGA1B.5.6	NM_001077276.1 Danio rerio high mobility group AT-hook 1b (hmga1b), mRNA	0,0091	0,0000	up	up	up	up	up	up
MPF_LOC101486255.2.2	XM_004540470.1 PREDICTED: Maylandia zebra mitochondrial fission regulator 1-like (LOC101486255), mRNA	0,0270	0,0013	down	up	up	up	up	up
MPF_contig_035601	NA	0,0341	0,0026	up	up	up	down	up	up
MPF_LOC100703335.1.1	XP_003444612.1 PREDICTED: death ligand signal enhancer-like [Oreochromis niloticus]	0,0383	0,0038	down	up	up	up	up	up
MPF_contig_035629	NA	0,0495	0,0075	down	up	up	up	up	up
MPF_LOC101471595.1.3	XM_004560274.1 PREDICTED: Maylandia zebra tubulin alpha-1A chain-like (LOC101471595), mRNA	0,0239	0,0009	down	up	up	up	up	up
MPF_LOC100707427.4.4	XM_003440083.1 PREDICTED: Oreochromis niloticus AN1-type zinc finger protein 5-like, transcript variant 5 (LOC100707427), mRNA	0,0371	0,0034	down	up	up	up	up	up
MPF_contig_035685	NA	0,0467	0,0063	down	down	up	up	up	up
MPF_LOC101068490.3.3	XP_003971983.1 PREDICTED: C-type lectin domain family 4 member F-like [Takifugu rubripes]	0,0213	0,0006	up	up	up	up	up	up
MPF_contig_035773	XM_004539186.1 PREDICTED: Maylandia zebra tropomodulin-1-like (LOC101483315), transcript variant X1, mRNA	0,0281	0,0015	down	up	up	up	up	up

MPF_LOC100695373.1.1	XM_003440950.1 PREDICTED: Oreochromis niloticus junctional adhesion molecule B-like (LOC100695373), mRNA	0,0341	0,0026	down	down	up	up	up	up
MPF_LOC100712519.4.4	XP_003439047.1 PREDICTED: cytosolic sulfotransferase 3-like [Oreochromis niloticus]	0,0313	0,0020	down	up	down	up	down	down
MPF_LOC101171896.1.1	XP_004086536.1 PREDICTED: polyadenylate-binding protein-interacting protein 2-like [Oryzias latipes]	0,0224	0,0007	down	up	up	up	up	up
MPF_LOC101066707.1.1	XM_003965418.1 PREDICTED: Takifugu rubripes zinc finger FYVE domain-containing protein 16-like (LOC101066707), mRNA	0,0277	0,0014	down	up	up	up	up	up
MPF_LOC101469436.1.3	XM_004543478.1 PREDICTED: Maylandia zebra dmX-like protein 2-like (LOC101469436), transcript variant X3, mRNA	0,0245	0,0010	up	up	up	up	up	up
MPF_LOC100710520.3.3	XM_003451402.1 PREDICTED: Oreochromis niloticus transcription factor 7-like 2-like (LOC100710520), mRNA	0,0429	0,0051	up	up	up	up	up	up
MPF_LOC101485781.3.4	XM_004542132.1 PREDICTED: Maylandia zebra bromo adjacent homology domain-containing 1 proteinlike (LOC101485781), mRNA	0,0341	0,0026	down	down	up	up	up	up
MPF_ZN569.1.1	ZN569_MOUSE (sp|Q80W31) Zinc finger protein 569 OS=Mus musculus GN=Znf569 PE=2 SV=2	0,0314	0,0021	up	up	up	up	up	up
MPF_LOC101467350.2.2	XM_004545794.1 PREDICTED: Maylandia zebra 60S ribosomal protein L36a-like (LOC101467350), transcript variant X2, mRNA	0,0371	0,0034	down	up	up	up	up	up
MPF_LOC100706983.1.11	XP_003460110.1 PREDICTED: 28S ribosomal protein S28, mitochondrial-like [Oreochromis niloticus]	0,0082	0,0000	down	down	down	down	down	down
MPF_LOC101477243.1.1	XM_004544896.1 PREDICTED: Maylandia zebra rho guanine nucleotide exchange factor 25-like (LOC101477243), transcript variant X3, mRNA	0,0143	0,0002	down	down	down	down	down	down
MPF_LOC101480516.1.2	XM_004537976.1 PREDICTED: Maylandia zebra protein phosphatase 1D-like (LOC101480516), mRNA	0,0225	0,0007	down	down	up	down	up	up
MPF_LOC101467994.1.1	XR_191159.1 PREDICTED: Maylandia zebra synaptotagmin-14-like (LOC101467994), transcript variant X3, misc_RNA	0,0438	0,0053	down	down	up	down	up	up
MPF_contig_036057	NA	0,0088	0,0000	down	up	up	up	up	up
MPF_contig_036071	NA	0,0270	0,0013	down	down	up	down	up	up
MPF_LOC101487672.1.1	XM_004557853.1 PREDICTED: Maylandia zebra Fanconi anemia group B protein-like (LOC101487672), mRNA	0,0208	0,0006	up	up	up	up	up	up
MPF_contig_036141	NA	0,0224	0,0007	up	up	up	up	up	up
MPF_LOC100702868.3.3	XM_003439549.1 PREDICTED: Oreochromis niloticus protein FAM169B-like (LOC100702868), mRNA	0,0270	0,0013	up	up	up	up	up	up
MPF_LOC101477159.2.2	XM_004547229.1 PREDICTED: Maylandia zebra mesoderm induction early response protein 3-like (LOC101477159), mRNA	0,0340	0,0026	up	up	up	up	up	up
MPF_LOC101487291.5.6	XM_004560239.1 PREDICTED: Maylandia zebra constitutive coactivator of PPAR-gamma-like protein 2like (LOC101487291), mRNA	0,0080	0,0000	down	up	up	up	up	up
MPF_LOC101479263.1.1	XM_004559378.1 PREDICTED: Maylandia zebra coronin-7-like (LOC101479263), mRNA	0,0388	0,0039	down	up	up	up	up	up
MPF_LOC101479551.1.1	XM_004555792.1 PREDICTED: Maylandia zebra SEC14-like protein 2-like (LOC101479551), mRNA	0,0371	0,0035	up	down	down	down	down	down

MPF_LOC101475578.1.1	XM_004555860.1 PREDICTED: Maylandia zebra RRP12-like protein-like (LOC101475578), transcript variant X1, mRNA	0,0418	0,0047	up	up	up	up	up	up
MPF_LOC101475225.1.1	XM_004546564.1 PREDICTED: Maylandia zebra protein phosphatase 1 regulatory subunit 16A-like (LOC101475225), mRNA	0,0213	0,0006	down	up	up	up	up	up
MPF_LOC101465079.2.2	XM_004551108.1 PREDICTED: Maylandia zebra basal cell adhesion molecule-like (LOC101465079), mRNA	0,0208	0,0005	down	down	down	down	down	down
MPF_LOC101468827.1.1	XM_004538856.1 PREDICTED: Maylandia zebra sodium channel and clathrin linker 1-like (LOC101468827), transcript variant X2, mRNA	0,0494	0,0075	down	up	up	up	up	up
MPF_LOC101464198.1.1	XM_004546987.1 PREDICTED: Maylandia zebra polyadenylate-binding protein-interacting protein 1-like (LOC101464198), mRNA	0,0324	0,0022	down	down	up	up	up	up
MPF_LOC101480954.1.2	XM_004572806.1 PREDICTED: Maylandia zebra versican core protein-like (LOC101480954), mRNA	0,0418	0,0047	down	down	up	up	up	up
MPF_LOC101463853.1.1	XM_004558959.1 PREDICTED: Maylandia zebra tRNA-splicing endonuclease subunit Sen2-like (LOC101463853), mRNA	0,0244	0,0010	up	up	up	up	up	up
MPF_contig_036406	NA	0,0219	0,0007	down	up	up	up	up	up
MPF_LOC101466761.1.1	XM_004564446.1 PREDICTED: Maylandia zebra transmembrane and TPR repeat-containing protein 3like (LOC101466761), transcript variant X2, mRNA	0,0424	0,0049	down	down	up	up	up	up

MPF_LOC101475504.1.1	XM_004544142.1 PREDICTED: Maylandia zebra solute carrier family 15 member 4-like (LOC101475504), mRNA	0,0431	0,0051	down	down	up	down	up	up
MPF_LOC101481869.1.9	XM_004538815.1 PREDICTED: Maylandia zebra mastermind-like protein 3-like (LOC101481869), mRNA	0,0352	0,0028	down	down	up	up	up	up
MPF_LOC101468652.1.1	XM_004547381.1 PREDICTED: Maylandia zebra POU domain, class 4, transcription factor 2-like (LOC101468652), mRNA	0,0488	0,0072	up	up	down	up	down	down
MPF_LOC101158949.1.1	XR_177430.1 PREDICTED: Oryzias latipes ubinuclein-2-like (LOC101158949), misc_RNA	0,0134	0,0001	down	down	up	up	up	up
MPF_LOC100709144.1.1	XM_003441930.1 PREDICTED: Oreochromis niloticus DNA cross-link repair 1A protein-like (LOC100709144), mRNA	0,0418	0,0047	up	up	up	up	up	up
MPF_CP250.2.2	CP250_MOUSE (sp|Q60952) Centrosome-associated protein CEP250 OS=Mus musculus GN=Cep250 PE=1 SV=4	0,0352	0,0028	down	up	up	up	up	up
MPF_contig_036677	XM_004573888.1 PREDICTED: Maylandia zebra c-Maf-inducing protein-like (LOC101478585), transcript variant X3, mRNA	0,0371	0,0034	up	up	up	up	up	up
MPF_contig_036695	NA	0,0150	0,0002	down	up	up	up	up	up
MPF_contig_036703	NA	0,0343	0,0026	up	up	up	up	up	up
MPF_SYJ2B.1.1	[BBH] SYJ2B_BOVIN (sp|Q3T0C9) Synaptojanin-2-binding protein OS=Bos taurus GN=SYNJ2BP PE=2 SV=1	0,0400	0,0042	down	up	up	up	up	up

MPF_LOC100703705.11.14	XM_003444236.1 PREDICTED: Oreochromis niloticus tumor necrosis factor receptor superfamily member 14-like (LOC100703705), mRNA	0,0339	0,0025	up	up	up	up	up	up
MPF_contig_036796	NA	0,0144	0,0002	up	up	up	up	up	up
MPF_LOC100710676.1.1	XP_003448392.1 PREDICTED: green-sensitive opsin-like [Oreochromis niloticus]	0,0232	0,0008	down	down	down	down	down	down
MPF_LOC100701403.2.2	XM_003454667.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100701403 (LOC100701403), mRNA	0,0491	0,0073	down	up	up	up	up	up
MPF_contig_036894	NA	0,0267	0,0012	up	up	up	up	up	up
MPF_LOC101487548.1.1	XM_004574179.1 PREDICTED: Maylandia zebra prostaglandin reductase 1-like (LOC101487548), mRNA	0,0371	0,0034	up	up	up	up	up	up
MPF_LOC101481957.1.1	XR_191362.1 PREDICTED: Maylandia zebra isobutyryl-CoA dehydrogenase, mitochondrial-like (LOC101481957), transcript variant X2, misc_RNA	0,0265	0,0012	up	up	up	up	up	up
MPF_LOC101487373.24.24	XM_004576282.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101487373), mRNA	0,0419	0,0048	down	down	down	down	down	down
MPF_contig_036988	NA	0,0231	0,0008	down	up	up	up	up	up
MPF_LOC101471364.1.1	XM_004549927.1 PREDICTED: Maylandia zebra tenascin-like (LOC101471364), transcript variant X5, mRNA	0,0228	0,0008	down	down	down	down	down	down
MPF_contig_037024	NA	0,0373	0,0035	down	up	up	up	up	up
MPF_LOC100710874.10.12	XP_003453997.1 PREDICTED: hypothetical protein LOC100710874 [Oreochromis niloticus]	0,0148	0,0002	down	down	down	up	down	down
MPF_contig_037084	NA	0,0294	0,0017	down	up	up	up	up	up
MPF_ZN234.2.2	ZN234_HUMAN (sp|Q14588) Zinc finger protein 234 OS=Homo sapiens GN=ZNF234 PE=2 SV=3	0,0432	0,0052	down	up	up	up	up	up
MPF_contig_037105	NA	0,0056	0,0000	up	down	down	down	down	down
MPF_contig_037163	NA	0,0247	0,0010	down	up	up	up	up	up
MPF_ZNF84.11.14	ZNF84_HUMAN (sp|P51523) Zinc finger protein 84 OS=Homo sapiens GN=ZNF84 PE=1 SV=2	0,0383	0,0038	up	up	up	up	up	up
MPF_contig_037214	NA	0,0316	0,0021	up	down	up	down	up	up
MPF_ZO6.4.6	ZO6_XENLA (sp|P18749) Oocyte zinc finger protein XlCOF6 (Fragment) OS=Xenopus laevis PE=3 SV=1	0,0371	0,0035	down	up	up	up	up	up
MPF_contig_037242	NA	0,0449	0,0055	down	down	down	down	down	down
MPF_ZG57.5.12	ZG57_XENLA (sp|P18729) Gastrula zinc finger protein XlCGF57.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0,0356	0,0030	up	up	up	up	up	up
MPF_LOC101468583.5.7	XM_004576296.1 PREDICTED: Maylandia zebra uncharacterized LOC101468583 (LOC101468583), mRNA	0,0130	0,0001	down	down	down	down	down	down
MPF_LOC100701849.2.5	XM_003453196.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100701849 (LOC100701849), mRNA	0,0332	0,0024	up	up	up	down	up	up

MPF_contig_037326	NA	0,0190	0,0004	down	up	up	up	up	up
MPF_contig_037327	NA	0,0371	0,0035	up	down	up	down	up	up
MPF_TCNA.2.4	TCNA_TRYCR (sp|P23253) Sialidase OS=Trypanosoma cruzi GN=TCNA PE=2 SV=1	0,0241	0,0009	up	down	up	down	up	up
MPF_LOC101481680.1.1	XR_191422.1 PREDICTED: Maylandia zebra uncharacterized LOC101481680 (LOC101481680), misc_RNA	0,0150	0,0002	down	down	down	up	down	down
MPF_contig_037377	NA	0,0419	0,0048	down	down	up	up	up	up
MPF_LOC101478994.1.1	XM_004537971.1 PREDICTED: Maylandia zebra fatty aldehyde dehydrogenase-like (LOC101478994), transcript variant X2, mRNA	0,0290	0,0017	down	up	up	up	up	up

MPF_ZNF84.13.14	ZNF84_HUMAN (sp|P51523) Zinc finger protein 84 OS=Homo sapiens GN=ZNF84 PE=1 SV=2	0,0401	0,0042	up	up	up	up	up	up
MPF_contig_037429	NA	0,0107	0,0001	up	up	down	down	down	down
MPF_ZN235.8.9	ZN235_HUMAN (sp|Q14590) Zinc finger protein 235 OS=Homo sapiens GN=ZNF235 PE=2 SV=3	0,0231	0,0008	up	up	up	up	up	up
MPF_LOC100693572.1.1	XM_003457590.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100693572 (LOC100693572), mRNA	0,0241	0,0009	down	up	up	up	up	up
MPF_LOC101170497.1.8	XP_004086004.1 PREDICTED: oocyte zinc finger protein XlCOF6-like [Oryzias latipes]	0,0366	0,0032	up	up	up	up	up	up
MPF_ZG20.1.1	ZG20_XENLA (sp|P18714) Gastrula zinc finger protein xFG20-1 OS=Xenopus laevis PE=3 SV=2	0,0421	0,0048	up	up	up	up	up	up
MPF_contig_037472	NA	0,0244	0,0010	down	up	up	up	up	up
MPF_ZNF22.1.1	ZNF22_PONAB (sp|Q5R4X5) Zinc finger protein 22 OS=Pongo abelii GN=ZNF22 PE=2 SV=1	0,0357	0,0030	up	up	up	up	up	up
MPF_LOC101170275.1.4	XM_004072328.1 PREDICTED: Oryzias latipes uncharacterized LOC101170275 (LOC101170275), mRNA	0,0256	0,0011	down	up	up	up	up	up
MPF_LOC100535956.1.1	XP_003198038.1 PREDICTED: hypothetical protein LOC100535956 [Danio rerio]	0,0367	0,0033	down	down	down	down	down	down
MPF_LOC101076349.1.1	XP_003966922.1 PREDICTED: LOW QUALITY PROTEIN: dysferlin-like [Takifugu rubripes]	0,0362	0,0031	up	up	up	up	up	up
MPF_LOC101484170.2.2	XM_004563148.1 PREDICTED: Maylandia zebra iduronate 2-sulfatase-like (LOC101484170), transcript variant X2, mRNA	0,0171	0,0003	up	up	up	up	up	up
MPF_LOC101464118.1.2	XM_004548946.1 PREDICTED: Maylandia zebra sterile alpha motif domain-containing protein 12-like (LOC101464118), transcript variant X2, mRNA	0,0451	0,0056	up	down	up	down	up	up
MPF_contig_037593	NA	0,0354	0,0029	down	up	up	up	up	up
MPF_contig_037633	NA	0,0293	0,0017	down	up	up	up	up	up
MPF_LOC100691506.16.16	XM_003460016.1 PREDICTED: Oreochromis niloticus zinc finger protein RFP-like (LOC100691506), mRNA	0,0160	0,0003	up	up	up	down	up	up
MPF_PHUM_PHUM529360.2	XP_002431439.1 ngd5/osm-6/ift52, putative [Pediculus humanus corporis]	0,0080	0,0000	down	down	down	down	down	down

MPF_PDZD8.1.1	XM_003454989.1 PREDICTED: Oreochromis niloticus PDZ domain containing 8 (PDZD8), mRNA	0,0364	0,0032 up	up	up	down	up	up
MPF_contig_037711	NA	0,0411	0,0045 down	up	up	up	up	up
MPF_LOC100695994.29.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0,0411	0,0045 up	up	up	down	up	up
MPF_CRE_07824.1.1	XP_003093184.1 hypothetical protein CRE_07824 [Caenorhabditis remanei]	0,0047	0,0000 down	down	down	down	down	down
MPF_LOC100119490.1.1	XP_001603259.2 PREDICTED: hypothetical protein LOC100119490 [Nasonia vitripennis]	0,0243	0,0010 down	down	down	up	down	down
MPF_NEMVEDRAFT_V1G24	XP_001627323.1 predicted protein [Nematostella vectensis]	0,0336	0,0025 down	up	up	up	up	up
MPF_contig_037771	NA	0,0253	0,0011 down	down	down	down	down	down
MPF_LOC101473738.1.2	XM_004538235.1 PREDICTED: Maylandia zebra matrix metalloproteinase-17-like (LOC101473738), mRNA	0,0402	0,0042 down	down	up	down	up	up
MPF_LOC100707133.10.12	XP_003457606.1 PREDICTED: hypothetical protein LOC100707133 [Oreochromis niloticus]	0,0094	0,0000 up	up	down	down	down	down
MPF_LOC100706947.1.1	XP_003452194.1 PREDICTED: proteasome-associated protein ECM29 homolog [Oreochromis niloticus]	0,0342	0,0026 down	up	up	up	up	up
MPF_CYYR1.3.19	NM_212882.1 Danio rerio cysteine and tyrosine-rich protein 1 (cyyr1), mRNA gb|BC066606.1| Danio rerio cysteine and tyrosine-rich protein 1, mRNA (cDNA clone MGC:77252 IMAGE:6963826), complete cds	0,0307	0,0019 up	up	up	up	up	up
MPF_LOC100695994.30.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0,0364	0,0032 down	up	up	up	up	up
MPF_ABLIM1A.5.5	NM_001114316.1 Danio rerio actin binding LIM protein 1a (ablim1a), mRNA gb|BC155652.1| Danio rerio zgc:172321, mRNA (cDNA clone MGC:172321 IMAGE:7043511), complete cds	0,0060	0,0000 down	up	up	up	up	up
MPF_LOC100618223.1.2	XP_003340934.1 PREDICTED: zinc finger protein 879-like [Monodelphis domestica]	0,0476	0,0067 up	up	up	up	up	up
MPF_contig_037860	NA	0,0329	0,0023 down	down	up	up	up	up
MPF_LOC101161026.1.1	XP_004084769.1 PREDICTED: oocyte zinc finger protein XlCOF8.4-like [Oryzias latipes]	0,0369	0,0033 up	up	up	up	up	up
MPF_contig_037880	NA	0,0265	0,0012 up	up	up	up	up	up
MPF_LOC101168923.4.7	XP_004085899.1 PREDICTED: oocyte zinc finger protein XlCOF22-like, partial [Oryzias latipes]	0,0397	0,0041 up	up	up	up	up	up
MPF_LOC100701582.9.9	XP_003455288.1 PREDICTED: zinc finger protein 236-like [Oreochromis niloticus]	0,0445	0,0055 down	up	up	up	up	up
MPF_contig_037930	NA	0,0351	0,0028 down	up	up	up	up	up
MPF_LOC100535897.1.1	XP_003198487.1 PREDICTED: zinc finger protein 729-like [Danio rerio]	0,0456	0,0058 down	up	up	up	up	up
MPF_LOC101483898.1.1	XM_004563146.1 PREDICTED: Maylandia zebra fragile X mental retardation protein 1-like (LOC101483898), mRNA	0,0262	0,0012 up	up	up	up	up	up
MPF_contig_037988	NA	0,0219	0,0006 down	up	up	up	up	up
MPF_LOC101475506.1.2	XM_004544241.1 PREDICTED: Maylandia zebra dihydropyrimidinase-related protein 2-like (LOC101475506), transcript variant X2, mRNA	0,0351	0,0028 up	up	up	up	up	up
MPF_LOC101167345.3.32	XM_004066051.1 PREDICTED: Oryzias latipes IQ domain-containing protein E-like (LOC101167345), mRNA	0,0454	0,0057 up	up	up	up	up	up

MPF_contig_038033	NA	0,0494	0,0075	down	up	up	up	up	up
MPF_contig_038087	XM_004542400.1 PREDICTED: Maylandia zebra microtubule-associated serine/threonine-protein kinase 3-like (LOC101482573), transcript variant X5, mRNA	0,0316	0,0021	up	down	up	down	up	up
MPF_contig_038107	XM_004542238.1 PREDICTED: Maylandia zebra neurexin-3b-like (LOC101486071), transcript variant X2, mRNA	0,0474	0,0066	up	down	up	down	up	up
MPF_contig_038161	NA	0,0472	0,0064	down	down	up	up	up	up
MPF_LOC100712339.1.2	XP_003460124.1 PREDICTED: protein JTB-like [Oreochromis niloticus]	0,0066	0,0000	up	up	up	up	up	up
MPF_LOC100692340.3.3	XM_003443685.1 PREDICTED: Oreochromis niloticus FXYD domain-containing ion transport regulator 3-like (LOC100692340), mRNA	0,0469	0,0063	down	down	down	down	down	down
MPF_LOC101066134.1.1	XP_003970138.1 PREDICTED: magnesium transporter protein 1-like [Takifugu rubripes]	0,0358	0,0030	down	down	down	down	down	down
MPF_SI_DKEY-65L23.2.1.1	NP_001093522.1 uncharacterized protein LOC793688 [Danio rerio] ref|XP_001923659.2| PREDICTED: hypothetical protein LOC100150789 [Danio rerio] ref|XP_001922919.2| PREDICTED: hypothetical protein LOC100150626 [Danio rerio]	0,0150	0,0002	down	up	up	up	up	up
MPF_LOC100695237.1.1	XR_134862.1 PREDICTED: Oreochromis niloticus UPF0765 protein C10orf58 homolog (LOC100695237), miscRNA	0,0153	0,0002	up	up	up	up	up	up
MPF_LOC100696870.1.2	XM_003442549.1 PREDICTED: Oreochromis niloticus WAS/WASL-interacting protein family member 2like (LOC100696870), mRNA	0,0330	0,0023	down	down	up	up	up	up
MPF_LOC101475582.1.2	XM_004558092.1 PREDICTED: Maylandia zebra mediator of RNA polymerase II transcription subunit 13-like (LOC101475582), mRNA	0,0327	0,0023	up	up	up	up	up	up
MPF_LOC100697286.1.1	XP_003455106.1 PREDICTED: phosphatidylinositol-binding clathrin assembly protein-like [Oreochromis niloticus]	0,0411	0,0045	up	down	up	down	up	up
MPF_LOC101079843.1.1	XM_003972061.1 PREDICTED: Takifugu rubripes coiled-coil and C2 domain-containing protein 1A-like (LOC101079843), mRNA	0,0160	0,0003	up	up	up	up	up	up
MPF_LOC101474004.1.1	XM_004550968.1 PREDICTED: Maylandia zebra replication protein A 32 kDa subunit-like (LOC101474004), transcript variant X2, mRNA	0,0101	0,0001	down	down	up	down	up	up
MPF_contig_038643	NA	0,0402	0,0042	down	up	up	up	up	up
MPF_LOC101480805.1.1	XM_004560594.1 PREDICTED: Maylandia zebra spartin-like (LOC101480805), transcript variant X2, mRNA	0,0089	0,0000	up	up	up	up	up	up
MPF_contig_003862	NA	0,0366	0,0032	down	down	up	up	up	up
MPF_LOC101484034.2.2	XM_004548471.1 PREDICTED: Maylandia zebra protein phosphatase 1 regulatory subunit 12A-like (LOC101484034), mRNA	0,0371	0,0035	up	up	up	up	up	up
MPF_COLI.1.1	COLI_THUOB (sp|Q9YGK2) Pro-opiomelanocortin OS=Thunnus obesus GN=pomc PE=2 SV=1	0,0195	0,0005	down	down	up	up	up	up
MPF_contig_038752	NA	0,0272	0,0014	down	down	up	down	up	up

MPF_LOC101154918.1.1	XM_004084703.1 PREDICTED: Oryzias latipes solute carrier family 2, facilitated glucose transporter member 11-like (LOC101154918), mRNA	0,0333	0,0024	up	up	up	down	up	up
MPF_LOC101477046.2.4	XM_004565575.1 PREDICTED: Maylandia zebra inhibin beta B chain-like (LOC101477046), mRNA	0,0247	0,0010	down	down	up	up	up	up
MPF_contig_038777	NA	0,0366	0,0032	down	up	up	up	up	up
MPF_contig_038789	NA	0,0213	0,0006	down	down	up	up	up	up
MPF_LOC101477600.1.1	XM_004540339.1 PREDICTED: Maylandia zebra phospholipase B1, membrane-associated-like (LOC101477600), mRNA	0,0112	0,0001	up	up	up	up	up	up
MPF_contig_003872	NA	0,0429	0,0051	down	down	up	down	up	up
MPF_LOC101473952.2.2	XM_004564949.1 PREDICTED: Maylandia zebra transportin-3-like (LOC101473952), mRNA	0,0483	0,0070	down	down	up	down	up	up
MPF_LOC101465583.6.7	XM_004562463.1 PREDICTED: Maylandia zebra histone H3.3-like (LOC101465583), mRNA	0,0353	0,0029	up	up	up	up	up	up
MPF_contig_038936	XM_004550255.1 PREDICTED: Maylandia zebra transcription elongation regulator 1-like (LOC101483186), transcript variant X1, mRNA	0,0371	0,0034	down	up	up	up	up	up
MPF_contig_038961	NA	0,0239	0,0009	down	up	up	up	up	up
MPF_LOC100707133.1.12	XP_003457606.1 PREDICTED: hypothetical protein LOC100707133 [Oreochromis niloticus]	0,0242	0,0009	down	down	down	up	down	down
MPF_contig_039068	NA	0,0485	0,0071	up	up	up	up	up	up
MPF_contig_039074	XM_004553126.1 PREDICTED: Maylandia zebra 40S ribosomal protein S27-like (LOC101477750), transcript variant X1, mRNA	0,0446	0,0055	up	up	up	up	up	up
MPF_contig_039110	NA	0,0247	0,0010	down	up	up	up	up	up
MPF_LOC101465495.1.1	XM_004538576.1 PREDICTED: Maylandia zebra lysine-specific demethylase 2B-like (LOC101465495), mRNA	0,0256	0,0011	up	up	up	up	up	up
MPF_DDC.1.5	NM_213342.1 Danio rerio dopa decarboxylase (ddc), mRNA gb|BC056292.1| Danio rerio dopa decarboxylase, mRNA (cDNA clone MGC:65801 IMAGE:6791927), complete cds	0,0446	0,0055	down	up	up	up	up	up
MPF_LOC101486252.1.1	XM_004563697.1 PREDICTED: Maylandia zebra PQ-loop repeat-containing protein 1-like (LOC101486252), transcript variant X2, mRNA	0,0247	0,0010	up	up	up	down	up	up
MPF_LOC101074351.1.1	XP_003968494.1 PREDICTED: double-strand break repair protein MRE11A-like [Takifugu rubripes]	0,0176	0,0004	up	up	up	up	up	up
MPF_LOC100707328.3.3	XM_003459711.1 PREDICTED: Oreochromis niloticus splicing factor 1-like, transcript variant 1 (LOC100707328), mRNA	0,0434	0,0052	down	up	up	up	up	up
MPF_HMGA1B.1.6	NM_001077276.1 Danio rerio high mobility group AT-hook 1b (hmga1b), mRNA	0,0277	0,0014	up	up	up	up	up	up
13MPF_LOC101466738.2.3	XM_004556678.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein subunit alpha-like (LOC101466738), mRNA	0,0406	0,0044	down	up	up	up	up	up
MPF_LOC101157961.1.1	XP_004075439.1 PREDICTED: 39S ribosomal protein L28, mitochondrial-like [Oryzias latipes]	0,0494	0,0075	up	up	up	up	up	up

MPF_contig_003919	NA	0,0160	0,0003	down	up	up	up	up	up
MPF_LOC100709648.13.13	XM_003457730.1 PREDICTED: Oreochromis niloticus 40S ribosomal protein S4-like (LOC100709648), mRNA	0,0371	0,0035	up	up	up	down	up	up
MPF_LOC101469156.2.2	XM_004568928.1 PREDICTED: Maylandia zebra zinc finger CCHC domain-containing protein 2-like (LOC101469156), mRNA	0,0472	0,0065	up	up	up	up	up	up
MPF_contig_039397	NA	0,0220	0,0007	down	down	down	down	down	down
MPF_LOC101463842.1.1	XM_004554815.1 PREDICTED: Maylandia zebra rab3 GTPase-activating protein non-catalytic subunitlike (LOC101463842), transcript variant X3, mRNA	0,0401	0,0042	down	up	up	up	up	up
MPF_LOC100534480.2.2	XM_003447448.1 PREDICTED: Oreochromis niloticus inducible cAMP early repressor (LOC100534480), mRNA	0,0267	0,0012	down	down	down	down	down	down
MPF_LOC101484751.1.1	XM_004545027.1 PREDICTED: Maylandia zebra natural resistance-associated macrophage protein 2like (LOC101484751), transcript variant X5, mRNA	0,0265	0,0012	up	up	up	up	up	up
MPF_KIF18A.1.1	XM_003445746.1 PREDICTED: Oreochromis niloticus kinesin family member 18A (KIF18A), mRNA	0,0289	0,0016	up	up	up	up	up	up
MPF_LOC101484486.1.1	XM_004571906.1 PREDICTED: Maylandia zebra protein FAM83D-like (LOC101484486), mRNA	0,0421	0,0049	up	up	up	up	up	up
MPF_contig_039525	NA	0,0430	0,0051	down	down	up	down	up	up
MPF_LOC101482508.1.1	XM_004547905.1 PREDICTED: Maylandia zebra calcium-binding mitochondrial carrier protein Aralar2like (LOC101482508), transcript variant X1, mRNA	0,0384	0,0038	down	down	up	up	up	up
MPF_LOC101474085.1.2	XM_004568504.1 PREDICTED: Maylandia zebra cyclin-Y-like (LOC101474085), transcript variant X4, mRNA	0,0267	0,0012	down	up	up	up	up	up
MPF_LOC100692770.1.1	XM_003459224.1 PREDICTED: Oreochromis niloticus PHD finger protein 12-like (LOC100692770), mRNA	0,0415	0,0046	down	up	up	up	up	up
MPF_contig_039665	XM_004573329.1 PREDICTED: Maylandia zebra poliovirus receptor-related protein 3-like (LOC101479710), transcript variant X1, mRNA	0,0429	0,0051	up	up	up	up	up	up
MPF_contig_003959	NA	0,0486	0,0072	down	up	up	up	up	up
MPF_LOC101482951.1.1	XM_004540645.1 PREDICTED: Maylandia zebra protein FAM161B-like (LOC101482951), mRNA	0,0380	0,0037	down	up	up	up	up	up
MPF_LOC101467816.1.1	XM_004562471.1 PREDICTED: Maylandia zebra mitochondrial Rho GTPase 2-like (LOC101467816), mRNA	0,0380	0,0037	up	up	up	up	up	up
MPF_contig_003963	XM_004541039.1 PREDICTED: Maylandia zebra clathrin light chain B-like (LOC101468249), transcript variant X1, mRNA	0,0114	0,0001	up	up	up	up	up	up
MPF_LOC101067778.1.1	XP_003966965.1 PREDICTED: rho guanine nucleotide exchange factor 15-like [Takifugu rubripes]	0,0333	0,0024	down	down	up	up	up	up
MPF_contig_039806	NA	0,0495	0,0075	down	up	up	up	up	up
MPF_LOC100712032.1.1	XM_003451995.1 PREDICTED: Oreochromis niloticus centrosomal protein of 55 kDa-like (LOC100712032), mRNA	0,0457	0,0059	up	up	up	up	up	up
MPF_LOC101474532.1.1	XM_004564475.1 PREDICTED: Maylandia zebra zinc finger protein 143-like (LOC101474532), transcript variant X2, mRNA	0,0264	0,0012	up	up	up	up	up	up

MPF_LOC101464352.1.1	XM_004538572.1 PREDICTED: Maylandia zebra uncharacterized LOC101464352 (LOC101464352), mRNA	0,0211	0,0006 down	up	up	up	up	up
MPF_LOC101156017.1.1	XP_004072239.1 PREDICTED: prostate stem cell antigen-like [Oryzias latipes]	0,0106	0,0001 down	down	down	down	down	down
MPF_LOC100638560.2.2	XP_003388433.1 PREDICTED: hypothetical protein LOC100638560 [Amphimedon queenslandica]	0,0091	0,0000 down	down	up	up	up	up
MPF_contig_039845	NA	0,0352	0,0028 up	down	up	down	up	up
MPF_LOC100699517.2.2	XP_003456582.1 PREDICTED: hypothetical protein LOC100699517 [Oreochromis niloticus]	0,0230	0,0008 down	up	up	up	up	up
MPF_LOC101168697.1.1	XP_004068278.1 PREDICTED: zinc finger CCCH domain-containing protein 3-like [Oryzias latipes]	0,0270	0,0013 down	up	up	up	up	up
MPF_LOC101469573.1.1	XM_004555762.1 PREDICTED: Maylandia zebra RING finger protein 214-like (LOC101469573), mRNA	0,0311	0,0020 down	up	up	up	up	up

MPF_DCAM.1.3	NM_001165344.1 Salmo salar S-adenosylmethionine decarboxylase proenzyme (dcam), mRNA gb|BT058814.1| Salmo salar clone ssal-rgf-504-333 S-adenosylmethionine decarboxylase proenzyme putative mRNA, complete cds	0,0474	0,0066 down	up	up	up	up	up
MPF_contig_040085	NA	0,0471	0,0064 down	up	up	up	up	up
MPF_LOC101466459.4.29	XM_004554283.1 PREDICTED: Maylandia zebra semaphorin-3G-like (LOC101466459), mRNA	0,0380	0,0037 down	up	up	up	up	up
MPF_LOC101475619.1.1	XM_004568507.1 PREDICTED: Maylandia zebra cullin-2-like (LOC101475619), transcript variant X1, mRNA	0,0467	0,0062 up	down	down	down	down	down
MPF_contig_004006	NA	0,0213	0,0006 down	up	up	up	up	up
MPF_PDPR.1.1	XP_003437743.1 PREDICTED: pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial [Oreochromis niloticus]	0,0403	0,0043 down	down	down	down	down	down
MPF_LOC100371306.1.2	XP_002733578.1 PREDICTED: hypothetical protein [Saccoglossus kowalevskii]	0,0357	0,0030 down	up	up	up	up	up
MPF_SEL1L.1.1	XM_003440777.1 PREDICTED: Oreochromis niloticus sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA	0,0181	0,0004 down	down	up	down	up	up
MPF_LOC100690613.1.1	XP_003458492.1 PREDICTED: CWF19-like protein 1-like [Oreochromis niloticus]	0,0376	0,0036 down	up	up	up	up	up
MPF_LOC101474298.1.1	XM_004551415.1 PREDICTED: Maylandia zebra rhotekin-2-like (LOC101474298), transcript variant X3, mRNA	0,0343	0,0026 up	up	up	up	up	up
MPF_LOC101469586.1.1	XM_004560825.1 PREDICTED: Maylandia zebra striatin-interacting protein 1 homolog (LOC101469586), transcript variant X3, mRNA	0,0301	0,0018 down	up	up	up	up	up
MPF_contig_040282	XM_004570345.1 PREDICTED: Maylandia zebra caskin-1-like (LOC101486956), transcript variant X2, mRNA	0,0097	0,0001 down	down	up	up	up	up
MPF_LOC101467475.1.1	XM_004551483.1 PREDICTED: Maylandia zebra coiled-coil domain-containing protein 6-like (LOC101467475), mRNA	0,0341	0,0026 down	up	up	up	up	up
MPF_LOC100700805.2.2	XM_003440887.1 PREDICTED: Oreochromis niloticus claudin-10-like (LOC100700805), mRNA	0,0098	0,0001 down	up	up	up	up	up

MPF_LOC101475864.1.1	XM_004556346.1 PREDICTED: Maylandia zebra protein FAM83F-like (LOC101475864), mRNA	0,0188	0,0004	up	up	up	up	up	up
MPF_contig_040466	NA	0,0244	0,0010	down	down	up	up	up	up
MPF_contig_004038	NA	0,0253	0,0011	down	down	down	up	down	down
MPF_contig_040515	NA	0,0373	0,0035	down	up	up	up	up	up
MPF_LOC101465938.1.1	XM_004570981.1 PREDICTED: Maylandia zebra ubiA prenyltransferase domain-containing protein 1like (LOC101465938), transcript variant X3, mRNA	0,0379	0,0036	down	up	up	up	up	up
MPF_LOC100705526.1.1	XM_003453520.1 PREDICTED: Oreochromis niloticus glutaredoxin-2, mitochondrial-like, transcript variant 4 (LOC100705526), mRNA	0,0131	0,0001	down	up	up	up	up	up
MPF_LOC101476819.7.7	XM_004576571.1 PREDICTED: Maylandia zebra uncharacterized LOC101476819 (LOC101476819), mRNA	0,0047	0,0000	down	down	down	down	down	down
MPF_LOC101476571.1.3	XM_004540817.1 PREDICTED: Maylandia zebra uncharacterized LOC101476571 (LOC101476571), transcript variant X3, mRNA	0,0476	0,0067	up	up	up	up	up	up
MPF_LOC101473792.1.1	XM_004570822.1 PREDICTED: Maylandia zebra tyrosine-protein phosphatase non-receptor type 5-like (LOC101473792), transcript variant X1, mRNA	0,0365	0,0032	up	up	up	down	up	up
MPF_LOC101075613.2.2	XP_003971057.1 PREDICTED: folliculin-interacting protein 1-like [Takifugu rubripes]	0,0438	0,0053	down	up	up	up	up	up
MPF_SH3GL3B.1.1	NP_956475.2 SH3-domain GRB2-like 3b [Danio rerio]	0,0303	0,0019	down	down	up	up	up	up
MPF_LOC100693187.1.1	XP_003453770.1 PREDICTED: leucine-rich repeat and WD repeat-containing protein 1-like [Oreochromis niloticus]	0,0485	0,0071	down	down	up	up	up	up
MPF_contig_040915	NA	0,0194	0,0005	up	down	down	down	down	down
MPF_LOC101476868.2.2	XM_004568867.1 PREDICTED: Maylandia zebra aryl hydrocarbon receptor nuclear translocator-like protein 2-like (LOC101476868), mRNA	0,0316	0,0021	down	down	down	down	down	down
MPF_LOC100371306.2.2	XP_002733578.1 PREDICTED: hypothetical protein [Saccoglossus kowalevskii]	0,0380	0,0037	down	up	up	up	up	up
MPF_LOC101472829.1.1	XM_004552259.1 PREDICTED: Maylandia zebra max-like protein X-like (LOC101472829), mRNA	0,0277	0,0014	down	up	up	up	up	up
MPF_LOC100700653.1.1	XP_003448440.1 PREDICTED: REM2- and Rab-like small GTPase 1-like [Oreochromis niloticus]	0,0419	0,0048	down	up	up	up	up	up
MPF_contig_004093	NA	0,0265	0,0012	up	up	up	up	up	up
MPF_UBQLN4.2.3	NP_998521.2 ubiquilin-4 [Danio rerio]	0,0333	0,0024	down	up	up	up	up	up
MPF_LOC101484010.1.1	XR_190959.1 PREDICTED: Maylandia zebra homeobox-containing protein 1-like (LOC101484010), transcript variant X6, misc_RNA	0,0428	0,0050	up	up	up	up	up	up
MPF_LOC101485038.1.1	XM_004568542.1 PREDICTED: Maylandia zebra uncharacterized LOC101485038 (LOC101485038), transcript variant X2, mRNA	0,0330	0,0023	up	up	up	up	up	up
MPF_LOC101465015.1.1	XM_004562273.1 PREDICTED: Maylandia zebra MKL/myocardin-like protein 2-like (LOC101465015), transcript variant X4, mRNA	0,0237	0,0009	down	down	down	down	down	down

MPF_LOC101472286.1.1	XM_004541888.1 PREDICTED: Maylandia zebra translation initiation factor eIF-2B subunit delta-like (LOC101472286), mRNA	0,0202	0,0005	up	up	up	up	up	up
MPF_LOC101469119.3.3	XM_004561571.1 PREDICTED: Maylandia zebra cadherin-2-like (LOC101469119), mRNA	0,0065	0,0000	down	up	up	up	up	up
MPF_contig_041220	NA	0,0294	0,0017	down	up	up	up	up	up
MPF_LOC100708246.1.1	XM_003442344.1 PREDICTED: Oreochromis niloticus GPI mannosyltransferase 3-like (LOC100708246), mRNA	0,0333	0,0024	down	up	up	up	up	up
MPF_LOC101077743.1.1	XP_003975039.1 PREDICTED: acetyl-CoA carboxylase 2-like [Takifugu rubripes]	0,0228	0,0008	up	up	up	up	up	up
MPF_LOC101173672.1.1	XM_004084030.1 PREDICTED: Oryzias latipes protein SCO2 homolog, mitochondrial-like (LOC101173672), mRNA	0,0422	0,0049	down	up	up	up	up	up
MPF_STK38.1.1	XP_003454311.1 PREDICTED: serine/threonine-protein kinase 38 [Oreochromis niloticus]	0,0494	0,0075	up	up	up	up	up	up
MPF_contig_004128	NA	0,0127	0,0001	down	down	down	down	down	down
MPF_LOC101158204.2.2	XM_004072523.1 PREDICTED: Oryzias latipes TBC1 domain family member 10A-like (LOC101158204), mRNA	0,0370	0,0033	down	up	up	up	up	up
MPF_LOC101485446.1.1	XM_004550723.1 PREDICTED: Maylandia zebra visinin-like (LOC101485446), mRNA	0,0277	0,0014	down	up	up	up	up	up
MPF_LOC101471500.2.2	XM_004562486.1 PREDICTED: Maylandia zebra telomere length regulation protein TEL2 homolog (LOC101471500), mRNA	0,0481	0,0069	down	up	up	up	up	up
MPF_LOC101483006.1.2	XR_191193.1 PREDICTED: Maylandia zebra unconventional myosin-XVI-like (LOC101483006), transcript variant X4, misc_RNA	0,0499	0,0077	down	up	up	up	up	up
MPF_LOC101474305.1.20	XM_004575475.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101474305), mRNA	0,0174	0,0004	up	up	down	up	down	down
MPF_LOC100690077.1.1	XP_003458490.1 PREDICTED: CCR4-NOT transcription complex subunit 2-like [Oreochromis niloticus]	0,0401	0,0042	down	down	up	up	up	up
MPF_LOC101483137.3.3	XM_004564978.1 PREDICTED: Maylandia zebra WD repeat-containing protein 62-like (LOC101483137), mRNA	0,0228	0,0008	down	up	up	up	up	up
MPF_MMS19.1.1	XM_003438539.1 PREDICTED: Oreochromis niloticus MMS19 nucleotide excision repair homolog (S. cerevisiae) (MMS19), mRNA	0,0208	0,0005	up	up	up	up	up	up
MPF_CC2D2A.1.1	XP_003439826.1 PREDICTED: coiled-coil and C2 domain-containing protein 2A [Oreochromis niloticus]	0,0250	0,0010	up	down	up	down	up	up
MPF_LOC100711371.1.1	XM_003443926.1 PREDICTED: Oreochromis niloticus transmembrane protein 168-like (LOC100711371), mRNA	0,0482	0,0069	down	up	up	up	up	up
MPF_LOC101465834.2.2	XM_004547185.1 PREDICTED: Maylandia zebra UPF0600 protein C5orf51 homolog (LOC101465834), transcript variant X1, mRNA	0,0474	0,0067	up	up	up	down	up	up
MPF_LOC100706983.9.11	XP_003460110.1 PREDICTED: 28S ribosomal protein S28, mitochondrial-like [Oreochromis niloticus]	0,0233	0,0008	down	down	up	up	up	up
MPF_LOC101483661.5.5	XM_004572907.1 PREDICTED: Maylandia zebra traf2 and NCK-interacting protein kinase-like (LOC101483661), transcript variant X1, mRNA	0,0319	0,0021	down	up	up	up	up	up

MPF_LOC100703239.1.1	XP_003440200.1 PREDICTED: hypothetical protein LOC100703239 [Oreochromis niloticus]	0,0089	0,0000 down	down	down	down	down	down
MPF_TASP1.1.2	XM_003441024.1 PREDICTED: Oreochromis niloticus taspase, threonine aspartase, 1 (TASP1), mRNA	0,0277	0,0014 down	down	up	down	up	up
MPF_LOC100695788.1.1	XP_003437652.1 PREDICTED: ribonuclease P protein subunit p29-like [Oreochromis niloticus]	0,0088	0,0000 up	up	up	up	up	up
MPF_LOC101482458.3.3	XM_004559758.1 PREDICTED: Maylandia zebra vitrin-like (LOC101482458), transcript variant X3, mRNA	0,0301	0,0018 down	down	up	up	up	up
MPF_contig_004162	NA	0,0361	0,0031 up	up	up	up	up	up
MPF_LOC100707818.1.1	XP_003447961.1 PREDICTED: signal recognition particle 68 kDa protein-like [Oreochromis niloticus]	0,0351	0,0028 down	up	up	up	up	up
MPF_LOC101485593.1.1	XM_004543054.1 PREDICTED: Maylandia zebra protein FAM65A-like (LOC101485593), transcript variant X2, mRNA	0,0262	0,0012 up	up	up	down	up	up
MPF_LOC100694289.1.1	XP_003437561.1 PREDICTED: gamma-taxilin-like [Oreochromis niloticus]	0,0169	0,0003 down	up	up	up	up	up
MPF_LOC100699374.1.1	XP_003443010.1 PREDICTED: hypothetical protein LOC100699374 [Oreochromis niloticus]	0,0403	0,0043 down	up	up	up	up	up
MPF_contig_041807	NA	0,0326	0,0022 down	up	up	up	up	up
MPF_LOC101465950.3.3	XM_004573375.1 PREDICTED: Maylandia zebra transcription initiation factor TFIID subunit 1-like (LOC101465950), transcript variant X5, mRNA	0,0354	0,0029 up	up	up	up	up	up
MPF_contig_041819	NA	0,0474	0,0067 down	up	up	up	up	up
MPF_LOC101467841.2.2	XM_004567099.1 PREDICTED: Maylandia zebra kin of IRRE-like protein 1-like (LOC101467841), transcript variant X2, mRNA	0,0130	0,0001 down	up	up	up	up	up
MPF_contig_004176	NA	0,0165	0,0003 down	up	up	up	up	up
MPF_LOC101478340.1.2	XM_004540060.1 PREDICTED: Maylandia zebra dual specificity protein phosphatase 23-like (LOC101478340), transcript variant X3, mRNA	0,0424	0,0049 up	up	up	up	up	up

MPF_LOC101478816.1.1	XM_004541641.1 PREDICTED: Maylandia zebra ubiquitin carboxyl-terminal hydrolase 45-like (LOC101478816), transcript variant X1, mRNA	0,0065	0,0000 down	down	down	down	down	down
MPF_LOC101469029.1.2	XM_004540592.1 PREDICTED: Maylandia zebra inositol-tetrakisphosphate 1-kinase-like (LOC101469029), mRNA	0,0248	0,0010 up	up	up	up	up	up
MPF_LOC101467621.8.8	XR_190852.1 PREDICTED: Maylandia zebra uncharacterized LOC101467621 (LOC101467621), misc_RNA	0,0334	0,0024 up	down	down	down	down	down
MPF_LOC101464537.3.3	XM_004563077.1 PREDICTED: Maylandia zebra trinucleotide repeat-containing gene 6B protein-like (LOC101464537), mRNA	0,0472	0,0065 down	up	up	up	up	up
MPF_LOC101467046.1.1	XM_004543467.1 PREDICTED: Maylandia zebra lysM and putative peptidoglycan-binding domaincontaining protein 2-like (LOC101467046), mRNA	0,0270	0,0013 down	up	up	up	up	up
MPF_LOC101078556.1.1	XM_003972456.1 PREDICTED: Takifugu rubripes zinc finger protein 330-like (LOC101078556), mRNA	0,0208	0,0005 down	up	up	up	up	up

MPF_contig_041939	NA	0,0474	0,0066	down	down	up	up	up	up
MPF_THAP9.1.1	[BBH] THAP9_HUMAN (sp|Q9H5L6) DNA transposase THAP9 OS=Homo sapiens GN=THAP9 PE=1 SV=2	0,0134	0,0001	down	down	down	down	down	down
MPF_LOC101486762.1.1	XM_004570077.1 PREDICTED: Maylandia zebra polyribonucleotide nucleotidyltransferase 1, mitochondrial-like (LOC101486762), mRNA	0,0333	0,0024	up	up	up	up	up	up
MPF_LOC101480445.3.3	XM_004543133.1 PREDICTED: Maylandia zebra nuclear factor of activated T-cells 5-like (LOC101480445), transcript variant X2, mRNA	0,0387	0,0038	down	up	up	up	up	up
MPF_LOC101161574.12.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0,0065	0,0000	down	down	down	down	down	down
MPF_LOC100712300.2.2	XP_003452130.1 PREDICTED: sister chromatid cohesion protein DCC1-like [Oreochromis niloticus]	0,0174	0,0004	up	up	up	up	up	up
MPF_LOC100691609.1.1	XP_003441572.1 PREDICTED: guanine nucleotide-binding protein-like 3-like [Oreochromis niloticus]	0,0277	0,0014	down	down	up	down	up	up
MPF_LOC101165259.2.2	XP_004079413.1 PREDICTED: desmoglein-2-like [Oryzias latipes]	0,0334	0,0024	up	down	down	down	down	down
MPF_LOC101471012.1.1	XM_004556045.1 PREDICTED: Maylandia zebra golgin subfamily A member 4-like (LOC101471012), transcript variant X2, mRNA	0,0187	0,0004	down	up	up	up	up	up
MPF_LOC101477689.1.1	XM_004564033.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily C member 18-like (LOC101477689), mRNA	0,0353	0,0029	up	up	up	up	up	up
MPF_LOC101170688.1.2	XP_004073787.1 PREDICTED: protein AF1q-like [Oryzias latipes]	0,0386	0,0038	up	up	up	up	up	up
MPF_LOC100700758.2.2	XP_003451835.1 PREDICTED: hypothetical protein LOC100700758 [Oreochromis niloticus]	0,0358	0,0030	down	up	up	up	up	up
MPF_LOC101469089.8.8	XM_004575775.1 PREDICTED: Maylandia zebra ubiquitin-40S ribosomal protein S27a-like (LOC101469089), mRNA	0,0080	0,0000	down	up	up	up	up	up
MPF_LOC101465348.1.6	XM_004570620.1 PREDICTED: Maylandia zebra protein ZNF365-like (LOC101465348), transcript variant X2, mRNA	0,0267	0,0012	up	up	up	up	up	up
MPF_LOC101472907.1.4	XM_004570821.1 PREDICTED: Maylandia zebra oxysterol-binding protein-related protein 5-like (LOC101472907), transcript variant X4, mRNA	0,0253	0,0011	up	up	up	up	up	up
MPF_LOC101469409.1.1	XM_004561191.1 PREDICTED: Maylandia zebra phospholysine phosphohistidine inorganic pyrophosphate phosphatase-like (LOC101469409), mRNA	0,0362	0,0031	down	up	up	up	up	up
MPF_LOC100697077.1.1	XP_003449585.1 PREDICTED: leishmanolysin-like peptidase-like [Oreochromis niloticus]	0,0256	0,0011	up	up	up	up	up	up
MPF_LOC100694722.1.1	XP_003456565.1 PREDICTED: aftiphilin-like [Oreochromis niloticus]	0,0492	0,0074	down	up	up	up	up	up
MPF_LOC100692146.1.1	XP_003441574.1 PREDICTED: serine/threonine-protein kinase SRPK1-like [Oreochromis niloticus]	0,0472	0,0065	down	up	up	up	up	up
MPF_MMP2.1.1	XM_003437534.1 PREDICTED: Oreochromis niloticus matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) (MMP2), mRNA	0,0342	0,0026	up	down	up	down	up	up
MPF_LOC100689949.1.1	XP_003452304.1 PREDICTED: ELMO domain-containing protein 2-like [Oreochromis niloticus]	0,0494	0,0074	down	down	up	down	up	up
MPF_LOC100696496.1.2	XM_003458306.1 PREDICTED: Oreochromis niloticus nucleolar protein 11-like (LOC100696496), mRNA	0,0317	0,0021	down	up	up	up	up	up

MPF_contig_042600	XM_004567440.1 PREDICTED: Maylandia zebra myb/SANT-like DNA-binding domain-containing protein 2-like (LOC101484373), transcript variant X1, mRNA	0,0485	0,0070	up	down	up	down	up	up
MPF_contig_042609	NA	0,0317	0,0021	up	up	up	up	up	up
MPF_LOC100689954.1.2	XM_003453546.1 PREDICTED: Oreochromis niloticus carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase protein-like (LOC100689954), mRNA	0,0172	0,0003	up	up	up	up	up	up
MPF_FRIM.1.1	FRIM_SALSA (sp|P49947) Ferritin, middle subunit OS=Salmo salar PE=2 SV=1	0,0290	0,0017	up	up	up	up	up	up
MPF_contig_042660	NA	0,0150	0,0002	down	up	up	up	up	up
MPF_LOC101480885.1.1	XM_004553596.1 PREDICTED: Maylandia zebra probable E3 SUMO-protein ligase RNF212-like (LOC101480885), transcript variant X2, mRNA	0,0477	0,0067	up	up	up	up	up	up
MPF_CYYR1.18.19	NM_212882.1 Danio rerio cysteine and tyrosine-rich protein 1 (cyyr1), mRNA gb|BC066606.1| Danio rerio cysteine and tyrosine-rich protein 1, mRNA (cDNA clone MGC:77252 IMAGE:6963826), complete cds	0,0270	0,0013	up	up	up	up	up	up
MPF_contig_042705	NA	0,0150	0,0002	down	down	up	up	up	up
MPF_contig_042733	NA	0,0449	0,0056	up	up	up	down	up	up
MPF_LOC100699407.3.3	XM_003451114.1 PREDICTED: Oreochromis niloticus stress-associated endoplasmic reticulum protein 1-like (LOC100699407), mRNA	0,0333	0,0024	down	down	up	down	up	up
MPF_LOC101471611.1.1	XM_004564014.1 PREDICTED: Maylandia zebra serine/arginine repetitive matrix protein 2-like (LOC101471611), transcript variant X2, mRNA	0,0283	0,0015	down	up	up	up	up	up
MPF_contig_042780	NA	0,0154	0,0002	up	up	up	up	up	up
MPF_LOC101473258.1.1	XM_004556246.1 PREDICTED: Maylandia zebra craniofacial development protein 1-like (LOC101473258), mRNA	0,0460	0,0060	down	down	up	up	up	up
MPF_NEMVEDRAFT_V1G19	XP_001639047.1 predicted protein [Nematostella vectensis]	0,0224	0,0007	down	down	up	up	up	up
MPF_LOC101479984.2.3	XM_004548360.1 PREDICTED: Maylandia zebra G1/S-specific cyclin-D2-like (LOC101479984), transcript variant X2, mRNA	0,0333	0,0024	up	up	up	up	up	up
MPF_LOC100707931.1.1	XM_003454934.1 PREDICTED: Oreochromis niloticus myosin-XV-like (LOC100707931), mRNA	0,0292	0,0017	up	up	up	up	up	up
MPF_KCTD9.3.3	KCTD9_HUMAN (sp|Q7L273) BTB/POZ domain-containing protein KCTD9 OS=Homo sapiens GN=KCTD9 PE=2 SV=1	0,0346	0,0027	up	up	up	up	up	up
MPF_contig_042890	NA	0,0147	0,0002	down	up	up	up	up	up
MPF_contig_042898	NA	0,0265	0,0012	down	up	up	up	up	up
MPF_contig_042931	NA	0,0060	0,0000	down	down	down	down	down	down
MPF_DEPDC5.2.2	XM_003459178.1 PREDICTED: Oreochromis niloticus DEP domain containing 5 (DEPDC5), mRNA	0,0131	0,0001	up	up	up	up	up	up

MPF_LOC100696002.1.1	XM_003445297.1 PREDICTED: Oreochromis niloticus carbamoyl-phosphate synthase [ammonia], mitochondrial-like (LOC100696002), mRNA	0,0295	0,0018	up	up	up	down	up	up
MPF_contig_042980	NA	0,0431	0,0051	up	up	up	up	up	up
MPF_DDA1.2.2	DDA1_DANRE (sp|Q7T2A3) DET1- and DDB1-associated protein 1 OS=Danio rerio GN=dda1 PE=2 SV=1	0,0241	0,0009	up	up	up	up	up	up
MPF_LOC101487220.1.1	XM_004566606.1 PREDICTED: Maylandia zebra NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial-like (LOC101487220), mRNA	0,0498	0,0076	down	down	down	down	down	down
MPF_contig_043008	NA	0,0289	0,0016	down	up	up	up	up	up
MPF_LOC101467510.1.4	XM_004561752.1 PREDICTED: Maylandia zebra folliculin-interacting protein 1-like (LOC101467510), transcript variant X2, mRNA	0,0224	0,0007	down	up	up	up	up	up
MPF_LOC100693046.1.1	XP_003459711.1 PREDICTED: ribosome biogenesis protein bop1-like [Oreochromis niloticus]	0,0266	0,0012	down	up	up	up	up	up
MPF_LOC101156990.1.1	XM_004074357.1 PREDICTED: Oryzias latipes upstream-binding protein 1-like (LOC101156990), mRNA	0,0288	0,0016	up	up	up	up	up	up
MPF_LOC101487084.1.4	XM_004554809.1 PREDICTED: Maylandia zebra neurofilament light polypeptide-like (LOC101487084), mRNA	0,0362	0,0031	down	up	up	up	up	up
MPF_LOC100690119.15.18	XP_003448733.1 PREDICTED: zinc finger protein 16-like [Oreochromis niloticus]	0,0453	0,0057	up	up	up	up	up	up
MPF_LOC101474504.4.5	XM_004557613.1 PREDICTED: Maylandia zebra anthrax toxin receptor 1-like (LOC101474504), mRNA	0,0333	0,0024	down	down	down	down	down	down
MPF_contig_043239	NA	0,0441	0,0054	down	down	up	up	up	up
MPF_LOC101464899.1.4	XM_004553991.1 PREDICTED: Maylandia zebra protein bassoon-like (LOC101464899), transcript variant X2, mRNA	0,0362	0,0031	down	up	up	up	up	up
MPF_contig_043293	NA	0,0268	0,0013	down	up	up	up	up	up
MPF_contig_043310	XM_004543936.1 PREDICTED: Maylandia zebra CMP-N-acetylneuraminate-beta-galactosamide-alpha-2, 3-sialyltransferase 4-like (LOC101465046), transcript variant X2, mRNA	0,0160	0,0003	down	up	up	up	up	up
MPF_LOC100709891.1.1	XP_003449549.1 PREDICTED: succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial-like [Oreochromis niloticus]	0,0347	0,0027	down	down	up	down	up	up
MPF_LOC101464899.2.4	XM_004553991.1 PREDICTED: Maylandia zebra protein bassoon-like (LOC101464899), transcript variant X2, mRNA	0,0200	0,0005	down	down	down	down	down	down
MPF_contig_043323	NA	0,0228	0,0008	down	down	down	up	down	down
MPF_LOC100618182.3.3	XP_003340880.1 PREDICTED: zinc finger protein 345-like [Monodelphis domestica]	0,0451	0,0056	down	up	up	up	up	up
MPF_LOC100695994.36.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0,0422	0,0049	down	up	up	up	up	up
MPF_contig_043407	NA	0,0265	0,0012	down	up	up	up	up	up
MPF_LOC100693387.2.2	XP_003457557.1 PREDICTED: coiled-coil-helix-coiled-coil-helix domain-containing protein 7-like isoform 2 [Oreochromis niloticus]	0,0301	0,0018	up	up	up	up	up	up

MPF_LOC100705814.2.2	XM_003437803.1 PREDICTED: Oreochromis niloticus eukaryotic initiation factor 4A-II-like (LOC100705814), mRNA	0,0352	0,0028	down	down	down	down	down	down
MPF_LOC100708302.1.1	XP_003458003.1 PREDICTED: F-box only protein 3-like [Oreochromis niloticus]	0,0477	0,0067	up	up	up	up	up	up
MPF_LOC100693393.1.1	XP_003459043.1 PREDICTED: beta-1,3-galactosyltransferase 1-like [Oreochromis niloticus]	0,0482	0,0069	down	down	up	up	up	up
MPF_contig_043487	NA	0,0213	0,0006	down	down	down	down	down	down
MPF_LOC101170497.8.8	XP_004086004.1 PREDICTED: oocyte zinc finger protein XlCOF6-like [Oryzias latipes]	0,0459	0,0059	down	down	up	up	up	up
MPF_contig_043522	NA	0,0134	0,0001	down	up	up	up	up	up
MPF_LOC101480205.1.1	XM_004554598.1 PREDICTED: Maylandia zebra exportin-1-like (LOC101480205), transcript variant X4, mRNA	0,0366	0,0032	up	up	up	up	up	up
MPF_contig_043533	NA	0,0143	0,0002	up	up	up	up	up	up
MPF_contig_043543	NA	0,0148	0,0002	up	up	up	up	up	up
MPF_LOC101470972.1.1	XM_004569116.1 PREDICTED: Maylandia zebra protein QN1 homolog (LOC101470972), mRNA	0,0414	0,0046	up	up	up	up	up	up
MPF_LOC101473217.1.1	XM_004572509.1 PREDICTED: Maylandia zebra ventral anterior homeobox 1-like (LOC101473217), mRNA	0,0143	0,0002	down	up	up	up	up	up
MPF_LOC101155904.1.1	XM_004065552.1 PREDICTED: Oryzias latipes uncharacterized LOC101155904 (LOC101155904), mRNA	0,0419	0,0047	up	up	up	up	up	up
MPF_LOC101468417.3.3	XM_004558511.1 PREDICTED: Maylandia zebra aspartate beta-hydroxylase domain-containing protein 2-like (LOC101468417), transcript variant X2, mRNA	0,0333	0,0024	down	up	up	up	up	up
MPF_LOC100695307.3.3	XM_003448117.1 PREDICTED: Oreochromis niloticus enoyl-CoA hydratase domain-containing protein 3, mitochondrial-like (LOC100695307), mRNA	0,0277	0,0014	up	up	up	up	up	up
MPF_LOC101064754.2.2	XM_003964223.1 PREDICTED: Takifugu rubripes calpain-2 catalytic subunit-like (LOC101064754), mRNA	0,0224	0,0007	up	down	up	down	up	up
MPF_LOC101487382.2.2	XM_004556477.1 PREDICTED: Maylandia zebra zinc finger protein 358-like (LOC101487382), mRNA	0,0346	0,0027	up	up	up	down	up	up
MPF_LOC101471367.5.5	XM_004573481.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase CBL-like (LOC101471367), mRNA	0,0472	0,0065	down	down	up	up	up	up
MPF_LOC101466696.1.1	XM_004545878.1 PREDICTED: Maylandia zebra uncharacterized LOC101466696 (LOC101466696), mRNA	0,0316	0,0021	down	up	up	up	up	up
MPF_LOC101478931.1.1	XM_004546204.1 PREDICTED: Maylandia zebra collagen alpha-3(IX) chain-like (LOC101478931), mRNA	0,0267	0,0012	down	down	up	down	up	up
MPF_contig_044061	NA	0,0302	0,0018	down	down	down	up	down	down
MPF_LOC101465129.16.18	XM_004542524.1 PREDICTED: Maylandia zebra cold-inducible RNA-binding protein A-like (LOC101465129), transcript variant X4, mRNA	0,0268	0,0013	down	up	up	up	up	up
MPF_LOC101486640.4.4	XM_004538564.1 PREDICTED: Maylandia zebra ubiquitin carboxyl-terminal hydrolase 32-like (LOC101486640), mRNA	0,0402	0,0042	up	up	up	up	up	up
MPF_contig_044118	NA	0,0435	0,0052	up	down	up	down	up	up
MPF_LOC101157745.7.7	XM_004082934.1 PREDICTED: Oryzias latipes uncharacterized LOC101157745 (LOC101157745), mRNA	0,0330	0,0023	up	up	up	up	up	up

MPF_APC10.1.1	[BBH] APC10_HUMAN (sp|Q9UM13) Anaphase-promoting complex subunit 10 OS=Homo sapiens GN=ANAPC10 PE=1 SV=1	0,0369	0,0033	down	up	up	up	up	up
MPF_contig_044171	NA	0,0149	0,0002	down	up	up	up	up	up
MPF_LOC101488047.1.1	XM_004561547.1 PREDICTED: Maylandia zebra calcium/calmodulin-dependent protein kinase type IVlike (LOC101488047), mRNA	0,0186	0,0004	down	down	down	down	down	down
MPF_LOC101482482.5.5	XM_004566239.1 PREDICTED: Maylandia zebra TGF-beta-activated kinase 1 and MAP3K7-binding protein 2-like (LOC101482482), transcript variant X5, mRNA	0,0430	0,0051	up	up	up	down	up	up
MPF_contig_044192	XM_004557088.1 PREDICTED: Maylandia zebra cytoplasmic polyadenylation element-binding protein 2like (LOC101483979), transcript variant X1, mRNA	0,0277	0,0014	down	down	up	up	up	up
MPF_LOC101469230.1.2	XM_004541970.1 PREDICTED: Maylandia zebra G patch domain-containing protein 2-like (LOC101469230), transcript variant X2, mRNA	0,0362	0,0031	down	up	up	up	up	up
MPF_LOC101483666.3.3	XM_004550438.1 PREDICTED: Maylandia zebra TATA box-binding protein-associated factor RNA polymerase I subunit A-like (LOC101483666), transcript variant X3, mRNA	0,0278	0,0015	down	down	down	down	down	down
MPF_CELF2.7.8	XM_003786821.1 PREDICTED: Otolemur garnettii CUGBP, Elav-like family member 2, transcript variant 4 (CELF2), mRNA	0,0267	0,0012	up	up	up	up	up	up
MPF_LOC101471048.6.7	XM_004568139.1 PREDICTED: Maylandia zebra cyclin-dependent kinase 16-like (LOC101471048), transcript variant X7, mRNA	0,0352	0,0028	up	up	up	up	up	up
MPF_ZG57.12.12	ZG57_XENLA (sp|P18729) Gastrula zinc finger protein XlCGF57.1 (Fragment) OS=Xenopus laevis PE=3 SV=1	0,0368	0,0033	down	up	up	up	up	up
MPF_LOC101464596.2.2	XM_004551025.1 PREDICTED: Maylandia zebra sodium/hydrogen exchanger 1-like (LOC101464596), transcript variant X2, mRNA	0,0066	0,0000	down	down	down	down	down	down
MPF_MYO16.1.1	XM_003452934.1 PREDICTED: Oreochromis niloticus myosin XVI (MYO16), mRNA	0,0277	0,0015	up	up	up	up	up	up
MPF_ZO6.6.6	ZO6_XENLA (sp|P18749) Oocyte zinc finger protein XlCOF6 (Fragment) OS=Xenopus laevis PE=3 SV=1	0,0335	0,0025	up	up	up	up	up	up
MPF_LOC101482347.1.1	XR_191458.1 PREDICTED: Maylandia zebra TBC1 domain family member 13-like (LOC101482347), transcript variant X2, misc_RNA	0,0461	0,0060	up	up	down	up	down	down
MPF_LOC100689749.1.1	XP_003445652.1 PREDICTED: G protein-coupled receptor kinase 5-like [Oreochromis niloticus]	0,0066	0,0000	down	up	up	up	up	up
MPF_contig_044368	NA	0,0265	0,0012	up	up	up	up	up	up
MPF_ZN425.2.2	ZN425_MACFA (sp|Q9N003) Zinc finger protein 425 (Fragment) OS=Macaca fascicularis GN=ZNF425 PE=2 SV=2	0,0454	0,0058	up	up	up	up	up	up
MPF_contig_044388	NA	0,0289	0,0016	down	up	up	up	up	up
MPF_contig_044394	NA	0,0410	0,0045	up	up	up	up	up	up
MPF_contig_044406	NA	0,0148	0,0002	down	up	up	up	up	up

MPF_LOC101483414.2.3	XM_004562959.1 PREDICTED: Maylandia zebra microtubule-associated serine/threonine-protein kinase 1-like (LOC101483414), mRNA	0,0421	0,0048	up	up	up	up	up	up
MPF_LOC100705401.1.1	XM_003441917.1 PREDICTED: Oreochromis niloticus delta-1-pyrroline-5-carboxylate synthase-like (LOC100705401), mRNA	0,0481	0,0069	up	up	up	up	up	up
MPF_contig_044512	NA	0,0206	0,0005	down	up	up	up	up	up
MPF_LOC101467415.3.4	XM_004562898.1 PREDICTED: Maylandia zebra lipid phosphate phosphatase-related protein type 5like (LOC101467415), transcript variant X5, mRNA	0,0220	0,0007	down	up	up	up	up	up
MPF_contig_044527	NA	0,0111	0,0001	down	up	up	up	up	up
MPF_contig_044528	NA	0,0359	0,0030	up	up	up	down	up	up
MPF_contig_044548	NA	0,0403	0,0043	down	down	down	up	down	down
MPF_LOC101473818.3.3	XM_004575140.1 PREDICTED: Maylandia zebra metallophosphoesterase MPPED2-like (LOC101473818), transcript variant X2, mRNA	0,0304	0,0019	down	up	up	up	up	up
MPF_LOC100699721.2.2	XP_003460016.1 PREDICTED: bifunctional protein NCOAT-like, partial [Oreochromis niloticus]	0,0174	0,0004	down	down	down	down	down	down
MPF_contig_044581	NA	0,0130	0,0001	up	up	up	up	up	up
MPF_LOC101480617.2.3	XM_004564970.1 PREDICTED: Maylandia zebra mucin-2-like (LOC101480617), mRNA	0,0410	0,0045	down	up	up	up	up	up
MPF_contig_044592	NA	0,0332	0,0023	down	up	up	up	up	up
MPF_LOC101477334.3.3	XM_004568161.1 PREDICTED: Maylandia zebra FYVE, RhoGEF and PH domain-containing protein 1like (LOC101477334), transcript variant X2, mRNA	0,0237	0,0009	down	up	up	up	up	up
MPF_LOC101470218.1.1	XM_004574288.1 PREDICTED: Maylandia zebra biotin--protein ligase-like (LOC101470218), transcript variant X1, mRNA	0,0308	0,0020	up	up	up	up	up	up
MPF_contig_044633	NA	0,0474	0,0066	down	up	up	up	up	up
MPF_contig_044669	NA	0,0357	0,0030	down	up	up	up	up	up
MPF_contig_044700	NA	0,0426	0,0050	down	up	up	up	up	up
MPF_contig_044705	NA	0,0401	0,0042	down	down	down	up	down	down
MPF_contig_044713	NA	0,0472	0,0065	down	up	up	up	up	up
MPF_LOC101074317.1.1	XP_003977744.1 PREDICTED: thrombospondin type-1 domain-containing protein 7A-like [Takifugu rubripes]	0,0267	0,0012	down	up	up	up	up	up
MPF_contig_044724	NA	0,0388	0,0039	up	up	up	up	up	up
MPF_contig_044730	NA	0,0259	0,0011	up	up	up	up	up	up
MPF_LOC101483308.2.3	XM_004559856.1 PREDICTED: Maylandia zebra lysine-specific demethylase phf2-like (LOC101483308), transcript variant X3, mRNA	0,0346	0,0027	down	up	up	up	up	up
MPF_LOC101465735.9.9	XM_004548780.1 PREDICTED: Maylandia zebra 40S ribosomal protein S23-like (LOC101465735), mRNA	0,0379	0,0036	up	up	up	up	up	up

MPF_contig_044768	NA	0,0290	0,0017	down	up	up	up	up	up
MPF_contig_044800	NA	0,0184	0,0004	up	up	up	up	up	up
MPF_LOC101476666.2.3	XM_004541357.1 PREDICTED: Maylandia zebra epithelial splicing regulatory protein 1-like (LOC101476666), transcript variant X2, mRNA	0,0286	0,0016	up	down	up	down	up	up
MPF_LOC101474478.3.3	XM_004572875.1 PREDICTED: Maylandia zebra neuritin-like (LOC101474478), mRNA	0,0041	0,0000	up	down	down	down	down	down
MPF_LOC101478686.3.4	XM_004553326.1 PREDICTED: Maylandia zebra SH3 and multiple ankyrin repeat domains protein 3like (LOC101478686), transcript variant X2, mRNA	0,0293	0,0017	down	up	up	up	up	up
MPF_LOC101483619.2.3	XM_004541289.1 PREDICTED: Maylandia zebra neuronal acetylcholine receptor subunit beta-2-like (LOC101483619), mRNA	0,0150	0,0002	up	up	up	down	up	up
MPF_contig_044869	XM_004575909.1 PREDICTED: Maylandia zebra neurabin-2-like (LOC101486611), transcript variant X1, mRNA	0,0054	0,0000	down	down	down	down	down	down
MPF_contig_044884	NA	0,0382	0,0037	down	up	up	up	up	up
MPF_LOC101481675.1.1	XM_004558563.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase CHFR-like (LOC101481675), transcript variant X4, mRNA	0,0371	0,0034	down	up	up	up	up	up
MPF_LOC101464081.1.3	XM_004540929.1 PREDICTED: Maylandia zebra gamma-aminobutyric acid receptor subunit beta-2-like (LOC101464081), transcript variant X2, mRNA	0,0325	0,0022	up	up	up	down	up	up
MPF_LOC100706980.1.1	XP_003459830.1 PREDICTED: hypothetical protein LOC100706980 [Oreochromis niloticus]	0,0408	0,0044	up	up	up	up	up	up
MPF_LOC100702758.9.10	XM_003455412.1 PREDICTED: Oreochromis niloticus 60S ribosomal protein L27a-like (LOC100702758), mRNA	0,0266	0,0012	up	up	up	up	up	up
MPF_LOC100696893.2.2	XM_003447708.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100696893 (LOC100696893), mRNA	0,0455	0,0058	down	down	up	up	up	up
MPF_MXAN_5876.1.1	YP_634013.1 hypothetical protein MXAN_5876 [Myxococcus xanthus DK 1622]	0,0147	0,0002	up	down	down	down	down	down
MPF_contig_045038	NA	0,0147	0,0002	up	down	up	down	up	up
MPF_contig_045090	NA	0,0330	0,0023	down	down	up	up	up	up
MPF_MYH10.2.2	MYH10_BOVIN (sp|Q27991) Myosin-10 OS=Bos taurus GN=MYH10 PE=2 SV=2	0,0333	0,0024	up	down	up	down	up	up
MPF_contig_045128	NA	0,0351	0,0028	down	down	up	up	up	up
MPF_LOC100705728.17.17	XM_003459563.1 PREDICTED: Oreochromis niloticus zinc finger protein RFP-like (LOC100705728), mRNA	0,0153	0,0002	up	up	down	down	down	down
MPF_LOC101467829.1.2	XM_004565458.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase pim-1-like (LOC101467829), mRNA	0,0210	0,0006	down	down	down	down	down	down
MPF_UBIQP.4.13	UBIQP_XENLA (sp|P62972) Polyubiquitin (Fragment) OS=Xenopus laevis PE=1 SV=2	0,0336	0,0025	down	down	up	up	up	up

MPF_LOC100709351.10.10	XM_003449499.1 PREDICTED: Oreochromis niloticus integral membrane protein 2B-like (LOC100709351), mRNA	0,0467	0,0062	up	up	up	up	up	up
MPF_LOC101483308.3.3	XM_004559856.1 PREDICTED: Maylandia zebra lysine-specific demethylase phf2-like (LOC101483308), transcript variant X3, mRNA	0,0293	0,0017	up	up	up	up	up	up
MPF_LOC100709639.2.2	XP_003455728.1 PREDICTED: hypothetical protein LOC100709639 [Oreochromis niloticus]	0,0481	0,0069	down	down	up	down	up	up
MPF_contig_045308	WP_006987701.1 hypothetical protein [Gillisia limnaea]	0,0332	0,0024	up	up	up	up	up	up
MPF_NRXN2B.1.1	NP_001073453.1 neurexin 2b precursor [Danio rerio]	0,0412	0,0046	up	down	up	down	up	up
MPF_contig_045318	NA	0,0173	0,0004	down	up	up	up	up	up
MPF_contig_045323	NA	0,0112	0,0001	down	down	down	down	down	down
MPF_LOC101475584.3.5	XM_004561039.1 PREDICTED: Maylandia zebra thrombospondin type-1 domain-containing protein 7Alike (LOC101475584), mRNA	0,0160	0,0003	down	down	down	down	down	down
MPF_LOC101474475.2.2	XM_004548245.1 PREDICTED: Maylandia zebra kelch domain-containing protein 10-like (LOC101474475), mRNA	0,0367	0,0033	down	up	up	up	up	up
MPF_LOC101468855.3.3	XM_004569017.1 PREDICTED: Maylandia zebra protein tweety homolog 3-like (LOC101468855), transcript variant X1, mRNA	0,0287	0,0016	down	down	down	down	down	down
MPF_LOC101482535.1.1	XM_004555438.1 PREDICTED: Maylandia zebra transformer-2 protein homolog beta-like (LOC101482535), transcript variant X3, mRNA	0,0498	0,0076	down	down	up	up	up	up
MPF_contig_045417	NA	0,0171	0,0003	down	up	up	up	up	up
MPF_contig_045428	NA	0,0270	0,0013	up	up	up	up	up	up
MPF_contig_045460	NA	0,0341	0,0026	down	up	up	up	up	up
MPF_AHNK.22.22	AHNK_HUMAN (sp|Q09666) Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0,0041	0,0000	down	down	down	down	down	down
MPF_contig_045495	NA	0,0262	0,0012	down	down	up	down	up	up
MPF_contig_045499	NA	0,0160	0,0003	up	up	up	up	up	up
MPF_contig_045514	NA	0,0340	0,0026	down	up	up	up	up	up
MPF_LOC101468323.2.2	XM_004561832.1 PREDICTED: Maylandia zebra exportin-7-like (LOC101468323), mRNA	0,0330	0,0023	up	up	up	up	up	up
MPF_LOC101480226.1.1	XM_004538168.1 PREDICTED: Maylandia zebra protein phosphatase PTC7 homolog (LOC101480226), mRNA	0,0160	0,0003	up	up	up	down	up	up
MPF_contig_045558	NA	0,0367	0,0033	down	up	up	up	up	up
MPF_LOC100534702.2.5	XR_117879.1 PREDICTED: Danio rerio hypothetical LOC100534702 (LOC100534702), miscRNA	0,0213	0,0006	up	up	up	up	up	up
MPF_LOC101163898.2.2	XP_004070391.1 PREDICTED: ATP synthase subunit epsilon, mitochondrial-like [Oryzias latipes]	0,0421	0,0049	down	up	up	up	up	up
MPF_LOC100705746.3.3	XP_003443116.1 PREDICTED: trafficking protein particle complex subunit 5-like [Oreochromis niloticus]	0,0371	0,0035	up	up	up	up	up	up

MPF_contig_045616	NA	0,0065	0,0000 down	down	down	down	down	down
MPF_LOC101481641.1.1	XM_004551444.1 PREDICTED: Maylandia zebra mitogen-activated protein kinase kinase kinase MLK4like (LOC101481641), transcript variant X2, mRNA	0,0370	0,0033 up	up	up	up	up	up
MPF_LOC101471940.1.1	XM_004570910.1 PREDICTED: Maylandia zebra TBC1 domain family member 25-like (LOC101471940), mRNA	0,0237	0,0009 down	up	up	up	up	up
MPF_LOC100712234.1.1	XM_003457656.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100712234 (LOC100712234), mRNA	0,0304	0,0019 up	down	down	down	down	down
MPF_ACTC.8.8	ACTC_TAKRU (sp|P53480) Actin, alpha cardiac OS=Takifugu rubripes PE=2 SV=1	0,0332	0,0024 down	down	up	up	up	up

MPF_contig_045776	NA	0,0458	0,0059 down	up	up	up	up	up
MPF_LOC101485385.2.2	XM_004537995.1 PREDICTED: Maylandia zebra zinc finger protein 618-like (LOC101485385), mRNA	0,0471	0,0064 down	up	up	up	up	up
MPF_LOC101472851.2.2	XR_191377.1 PREDICTED: Maylandia zebra homeobox protein Hox-C4a-like (LOC101472851), transcript variant X3, misc_RNA	0,0171	0,0003 down	up	up	up	up	up
MPF_LOC100694405.1.2	XM_003443693.1 PREDICTED: Oreochromis niloticus uncharacterized protein C8orf76-like (LOC100694405), mRNA	0,0222	0,0007 up	up	up	up	up	up
MPF_LOC101484522.1.1	XM_004554979.1 PREDICTED: Maylandia zebra transducin-like enhancer protein 1-like (LOC101484522), mRNA	0,0471	0,0064 up	up	up	up	up	up
MPF_LOC101463657.2.2	XM_004557477.1 PREDICTED: Maylandia zebra cerebellar degeneration-related protein 2-like (LOC101463657), mRNA	0,0451	0,0057 up	up	up	down	up	up
MPF_LOC101486956.2.2	XM_004570349.1 PREDICTED: Maylandia zebra caskin-1-like (LOC101486956), transcript variant X6, mRNA	0,0270	0,0013 up	up	up	up	up	up
MPF_LOC101477256.2.2	XM_004570210.1 PREDICTED: Maylandia zebra TGF-beta-activated kinase 1 and MAP3K7-binding protein 3-like (LOC101477256), mRNA	0,0394	0,0040 down	down	up	up	up	up
MPF_LOC101484448.2.3	XM_004540186.1 PREDICTED: Maylandia zebra lipid phosphate phosphatase-related protein type 3like (LOC101484448), transcript variant X2, mRNA	0,0228	0,0008 down	up	up	up	up	up
MPF_LOC101482618.1.1	XM_004555539.1 PREDICTED: Maylandia zebra A-kinase anchor protein 17A-like (LOC101482618), transcript variant X3, mRNA	0,0339	0,0025 up	up	up	up	up	up
MPF_LOC101479448.4.4	XM_004553132.1 PREDICTED: Maylandia zebra Krueppel-like factor 13-like (LOC101479448), mRNA	0,0380	0,0037 down	up	up	up	up	up
MPF_TYRO3.2.2	NM_131432.1 Danio rerio TYRO3 protein tyrosine kinase (tyro3), mRNA gb|AF021344.1|AF021344 Danio rerio developmental receptor tyrosine kinase (Dtk) mRNA, complete cds	0,0285	0,0016 down	up	up	up	up	up
MPF_LOC101485687.1.1	XM_004567815.1 PREDICTED: Maylandia zebra polycomb protein suz12-B-like (LOC101485687), transcript variant X1, mRNA	0,0224	0,0007 up	up	up	up	up	up
MPF_contig_046161	XM_004559166.1 PREDICTED: Maylandia zebra PTB domain-containing engulfment adapter protein 1like (LOC101471107), transcript variant X1, mRNA	0,0439	0,0053 up	up	up	up	up	up

MPF_LOC101471394.1.1	XM_004557138.1 PREDICTED: Maylandia zebra GS homeobox 2-like (LOC101471394), mRNA	0,0169	0,0003	up	up	up	down	up	up
MPF_LOC101161574.14.14	XR_177502.1 PREDICTED: Oryzias latipes uncharacterized LOC101161574 (LOC101161574), misc_RNA	0,0155	0,0002	up	down	down	down	down	down
MPF_LOC100703973.1.1	XM_003444318.1 PREDICTED: Oreochromis niloticus protein FAM136A-like (LOC100703973), mRNA	0,0374	0,0036	down	up	up	up	up	up
MPF_contig_046286	NA	0,0047	0,0000	up	up	up	down	up	up
MPF_LOC101473550.1.1	XM_004558529.1 PREDICTED: Maylandia zebra ribonuclease P/MRP protein subunit POP5-like (LOC101473550), mRNA	0,0169	0,0003	up	up	up	up	up	up
MPF_LOC100703754.1.1	XM_003456632.1 PREDICTED: Oreochromis niloticus mannosyl-oligosaccharide 1,2-alphamannosidase IA-like (LOC100703754), mRNA	0,0320	0,0022	down	down	down	down	down	down
MPF_LOC101473892.1.1	XM_004569569.1 PREDICTED: Maylandia zebra transforming growth factor beta-1-like (LOC101473892), transcript variant X2, mRNA	0,0168	0,0003	down	down	down	down	down	down
MPF_LOC101472522.2.2	XM_004547397.1 PREDICTED: Maylandia zebra nucleolar protein 8-like (LOC101472522), mRNA	0,0497	0,0076	down	down	up	up	up	up
MPF_contig_004625	XM_004542709.1 PREDICTED: Maylandia zebra histone-lysine N-methyltransferase MLL3-like (LOC101465418), transcript variant X4, mRNA	0,0406	0,0044	down	down	up	down	up	up
MPF_LOC100700981.1.1	XM_003440559.1 PREDICTED: Oreochromis niloticus rab-like protein 2A-like (LOC100700981), mRNA	0,0464	0,0061	down	up	up	up	up	up
MPF_LOC101469584.2.2	XM_004559799.1 PREDICTED: Maylandia zebra serum response factor-like (LOC101469584), mRNA	0,0465	0,0062	up	up	up	up	up	up
MPF_LOC101482448.2.2	XM_004555347.1 PREDICTED: Maylandia zebra protein kinase C iota type-like (LOC101482448), mRNA	0,0344	0,0026	down	up	up	up	up	up
MPF_LOC101487315.1.1	XM_004543356.1 PREDICTED: Maylandia zebra protocadherin-17-like (LOC101487315), transcript variant X1, mRNA	0,0420	0,0048	up	down	up	down	up	up
MPF_LOC101474190.1.1	XM_004547121.1 PREDICTED: Maylandia zebra RING finger protein 122-like (LOC101474190), transcript variant X1, mRNA	0,0047	0,0000	down	up	up	up	up	up
MPF_LOC101482740.1.1	XM_004559578.1 PREDICTED: Maylandia zebra LIM homeobox transcription factor 1-alpha-like (LOC101482740), transcript variant X2, mRNA	0,0253	0,0011	down	up	up	up	up	up
MPF_LOC100709092.1.1	XM_003453780.1 PREDICTED: Oreochromis niloticus solute carrier family 2, facilitated glucose transporter member 9-like (LOC100709092), mRNA	0,0336	0,0025	down	up	up	up	up	up

MPF_LOC100693334.1.1	XP_003443821.1 PREDICTED: 39S ribosomal protein L36, mitochondrial-like [Oreochromis niloticus]	0,0320	0,0022	down	up	up	up	up	up
MPF_LOC101466706.1.1	XM_004548787.1 PREDICTED: Maylandia zebra coiled-coil domain-containing protein 66-like (LOC101466706), transcript variant X4, mRNA	0,0170	0,0003	down	up	up	up	up	up
MPF_LOC100705821.1.1	XM_003459705.1 PREDICTED: Oreochromis niloticus RWD domain-containing protein 4-like (LOC100705821), mRNA	0,0272	0,0014	up	up	up	up	up	up
MPF_APOC2.2.2	XP_003450543.1 PREDICTED: hypothetical protein LOC100712561 [Oreochromis niloticus]	0,0271	0,0014	down	down	up	down	up	up

MPF_contig_046607	XM_004570275.1 PREDICTED: Maylandia zebra paired amphipathic helix protein Sin3a-like (LOC101468364), transcript variant X2, mRNA	0,0412	0,0046	down	down	up	up	up	up
MPF_LOC100690836.1.1	XP_003447492.1 PREDICTED: presequence protease, mitochondrial-like [Oreochromis niloticus]	0,0224	0,0007	up	up	up	up	up	up
MPF_contig_046648	XM_004545215.1 PREDICTED: Maylandia zebra protein FAM219A-like (LOC101484940), transcript variant X2, mRNA	0,0347	0,0027	up	up	up	down	up	up
MPF_TCB1.7.8	TCB1_CAEBR (sp|P35072) Transposable element Tcb1 transposase OS=Caenorhabditis briggsae PE=3 SV=1	0,0367	0,0033	down	up	up	up	up	up
MPF_LOC101465258.1.1	XM_004572743.1 PREDICTED: Maylandia zebra transmembrane and coiled-coil domain-containing protein 4-like (LOC101465258), transcript variant X2, mRNA	0,0289	0,0016	up	up	up	up	up	up
MPF_LOC100692576.1.3	XM_003437754.1 PREDICTED: Oreochromis niloticus GPN-loop GTPase 1-like (LOC100692576), mRNA	0,0371	0,0034	up	up	up	up	up	up
MPF_contig_046735	NA	0,0145	0,0002	up	up	up	up	up	up
MPF_LOC101068645.2.2	XM_003975361.1 PREDICTED: Takifugu rubripes guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5-like (LOC101068645), mRNA	0,0390	0,0039	down	down	up	down	up	up
MPF_contig_046797	NA	0,0494	0,0074	up	up	up	down	up	up
MPF_LOC101074201.1.1	XM_003971402.1 PREDICTED: Takifugu rubripes creatine kinase B-type-like (LOC101074201), mRNA	0,0451	0,0056	down	up	up	up	up	up
MPF_contig_046856	NA	0,0172	0,0003	down	up	up	up	up	up
MPF_LOC101472088.1.1	XR_190951.1 PREDICTED: Maylandia zebra uncharacterized LOC101472088 (LOC101472088), misc_RNA	0,0308	0,0020	down	down	up	up	up	up
MPF_contig_046862	NA	0,0332	0,0024	up	up	up	up	up	up
MPF_LOC101480012.2.2	XM_004555338.1 PREDICTED: Maylandia zebra hippocampus abundant transcript 1 protein-like (LOC101480012), mRNA	0,0380	0,0037	down	down	up	up	up	up
MPF_LOC101157089.1.1	XP_004079208.1 PREDICTED: coatomer subunit beta'-like [Oryzias latipes]	0,0352	0,0028	down	up	up	up	up	up
MPF_LOC101482239.1.1	XM_004553768.1 PREDICTED: Maylandia zebra LIM/homeobox protein Lhx9-like (LOC101482239), transcript variant X1, mRNA	0,0346	0,0027	up	up	up	down	up	up
MPF_LOC101469226.1.1	XM_004541233.1 PREDICTED: Maylandia zebra uncharacterized LOC101469226 (LOC101469226), mRNA	0,0294	0,0017	up	up	up	down	up	up
MPF_LOC101473936.1.1	XM_004559270.1 PREDICTED: Maylandia zebra PQ-loop repeat-containing protein 3-like (LOC101473936), mRNA	0,0285	0,0016	down	up	up	up	up	up
MPF_LOC101476666.3.3	XM_004541357.1 PREDICTED: Maylandia zebra epithelial splicing regulatory protein 1-like (LOC101476666), transcript variant X2, mRNA	0,0282	0,0015	up	down	up	down	up	up
MPF_LOC101466805.1.1	XM_004574191.1 PREDICTED: Maylandia zebra general transcription factor IIH subunit 2-like (LOC101466805), transcript variant X2, mRNA	0,0422	0,0049	down	up	up	up	up	up
MPF_LOC101479710.1.1	XM_004573330.1 PREDICTED: Maylandia zebra poliovirus receptor-related protein 3-like (LOC101479710), transcript variant X2, mRNA	0,0410	0,0045	up	up	up	up	up	up
MPF_LOC101482766.4.4	XM_004543433.1 PREDICTED: Maylandia zebra cyclin-dependent kinase-like 5-like (LOC101482766), mRNA	0,0363	0,0032	down	up	up	up	up	up

MPF_LOC101468054.1.1	XM_004569557.1 PREDICTED: Maylandia zebra phosphoenolpyruvate carboxykinase [GTP], mitochondrial-like (LOC101468054), mRNA	0,0414	0,0046	down	up	up	up	up	up
MPF_LOC101483327.1.1	XM_004541476.1 PREDICTED: Maylandia zebra chromobox protein homolog 3-like (LOC101483327), transcript variant X2, mRNA	0,0277	0,0014	up	up	up	up	up	up
MPF_LOC101477081.3.3	XM_004549844.1 PREDICTED: Maylandia zebra noelin-like (LOC101477081), transcript variant X2, mRNA	0,0172	0,0003	down	down	up	down	up	up
MPF_contig_047119	NA	0,0308	0,0020	down	down	down	down	down	down
MPF_LOC101481920.2.2	XM_004572350.1 PREDICTED: Maylandia zebra zinc finger protein 143-like (LOC101481920), mRNA	0,0347	0,0027	up	down	up	down	up	up
MPF_LOC101464577.1.1	XM_004547080.1 PREDICTED: Maylandia zebra betaine--homocysteine S-methyltransferase 1-like (LOC101464577), mRNA	0,0427	0,0050	down	down	up	up	up	up
MPF_LOC101472703.2.2	XM_004569035.1 PREDICTED: Maylandia zebra axin-1-like (LOC101472703), transcript variant X3, mRNA	0,0404	0,0043	down	up	up	up	up	up
MPF_LOC101469738.2.2	XM_004551780.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase MSL2-like (LOC101469738), mRNA	0,0180	0,0004	up	up	up	down	up	up

MPF_contig_047313	XM_004560032.1 PREDICTED: Maylandia zebra E3 ubiquitin-protein ligase RNF19A-like (LOC101479921), transcript variant X1, mRNA	0,0377	0,0036	down	down	up	down	up	up
MPF_LOC100703053.1.1	XM_003440732.1 PREDICTED: Oreochromis niloticus ATP-dependent RNA helicase DDX1-like (LOC100703053), mRNA	0,0232	0,0008	down	up	up	up	up	up
MPF_LOC101465092.2.3	XM_004554364.1 PREDICTED: Maylandia zebra serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform-like (LOC101465092), transcript variant X2, mRNA	0,0142	0,0001	up	up	up	up	up	up
MPF_THOC1.1.1	XM_003437855.1 PREDICTED: Oreochromis niloticus THO complex 1 (THOC1), mRNA	0,0499	0,0077	down	down	up	down	up	up
MPF_LOC100707167.1.1	XM_003442256.1 PREDICTED: Oreochromis niloticus calretinin-like (LOC100707167), mRNA	0,0270	0,0013	down	down	up	up	up	up
MPF_LOC101479508.1.1	XM_004545378.1 PREDICTED: Maylandia zebra leucine-rich repeats and immunoglobulin-like domains protein 1-like (LOC101479508), mRNA	0,0486	0,0072	up	down	up	down	up	up
MPF_contig_047564	NA	0,0243	0,0009	down	up	up	up	up	up
MPF_contig_047566	NA	0,0078	0,0000	down	down	down	down	down	down
MPF_LOC101164389.1.1	XP_004067408.1 PREDICTED: ATP-dependent RNA helicase SUPV3L1, mitochondrial-like [Oryzias latipes]	0,0270	0,0013	up	up	up	up	up	up
MPF_contig_047601	NA	0,0213	0,0006	down	down	down	down	down	down
MPF_LOC100697918.2.2	XP_003438738.1 PREDICTED: nuclear prelamin A recognition factor-like [Oreochromis niloticus]	0,0269	0,0013	down	up	up	up	up	up
MPF_LOC100698395.2.2	XM_003442470.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100698395 (LOC100698395), mRNA	0,0358	0,0030	down	up	up	up	up	up
MPF_LOC101075879.1.1	XP_003961756.1 PREDICTED: leucine-rich repeat-containing protein 58-like [Takifugu rubripes]	0,0277	0,0015	up	up	up	up	up	up

MPF_contig_047695	NA	0,0387	0,0038	up	up	up	up	up	up
MPF_LOC101474919.1.1	XM_004544715.1 PREDICTED: Maylandia zebra bone morphogenetic protein 1-like (LOC101474919), mRNA	0,0450	0,0056	down	up	up	up	up	up
MPF_LOC101481962.1.2	XM_004559755.1 PREDICTED: Maylandia zebra striatin-like (LOC101481962), transcript variant X2, mRNA	0,0487	0,0072	down	up	down	up	down	down
MPF_LOC101484122.9.9	XM_004572909.1 PREDICTED: Maylandia zebra eukaryotic translation initiation factor 5A-1-like (LOC101484122), mRNA	0,0224	0,0007	up	down	up	down	up	up
MPF_contig_047843	NA	0,0457	0,0059	down	up	up	up	up	up
MPF_LOC101473158.1.1	XM_004563202.1 PREDICTED: Maylandia zebra bromodomain-containing protein 8-like (LOC101473158), transcript variant X2, mRNA	0,0338	0,0025	up	up	up	up	up	up
MPF_LOC101476857.3.3	XM_004566214.1 PREDICTED: Maylandia zebra 5'-nucleotidase domain-containing protein 1-like (LOC101476857), mRNA	0,0147	0,0002	down	up	up	up	up	up
MPF_LOC101479065.1.1	XM_004552479.1 PREDICTED: Maylandia zebra synaptotagmin-C-like (LOC101479065), mRNA	0,0110	0,0001	down	up	up	up	up	up
MPF_LOC101173666.1.1	XP_004082016.1 PREDICTED: poliovirus receptor-related protein 2-like [Oryzias latipes]	0,0160	0,0003	down	down	down	down	down	down
MPF_LOC101472989.6.6	XM_004566934.1 PREDICTED: Maylandia zebra CAP-Gly domain-containing linker protein 1-like (LOC101472989), transcript variant X5, mRNA	0,0364	0,0032	down	up	up	up	up	up
MPF_LOC101467664.1.2	XM_004569013.1 PREDICTED: Maylandia zebra serine/threonine-protein kinase PLK1-like (LOC101467664), mRNA	0,0406	0,0044	up	up	up	up	up	up
MPF_LOC101066223.1.1	XP_003974027.1 PREDICTED: cytochrome b-c1 complex subunit 6, mitochondrial-like [Takifugu rubripes]	0,0187	0,0004	up	up	up	up	up	up
MPF_contig_047973	NA	0,0208	0,0006	up	up	up	up	up	up
MPF_contig_004789	NA	0,0359	0,0030	down	up	down	up	down	down
MPF_LOC100690938.3.3	XP_003451378.1 PREDICTED: microtubule-associated protein 1B-like [Oreochromis niloticus]	0,0268	0,0013	down	up	up	up	up	up
MPF_LOC100706983.10.11	XM_003460062.1 PREDICTED: Oreochromis niloticus 28S ribosomal protein S28, mitochondrial-like (LOC100706983), mRNA	0,0091	0,0000	down	down	down	up	down	down
2MPF_contig_048033	XM_004563944.1 PREDICTED: Maylandia zebra signal-induced proliferation-associated 1-like protein like (LOC101477688), transcript variant X1, mRNA	0,0338	0,0025	up	up	up	up	up	up
MPF_LOC101474085.2.2	XM_004568504.1 PREDICTED: Maylandia zebra cyclin-Y-like (LOC101474085), transcript variant X4, mRNA	0,0123	0,0001	up	up	up	up	up	up
MPF_LOC101172433.1.1	XP_004077062.1 PREDICTED: uncharacterized protein LOC101172433 [Oryzias latipes]	0,0208	0,0005	up	up	up	down	up	up
MPF_HMGA2.2.3	NM_010441.2 Mus musculus high mobility group AT-hook 2 (Hmga2), mRNA	0,0144	0,0002	down	down	up	up	up	up
MPF_contig_048139	XM_004545214.1 PREDICTED: Maylandia zebra protein FAM219A-like (LOC101484940), transcript variant X1, mRNA	0,0248	0,0010	up	down	up	down	up	up
MPF_LOC101479795.2.2	XM_004547426.1 PREDICTED: Maylandia zebra uncharacterized LOC101479795 (LOC101479795), mRNA	0,0065	0,0000	down	up	up	up	up	up

MPF_LOC101072633.13.15	XM_003970117.1 PREDICTED: Takifugu rubripes non-histone chromosomal protein HMG-14A-like (LOC101072633), mRNA	0,0381	0,0037	up	down	up	down	up	up

MPF_LOC101483950.1.2	XM_004549875.1 PREDICTED: Maylandia zebra FCH domain only protein 2-like (LOC101483950), transcript variant X3, mRNA	0,0308	0,0020	down	down	up	up	up	up
MPF_LOC101479312.2.2	XM_004548084.1 PREDICTED: Maylandia zebra tribbles homolog 1-like (LOC101479312), mRNA	0,0097	0,0000	down	down	down	down	down	down
MPF_LOC101485482.1.1	XM_004563248.1 PREDICTED: Maylandia zebra POU domain, class 3, transcription factor 4-like (LOC101485482), mRNA	0,0290	0,0017	down	down	up	up	up	up
MPF_LOC100691587.1.1	XM_003458842.1 PREDICTED: Oreochromis niloticus mitochondrial chaperone BCS1-like (LOC100691587), mRNA	0,0139	0,0001	down	up	up	up	up	up
MPF_LOC101481069.1.1	XM_004556635.1 PREDICTED: Maylandia zebra sideroflexin-2-like (LOC101481069), mRNA	0,0387	0,0038	up	up	up	up	up	up
MPF_LOC101468719.1.2	XM_004559706.1 PREDICTED: Maylandia zebra kinesin light chain 1-like (LOC101468719), transcript variant X6, mRNA	0,0326	0,0022	up	up	up	up	up	up
MPF_LOC101078751.2.2	XM_003963635.1 PREDICTED: Takifugu rubripes cytoplasmic tRNA 2-thiolation protein 2-like (LOC101078751), mRNA	0,0432	0,0051	down	up	up	up	up	up
MPF_LOC101470981.2.2	XM_004547952.1 PREDICTED: Maylandia zebra mitochondrial import receptor subunit TOM7 homolog (LOC101470981), mRNA	0,0354	0,0029	up	up	up	up	up	up
MPF_contig_048334	NA	0,0403	0,0043	down	up	up	up	up	up
MPF_LOC101469923.2.2	XM_004573293.1 PREDICTED: Maylandia zebra GTP cyclohydrolase 1-like (LOC101469923), mRNA	0,0243	0,0009	down	up	up	up	up	up
MPF_LOC101477539.2.2	XM_004570211.1 PREDICTED: Maylandia zebra transmembrane protein 47-like (LOC101477539), mRNA	0,0277	0,0015	down	up	up	up	up	up
MPF_LOC446087.1.1	XM_003963804.1 PREDICTED: Takifugu rubripes nicotinic acetylcholine receptor alpha 1a subunit (LOC446087), mRNA	0,0486	0,0072	down	up	up	up	up	up
MPF_contig_048479	NA	0,0204	0,0005	down	up	up	up	up	up
MPF_contig_048489	NA	0,0288	0,0016	down	down	up	up	up	up
MPF_contig_048528	NA	0,0363	0,0032	up	up	up	up	up	up
MPF_contig_048529	NA	0,0388	0,0039	down	up	up	up	up	up
MPF_LOC101167735.1.1	XM_004078595.1 PREDICTED: Oryzias latipes heterogeneous nuclear ribonucleoprotein C-like (LOC101167735), mRNA	0,0323	0,0022	up	up	up	up	up	up
MPF_contig_048538	NA	0,0115	0,0001	up	up	up	up	up	up
MPF_ACTBA.4.4	XM_003964421.1 PREDICTED: Takifugu rubripes actin, cytoplasmic 1-like (LOC101073736), mRNA	0,0147	0,0002	up	up	up	up	up	up
MPF_LOC100695937.1.1	XM_003449613.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100695937 (LOC100695937), mRNA	0,0144	0,0002	down	down	down	down	down	down

MPF_contig_048639	NA	0,0236	0,0009	up	up	up	up	up	up
MPF_LOC101172338.1.1	XP_004072456.1 PREDICTED: leucine-zipper-like transcriptional regulator 1-like [Oryzias latipes]	0,0461	0,0060	down	down	up	up	up	up
MPF_contig_004858	NA	0,0228	0,0008	down	down	down	down	down	down
MPF_contig_048760	NA	0,0130	0,0001	down	up	up	up	up	up
MPF_contig_048812	NA	0,0411	0,0045	down	up	up	up	up	up
MPF_LOC101470086.1.1	XM_004569475.1 PREDICTED: Maylandia zebra tomoregulin-1-like (LOC101470086), transcript variant X2, mRNA	0,0343	0,0026	up	down	up	down	up	up
MPF_LOC101464911.1.1	XM_004560530.1 PREDICTED: Maylandia zebra protein FAM181B-like (LOC101464911), mRNA	0,0228	0,0008	up	up	up	up	up	up
MPF_LOC101465780.2.3	XM_004560720.1 PREDICTED: Maylandia zebra voltage-dependent calcium channel gamma-3 subunitlike (LOC101465780), transcript variant X2, mRNA	0,0491	0,0073	down	up	up	up	up	up
MPF_LOC100689805.1.1	XP_003457862.1 PREDICTED: probable signal peptidase complex subunit 2-like [Oreochromis niloticus]	0,0138	0,0001	down	up	up	up	up	up
MPF_LELG_02721.2.2	XP_001526163.1 hypothetical protein LELG_02721 [Lodderomyces elongisporus NRRL YB-4239]	0,0224	0,0007	down	down	up	up	up	up
MPF_LOC100703964.3.3	XM_003442244.1 PREDICTED: Oreochromis niloticus cytochrome c oxidase subunit 4 isoform 1, mitochondrial-like (LOC100703964), mRNA	0,0208	0,0005	down	up	up	up	up	up
MPF_LOC100699693.1.1	XP_003455536.1 PREDICTED: glutathione S-transferase theta-1-like [Oreochromis niloticus]	0,0344	0,0027	up	up	up	up	up	up
MPF_contig_049020	NA	0,0175	0,0004	up	up	up	up	up	up
MPF_LOC101161784.1.1	XP_004086111.1 PREDICTED: stathmin-4-like [Oryzias latipes]	0,0443	0,0054	down	down	up	up	up	up
MPF_LOC100708634.4.4	XP_003449376.1 PREDICTED: apolipoprotein A-I-like [Oreochromis niloticus]	0,0207	0,0005	down	up	up	up	up	up
MPF_LOC101481351.1.1	XM_004551535.1 PREDICTED: Maylandia zebra transcription factor COE3-like (LOC101481351), transcript variant X2, mRNA	0,0336	0,0025	up	up	up	down	up	up
MPF_contig_004895	NA	0,0207	0,0005	up	up	up	up	up	up
MPF_LOC101466312.1.2	XM_004569463.1 PREDICTED: Maylandia zebra protein EFR3 homolog A-like (LOC101466312), transcript variant X4, mRNA	0,0232	0,0008	up	up	up	up	up	up
MPF_LOC100690594.1.1	XP_003453678.1 PREDICTED: serine/threonine-protein phosphatase 2B catalytic subunit alpha isoformlike [Oreochromis niloticus]	0,0357	0,0030	up	down	up	down	up	up
MPF_LOC101475900.1.3	XM_004566477.1 PREDICTED: Maylandia zebra ras-related protein Rab-21-like (LOC101475900), mRNA	0,0332	0,0024	up	up	up	up	up	up
MPF_LOC101485630.2.2	XM_004552028.1 PREDICTED: Maylandia zebra transcription factor COE3-like (LOC101485630), transcript variant X3, mRNA	0,0303	0,0019	up	up	up	up	up	up
MPF_LOC101475584.5.5	XM_004561039.1 PREDICTED: Maylandia zebra thrombospondin type-1 domain-containing protein 7Alike (LOC101475584), mRNA	0,0208	0,0006	up	up	up	up	up	up

MPF_UTRN.2.2	XM_003449882.1 PREDICTED: Oreochromis niloticus utrophin (UTRN), mRNA	0,0333	0,0024	up	down	up	down	up	up
MPF_contig_049193	NA	0,0243	0,0009	down	down	up	down	up	up
MPF_contig_004922	NA	0,0080	0,0000	down	down	down	down	down	down
MPF_contig_000493	XM_004550861.1 PREDICTED: Maylandia zebra INO80 complex subunit E-like (LOC101470596), transcript variant X2, mRNA	0,0333	0,0024	up	down	up	down	up	up
MPF_contig_004932	NA	0,0150	0,0002	down	up	up	up	up	up
MPF_LOC101478094.1.1	XM_004569499.1 PREDICTED: Maylandia zebra matrix metalloproteinase-16-like (LOC101478094), transcript variant X1, mRNA	0,0277	0,0014	up	up	up	up	up	up
MPF_LOC101470505.1.1	XM_004550481.1 PREDICTED: Maylandia zebra mRNA-capping enzyme-like (LOC101470505), mRNA	0,0307	0,0019	up	up	up	up	up	up
MPF_LOC101470646.1.1	XM_004562113.1 PREDICTED: Maylandia zebra ephrin type-B receptor 1-like (LOC101470646), mRNA	0,0380	0,0037	up	up	up	up	up	up
MPF_LOC100692410.1.1	XP_003440487.1 PREDICTED: calcium and integrin-binding family member 2-like [Oreochromis niloticus]	0,0276	0,0014	down	up	up	up	up	up
MPF_contig_005114	NA	0,0340	0,0026	down	down	up	up	up	up
MPF_LOC101477320.1.1	XM_004540156.1 PREDICTED: Maylandia zebra solute carrier family 35 member G2-like (LOC101477320), mRNA	0,0171	0,0003	down	up	up	up	up	up
MPF_LOC100695830.1.2	XM_003445456.1 PREDICTED: Oreochromis niloticus serine/arginine-rich splicing factor 4-like, transcript variant 1 (LOC100695830), mRNA	0,0060	0,0000	up	down	down	down	down	down
MPF_LOC101487935.1.1	XM_004551853.1 PREDICTED: Maylandia zebra myeloma-overexpressed gene 2 protein homolog (LOC101487935), mRNA	0,0270	0,0013	up	up	up	up	up	up
MPF_contig_000517	NA	0,0265	0,0012	up	up	up	up	up	up
MPF_contig_005232	NA	0,0421	0,0048	down	up	up	up	up	up
MPF_LOC101478384.1.1	XM_004547890.1 PREDICTED: Maylandia zebra coiled-coil domain-containing protein 126-like (LOC101478384), transcript variant X3, mRNA	0,0270	0,0013	up	up	up	up	up	up
MPF_contig_000535	NA	0,0360	0,0031	down	up	up	up	up	up
MPF_contig_005369	XM_004566994.1 PREDICTED: Maylandia zebra rap1 GTPase-activating protein 2-like (LOC101464757), transcript variant X2, mRNA	0,0098	0,0001	down	up	up	up	up	up
MPF_LOC100698574.1.2	XP_003445184.1 PREDICTED: receptor-type tyrosine-protein phosphatase C-like [Oreochromis niloticus]	0,0098	0,0001	down	down	down	down	down	down
MPF_LOC101487987.1.1	XM_004543163.1 PREDICTED: Maylandia zebra switch-associated protein 70-like (LOC101487987), mRNA	0,0430	0,0051	up	down	up	down	up	up
MPF_LOC101486654.1.1	XM_004542792.1 PREDICTED: Maylandia zebra dystrobrevin alpha-like (LOC101486654), transcript variant X6, mRNA	0,0352	0,0028	down	down	up	up	up	up
MPF_LOC101174705.1.1	XP_004080443.1 PREDICTED: adenosine kinase-like isoform 2 [Oryzias latipes]	0,0438	0,0053	up	up	up	down	up	up
MPF_LOC101485709.2.4	XM_004548564.1 PREDICTED: Maylandia zebra synapsin-1-like (LOC101485709), mRNA	0,0150	0,0002	down	up	up	up	up	up

MPF_contig_005519	NA	0,0406	0,0044	down	down	down	down	down	down
MPF_LECG.1.42	LECG_THANI (sp|Q66S03) Galactose-specific lectin nattectin OS=Thalassophryne nattereri PE=1 SV=1	0,0306	0,0019	down	up	up	up	up	up
MPF_LOC101476056.1.2	XM_004559923.1 PREDICTED: Maylandia zebra phosphatase and actin regulator 3-like (LOC101476056), transcript variant X2, mRNA	0,0411	0,0045	down	up	up	up	up	up
MPF_LOC101482596.1.5	XM_004548845.1 PREDICTED: Maylandia zebra transmembrane prostate androgen-induced proteinlike (LOC101482596), transcript variant X2, mRNA	0,0084	0,0000	down	up	up	up	up	up
MPF_COX1.2.7	COX1_LATCH (sp|O03167) Cytochrome c oxidase subunit 1 OS=Latimeria chalumnae GN=MT-CO1 PE=3 SV=1	0,0287	0,0016	up	down	up	down	up	up
MPF_contig_005660	NA	0,0147	0,0002	down	up	up	up	up	up
MPF_LOC101469304.1.8	XM_004556584.1 PREDICTED: Maylandia zebra synuclein-like (LOC101469304), mRNA	0,0247	0,0010	down	up	up	up	up	up
MPF_LOC101483692.1.1	XM_004555993.1 PREDICTED: Maylandia zebra protein FAM135A-like (LOC101483692), transcript variant X2, mRNA	0,0265	0,0012	down	up	up	up	up	up
MPF_LOC101478422.1.2	XM_004560767.1 PREDICTED: Maylandia zebra parvalbumin-7-like (LOC101478422), transcript variant X2, mRNA	0,0268	0,0013	up	up	up	up	up	up
MPF_LOC101484349.1.2	XM_004538184.1 PREDICTED: Maylandia zebra sorting nexin-24-like (LOC101484349), mRNA	0,0481	0,0069	up	down	up	down	up	up
MPF_LOC101470261.1.1	XM_004541142.1 PREDICTED: Maylandia zebra teneurin-2-like (LOC101470261), transcript variant X2, mRNA	0,0171	0,0003	down	up	up	up	up	up
MPF_contig_005929	NA	0,0178	0,0004	down	up	up	up	up	up
MPF_LOC101484948.1.2	XM_004569795.1 PREDICTED: Maylandia zebra chromodomain-helicase-DNA-binding protein 4-like (LOC101484948), mRNA	0,0362	0,0031	up	down	up	down	up	up
MPF_LOC101480093.2.8	XM_004574589.1 PREDICTED: Maylandia zebra tripartite motif-containing protein 16-like (LOC101480093), mRNA	0,0461	0,0060	up	up	up	down	up	up
MPF_LOC100690512.1.1	XP_003438469.1 PREDICTED: hypothetical protein LOC100690512 [Oreochromis niloticus]	0,0256	0,0011	down	down	down	down	down	down
MPF_LOC101484118.1.2	XM_004570768.1 PREDICTED: Maylandia zebra SLIT-ROBO Rho GTPase-activating protein 1-like (LOC101484118), transcript variant X4, mRNA	0,0187	0,0004	down	down	down	up	down	down
MPF_LOC101475515.1.1	XM_004545728.1 PREDICTED: Maylandia zebra cleavage stimulation factor subunit 2-like (LOC101475515), transcript variant X3, mRNA	0,0225	0,0007	up	up	up	up	up	up
MPF_LOC101472211.3.4	XM_004545811.1 PREDICTED: Maylandia zebra BEN domain-containing protein 4-like (LOC101472211), mRNA	0,0228	0,0008	down	up	up	up	up	up
MPF_LOC101465466.1.1	XM_004553276.1 PREDICTED: Maylandia zebra dnaJ homolog subfamily A member 2-like (LOC101465466), mRNA	0,0303	0,0019	up	up	up	up	up	up
MPF_contig_006069	NA	0,0041	0,0000	down	down	down	down	down	down

MPF_LOC101469201.1.1	XM_004557967.1 PREDICTED: Maylandia zebra acidic leucine-rich nuclear phosphoprotein 32 family member A-like (LOC101469201), transcript variant X3, mRNA	0,0388	0,0039	up	up	up	up	up	up
MPF_LOC100692493.1.1	XP_003457870.1 PREDICTED: autophagy-related protein 16-1-like [Oreochromis niloticus]	0,0160	0,0002	up	up	up	up	up	up
MPF_LOC101483250.1.1	XM_004543044.1 PREDICTED: Maylandia zebra guanine nucleotide-binding protein G(o) subunit alphalike (LOC101483250), mRNA	0,0403	0,0043	up	up	up	up	up	up
MPF_LOC101470756.1.1	XM_004540502.1 PREDICTED: Maylandia zebra membrane-bound O-acyltransferase domaincontaining protein 2-like (LOC101470756), mRNA	0,0421	0,0049	down	down	up	up	up	up
MPF_LOC101483869.1.1	XM_004574429.1 PREDICTED: Maylandia zebra coiled-coil domain-containing protein 130 homolog (LOC101483869), mRNA	0,0286	0,0016	down	up	up	up	up	up
MPF_LOC101480346.1.4	XM_004567337.1 PREDICTED: Maylandia zebra myotubularin-related protein 3-like (LOC101480346), transcript variant X4, mRNA	0,0428	0,0050	up	up	up	up	up	up
MPF_LOC101485801.1.2	XM_004569981.1 PREDICTED: Maylandia zebra transcription factor GATA-3-like (LOC101485801), transcript variant X9, mRNA	0,0180	0,0004	down	up	up	up	up	up
MPF_LOC101477305.1.1	XM_004560761.1 PREDICTED: Maylandia zebra uncharacterized LOC101477305 (LOC101477305), mRNA	0,0365	0,0032	down	up	up	up	up	up
MPF_LOC100691830.1.1	XP_003453451.1 PREDICTED: DPY30 domain-containing protein 1-like [Oreochromis niloticus]	0,0371	0,0034	up	up	up	down	up	up
MPF_contig_006449	XM_004560824.1 PREDICTED: Maylandia zebra striatin-interacting protein 1 homolog (LOC101469586), transcript variant X2, mRNA	0,0321	0,0022	up	up	up	down	up	up
MPF_LOC101474478.2.3	XM_004572875.1 PREDICTED: Maylandia zebra neuritin-like (LOC101474478), mRNA	0,0432	0,0052	up	down	down	down	down	down
MPF_contig_006466	NA	0,0094	0,0000	down	up	up	up	up	up
MPF_COX2.3.4	COX2_DANRE (sp|Q9MIY7) Cytochrome c oxidase subunit 2 OS=Danio rerio GN=mt-co2 PE=3 SV=1	0,0314	0,0021	up	up	up	down	up	up
MPF_LOC101483595.1.1	XM_004537989.1 PREDICTED: Maylandia zebra deleted in bladder cancer protein 1 homolog (LOC101483595), mRNA	0,0160	0,0003	up	up	up	up	up	up
MPF_LOC101464641.1.1	XM_004540006.1 PREDICTED: Maylandia zebra polypeptide N-acetylgalactosaminyltransferase 16-like (LOC101464641), mRNA	0,0171	0,0003	down	up	up	up	up	up
MPF_LOC101475366.1.1	XM_004557617.1 PREDICTED: Maylandia zebra rho GTPase-activating protein 22-like (LOC101475366), transcript variant X2, mRNA	0,0404	0,0043	down	down	up	up	up	up
MPF_LOC100691148.1.2	XM_003458290.1 PREDICTED: Oreochromis niloticus diacylglycerol kinase zeta-like (LOC100691148), mRNA	0,0228	0,0008	up	up	up	up	up	up
MPF_LOC101479577.1.1	XM_004542105.1 PREDICTED: Maylandia zebra uncharacterized LOC101479577 (LOC101479577), transcript variant X1, mRNA	0,0184	0,0004	up	up	up	up	up	up
MPF_LOC101165232.1.1	XP_004070172.1 PREDICTED: N-terminal EF-hand calcium-binding protein 2-like [Oryzias latipes]	0,0228	0,0008	up	down	up	down	up	up
MPF_ND5.2.8	YP_003127104.1 NADH dehydrogenase subunit 5 [Hyperoglyphe japonica]	0,0352	0,0028	up	up	up	up	up	up
MPF_LOC101469939.1.2	XM_004552621.1 PREDICTED: Maylandia zebra peripheral plasma membrane protein CASK-like (LOC101469939), transcript variant X3, mRNA	0,0268	0,0013	down	down	up	down	up	up

MPF_LOC101479776.1.2	XM_004568261.1 PREDICTED: Maylandia zebra transmembrane and TPR repeat-containing protein 2like (LOC101479776), mRNA	0,0238	0,0009	down	up	up	up	up	up
MPF_LOC100699934.1.1	XP_003448851.1 PREDICTED: probable G-protein coupled receptor 19-like [Oreochromis niloticus]	0,0189	0,0004	down	up	up	up	up	up
MPF_LOC100689854.4.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0,0228	0,0007	up	up	up	up	up	up
MPF_contig_006725	NA	0,0467	0,0063	down	down	down	up	down	down

MPF_LOC100706747.1.1	XM_003446414.1 PREDICTED: Oreochromis niloticus enoyl-CoA delta isomerase 1, mitochondrial-like (LOC100706747), mRNA	0,0430	0,0051	up	up	up	down	up	up
MPF_LOC101472313.1.1	XM_004546377.1 PREDICTED: Maylandia zebra polyglutamine-binding protein 1-like (LOC101472313), transcript variant X2, mRNA	0,0244	0,0010	up	up	up	up	up	up
MPF_LOC101478179.1.1	XM_004546668.1 PREDICTED: Maylandia zebra transgelin-3-like (LOC101478179), mRNA	0,0406	0,0044	up	up	up	up	up	up
MPF_contig_006781	XM_004572062.1 PREDICTED: Maylandia zebra polypyrimidine tract-binding protein 2-like (LOC101478106), transcript variant X2, mRNA	0,0069	0,0000	down	up	up	up	up	up
MPF_LOC101479404.3.4	XM_004570313.1 PREDICTED: Maylandia zebra prolactin-1-like (LOC101479404), mRNA	0,0130	0,0001	down	down	down	down	down	down
MPF_LOC100694516.1.1	XP_003449159.1 PREDICTED: copine-9-like [Oreochromis niloticus]	0,0301	0,0018	down	down	up	down	up	up
MPF_LOC101481918.2.3	XM_004548550.1 PREDICTED: Maylandia zebra dual specificity protein phosphatase 7-like (LOC101481918), mRNA	0,0060	0,0000	down	down	down	down	down	down
MPF_PDE4DIP.2.2	XP_003438008.1 PREDICTED: myomegalin [Oreochromis niloticus]	0,0065	0,0000	up	up	up	up	up	up
MPF_LOC101480151.1.1	XM_004542860.1 PREDICTED: Maylandia zebra abhydrolase domain-containing protein 3-like (LOC101480151), mRNA	0,0407	0,0044	down	up	up	up	up	up
MPF_contig_006877	NA	0,0151	0,0002	down	up	up	up	up	up
MPF_LOC100700605.2.27	XM_003458555.1 PREDICTED: Oreochromis niloticus nuclear factor 7, ovary-like (LOC100700605), mRNA	0,0241	0,0009	up	up	up	up	up	up
MPF_contig_006984	NA	0,0224	0,0007	up	up	up	up	up	up
MPF_LOC101486203.1.2	XM_004572644.1 PREDICTED: Maylandia zebra flotillin-1-like (LOC101486203), mRNA	0,0440	0,0054	up	down	up	down	up	up
MPF_contig_007070	NA	0,0195	0,0005	down	up	up	up	up	up
MPF_LOC101474475.1.2	XM_004548245.1 PREDICTED: Maylandia zebra kelch domain-containing protein 10-like (LOC101474475), mRNA	0,0351	0,0028	up	down	up	down	up	up
MPF_LOC101067996.1.1	XP_003964368.1 PREDICTED: caskin-1-like [Takifugu rubripes]	0,0309	0,0020	down	up	up	up	up	up
MPF_LOC101463592.1.3	XM_004543454.1 PREDICTED: Maylandia zebra high affinity cAMP-specific and IBMX-insensitive 3',5'cyclic phosphodiesterase 8A-like (LOC101463592), mRNA	0,0421	0,0048	down	down	up	up	up	up
MPF_contig_007138	XM_004574682.1 PREDICTED: Maylandia zebra synaptogyrin-1-like (LOC101484327), transcript variant X1, mRNA	0,0269	0,0013	up	up	up	up	up	up

MPF_LOC100698387.1.1	XP_003440011.1 PREDICTED: leucine-rich repeat-containing protein 15-like [Oreochromis niloticus]	0,0130	0,0001	up	down	up	down	up	up
MPF_LOC100700827.1.1	XM_003446806.1 PREDICTED: Oreochromis niloticus uncharacterized protein C21orf59 homolog (LOC100700827), mRNA	0,0277	0,0015	up	up	up	up	up	up
MPF_LOC101479997.1.1	XM_004574065.1 PREDICTED: Maylandia zebra cytochrome b-c1 complex subunit Rieske, mitochondrial-like (LOC101479997), mRNA	0,0342	0,0026	up	up	up	up	up	up
MPF_LOC100712461.1.1	XM_003446184.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100712461 (LOC100712461), mRNA	0,0419	0,0048	down	down	up	up	up	up
MPF_contig_007184	NA	0,0371	0,0035	down	up	up	up	up	up
MPF_LOC100697283.1.3	XM_003454317.1 PREDICTED: Oreochromis niloticus short coiled-coil protein A-like (LOC100697283), mRNA	0,0414	0,0046	down	up	up	up	up	up
MPF_LOC101485100.1.2	XM_004560980.1 PREDICTED: Maylandia zebra chromatin target of PRMT1 protein-like (LOC101485100), mRNA	0,0362	0,0031	down	up	up	up	up	up
MPF_contig_007341	NA	0,0457	0,0059	down	down	up	down	up	up
MPF_TBA.2.17	TBA_LYTPI (sp|P02553) Tubulin alpha chain (Fragment) OS=Lytechinus pictus PE=3 SV=1	0,0194	0,0005	up	up	up	up	up	up
MPF_NU1M.1.2	NU1M_DANRE (sp|Q9MIZ0) NADH-ubiquinone oxidoreductase chain 1 OS=Danio rerio GN=mt-nd1 PE=3 SV=1	0,0304	0,0019	up	up	up	up	up	up
MPF_LOC101166342.1.1	XM_004080448.1 PREDICTED: Oryzias latipes receptor-type tyrosine-protein phosphatase epsilon-like (LOC101166342), mRNA	0,0211	0,0006	up	up	up	up	up	up
MPF_contig_007515	NA	0,0403	0,0043	down	down	up	down	up	up
MPF_LOC101472989.2.6	XM_004566934.1 PREDICTED: Maylandia zebra CAP-Gly domain-containing linker protein 1-like (LOC101472989), transcript variant X5, mRNA	0,0319	0,0022	up	down	up	down	up	up
MPF_LOC101471000.1.1	XM_004575946.1 PREDICTED: Maylandia zebra rap1 GTPase-GDP dissociation stimulator 1-like (LOC101471000), transcript variant X2, mRNA	0,0307	0,0019	down	up	up	up	up	up
MPF_LOC100695240.1.2	XP_003452569.1 PREDICTED: calcium/calmodulin-dependent protein kinase type IV-like [Oreochromis niloticus]	0,0054	0,0000	down	down	down	down	down	down
MPF_LOC101479799.1.3	XM_004571889.1 PREDICTED: Maylandia zebra protein NDRG3-like (LOC101479799), mRNA	0,0335	0,0025	down	up	down	up	down	down
MPF_LOC101470650.1.2	XM_004540130.1 PREDICTED: Maylandia zebra nesprin-1-like (LOC101470650), transcript variant X2, mRNA	0,0433	0,0052	down	down	down	down	down	down
MPF_LOC100708198.1.1	XP_003453989.1 PREDICTED: wiskott-Aldrich syndrome protein family member 3-like [Oreochromis niloticus]	0,0236	0,0008	down	up	up	up	up	up
MPF_LOC101478889.2.3	XM_004561424.1 PREDICTED: Maylandia zebra protein yippee-like 2-like (LOC101478889), transcript variant X2, mRNA	0,0107	0,0001	down	down	up	up	up	up
MPF_LOC101464804.1.1	XM_004556769.1 PREDICTED: Maylandia zebra ankyrin-3-like (LOC101464804), transcript variant X1, mRNA	0,0327	0,0023	down	down	down	up	down	down
MPF_contig_007919	NA	0,0279	0,0015	down	down	down	up	down	down

MPF_contig_000796	XM_004539264.1 PREDICTED: Maylandia zebra alpha-1,6-mannosylglycoprotein 6-beta-Nacetylglucosaminyltransferase B-like (LOC101479752), transcript variant X1, mRNA	0,0098	0,0001 up	up	up	up	up	up
MPF_contig_007959	NA	0,0139	0,0001 down	down	down	down	down	down
MPF_LOC100703329.1.1	XP_003443108.1 PREDICTED: ras-related protein Rab-3D-like [Oreochromis niloticus]	0,0364	0,0032 down	up	up	up	up	up
MPF_LOC100696224.1.1	XP_003457485.1 PREDICTED: chromodomain-helicase-DNA-binding protein 8-like [Oreochromis niloticus]	0,0084	0,0000 up	up	up	down	up	up
MPF_LOC101486993.1.1	XM_004554270.1 PREDICTED: Maylandia zebra sodium-dependent neutral amino acid transporter SLC6A17-like (LOC101486993), mRNA	0,0205	0,0005 down	down	down	up	down	down
MPF_contig_008114	NA	0,0294	0,0017 down	up	up	up	up	up
MPF_LOC101474542.1.1	XM_004565746.1 PREDICTED: Maylandia zebra stathmin-4-like (LOC101474542), transcript variant X2, mRNA	0,0188	0,0004 down	down	up	down	up	up
MPF_contig_008128	NA	0,0213	0,0006 up	up	down	down	down	down
MPF_LOC101163366.1.1	XM_004081463.1 PREDICTED: Oryzias latipes tetraspanin-7-like (LOC101163366), mRNA	0,0222	0,0007 down	up	up	up	up	up
MPF_contig_008143	NA	0,0291	0,0017 up	up	up	down	up	up
MPF_contig_008230	NA	0,0154	0,0002 up	down	down	down	down	down
MPF_LOC101484672.1.6	XM_004548379.1 PREDICTED: Maylandia zebra lysine-specific demethylase 7A-like (LOC101484672), transcript variant X2, mRNA	0,0410	0,0045 up	up	up	up	up	up
MPF_LOC100698899.1.1	XM_003457691.1 PREDICTED: Oreochromis niloticus protein PAT1 homolog 1-like (LOC100698899), mRNA	0,0290	0,0017 up	up	up	up	up	up
MPF_contig_008263	NA	0,0304	0,0019 up	up	up	down	up	up
MPF_LOC100693817.1.1	XM_003454059.1 PREDICTED: Oreochromis niloticus methionine synthase-like (LOC100693817), mRNA	0,0493	0,0074 down	down	up	up	up	up
MPF_contig_008294	NA	0,0143	0,0002 up	up	up	up	up	up
MPF_LOC100696737.1.2	XM_003451435.1 PREDICTED: Oreochromis niloticus hypothetical protein LOC100696737 (LOC100696737), mRNA	0,0413	0,0046 down	up	up	up	up	up
MPF_LOC101469329.1.2	XM_004564739.1 PREDICTED: Maylandia zebra nogo-B receptor-like (LOC101469329), mRNA	0,0371	0,0034 down	up	up	up	up	up
MPF_contig_008402	NA	0,0315	0,0021 up	down	down	down	down	down
MPF_contig_008419	NA	0,0150	0,0002 down	down	up	up	up	up
MPF_LOC101472438.1.4	XM_004575387.1 PREDICTED: Maylandia zebra collagen alpha-5(IV) chain-like (LOC101472438), mRNA	0,0109	0,0001 down	down	down	down	down	down
MPF_LOC101482364.1.4	XM_004541093.1 PREDICTED: Maylandia zebra cytoplasmic polyadenylation element-binding protein 4like (LOC101482364), mRNA	0,0210	0,0006 down	up	up	up	up	up
MPF_contig_008514	NA	0,0470	0,0064 down	up	up	up	up	up
MPF_LOC100705473.1.1	XM_003439642.1 PREDICTED: Oreochromis niloticus probable ATP-dependent RNA helicase YTHDC2like (LOC100705473), mRNA	0,0270	0,0013 down	up	up	up	up	up

MPF_LOC101476160.2.2	XM_004557247.1 PREDICTED: Maylandia zebra unconventional myosin-X-like (LOC101476160), mRNA	0,0401	0,0042	down	up	up	up	up	up
MPF_LOC101063630.1.1	XM_003979835.1 PREDICTED: Takifugu rubripes high mobility group-T protein-like (LOC101063630), mRNA	0,0394	0,0040	down	down	up	down	up	up
MPF_LOC100709406.1.1	XP_003440884.1 PREDICTED: interleukin-17F-like [Oreochromis niloticus]	0,0084	0,0000	up	up	up	up	up	up
MPF_LOC101477952.1.2	XM_004553681.1 PREDICTED: Maylandia zebra transmembrane protein 33-like (LOC101477952), mRNA	0,0419	0,0048	down	down	up	up	up	up
MPF_contig_008757	NA	0,0233	0,0008	down	up	up	up	up	up
MPF_contig_000877	NA	0,0213	0,0006	down	up	up	up	up	up
MPF_LOC101481643.1.2	XM_004574978.1 PREDICTED: Maylandia zebra sesquipedalian-1-like (LOC101481643), transcript variant X2, mRNA	0,0084	0,0000	down	up	up	up	up	up
MPF_LOC101468845.1.1	XM_004567562.1 PREDICTED: Maylandia zebra melanoma-associated antigen G1-like (LOC101468845), mRNA	0,0401	0,0042	down	up	up	up	up	up
MPF_contig_008801	NA	0,0459	0,0059	up	up	up	up	up	up
MPF_contig_008885	NA	0,0127	0,0001	down	up	up	up	up	up
MPF_LOC100712420.1.5	XP_003456711.1 PREDICTED: adenine phosphoribosyltransferase-like [Oreochromis niloticus]	0,0218	0,0006	down	down	down	down	down	down
MPF_contig_008944	XM_004556098.1 PREDICTED: Maylandia zebra transforming acidic coiled-coil-containing protein 2-like (LOC101481661), transcript variant X12, mRNA	0,0470	0,0064	down	up	up	up	up	up
MPF_LOC100698619.1.1	XP_003455532.1 PREDICTED: hypothetical protein LOC100698619 [Oreochromis niloticus]	0,0134	0,0001	down	up	up	up	up	up
MPF_LOC100151239.1.1	XP_001921419.1 PREDICTED: protein FAM89A-like [Danio rerio]	0,0243	0,0009	down	up	up	up	up	up
MPF_LOC101465301.1.1	XM_004538299.1 PREDICTED: Maylandia zebra procollagen galactosyltransferase 2-like (LOC101465301), mRNA	0,0174	0,0004	down	up	up	up	up	up
MPF_LOC101073876.1.2	XM_003978783.1 PREDICTED: Takifugu rubripes uncharacterized LOC101073876 (LOC101073876), mRNA	0,0411	0,0045	down	up	up	up	up	up
MPF_LOC101062903.1.1	XP_003965204.1 PREDICTED: protein phosphatase 1 regulatory subunit 3B-like [Takifugu rubripes]	0,0408	0,0044	down	up	up	up	up	up
MPF_LOC101483580.1.1	XM_004556746.1 PREDICTED: Maylandia zebra leucine zipper putative tumor suppressor 2 homolog (LOC101483580), mRNA	0,0332	0,0024	up	up	up	up	up	up
MPF_LOC101469799.2.5	XM_004544977.1 PREDICTED: Maylandia zebra zinc finger protein Xfin-like (LOC101469799), transcript variant X17, mRNA	0,0195	0,0005	down	down	down	up	down	down
MPF_LOC101467410.1.1	XM_004562377.1 PREDICTED: Maylandia zebra protein FAM20A-like (LOC101467410), mRNA	0,0472	0,0065	up	up	up	up	up	up
MPF_LOC100707640.1.2	XP_003451524.1 PREDICTED: hypothetical protein LOC100707640 [Oreochromis niloticus]	0,0128	0,0001	down	down	down	down	down	down
MPF_LOC101169532.9.45	XP_004070110.1 PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Oryzias latipes]	0,0060	0,0000	down	down	down	down	down	down

MPF_LOC100701582.4.9	XP_003455288.1 PREDICTED: zinc finger protein 236-like [Oreochromis niloticus]	0,0456	0,0058	down	up	up	up	up	up
MPF_contig_009137	NA	0,0171	0,0003	down	down	down	up	down	down
MPF_LOC100689854.5.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0,0277	0,0014	down	up	up	up	up	up
MPF_contig_009192	NA	0,0289	0,0016	down	up	up	up	up	up
MPF_contig_009278	NA	0,0232	0,0008	down	up	up	up	up	up
MPF_LOC101477924.3.5	XM_004571254.1 PREDICTED: Maylandia zebra carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1-like (LOC101477924), mRNA	0,0237	0,0009	up	down	down	down	down	down
MPF_contig_009283	NA	0,0228	0,0008	down	down	down	down	down	down
MPF_LOC101169293.1.10	XM_004072324.1 PREDICTED: Oryzias latipes pogo transposable element with KRAB domain-like (LOC101169293), mRNA	0,0130	0,0001	down	down	down	down	down	down
MPF_LOC101482903.1.2	XM_004550060.1 PREDICTED: Maylandia zebra superoxide dismutase [Cu-Zn]-like (LOC101482903), mRNA	0,0486	0,0072	up	up	up	up	up	up
MPF_LOC100689895.3.13	XP_003459184.1 PREDICTED: coxsackievirus and adenovirus receptor homolog [Oreochromis niloticus]	0,0461	0,0060	down	down	down	down	down	down
MPF_LOC101482781.1.4	XM_004569427.1 PREDICTED: Maylandia zebra ran-binding protein 9-like (LOC101482781), mRNA	0,0228	0,0008	up	up	up	up	up	up
MPF_LOC101064585.1.2	XM_003975501.1 PREDICTED: Takifugu rubripes DEP domain-containing protein 5-like (LOC101064585), mRNA	0,0169	0,0003	up	up	up	up	up	up
MPF_B2MG.1.10	B2MG_CYPCA (sp|Q03422) Beta-2-microglobulin OS=Cyprinus carpio GN=b2m PE=3 SV=1	0,0329	0,0023	down	up	up	up	up	up
MPF_MYO5A.1.1	MYO5A_CHICK (sp|Q02440) Unconventional myosin-Va OS=Gallus gallus GN=MYO5A PE=1 SV=1	0,0491	0,0073	down	down	up	up	up	up
MPF_contig_009396	NA	0,0380	0,0037	down	down	up	up	up	up
MPF_LOC100695994.10.40	XP_003443831.1 PREDICTED: zinc finger protein 850-like [Oreochromis niloticus]	0,0210	0,0006	down	up	up	up	up	up
MPF_LOC100148223.1.2	XP_003201586.1 PREDICTED: zinc finger protein 729-like [Danio rerio]	0,0394	0,0040	down	down	up	down	up	up
MPF_LOC101471502.1.1	XM_004539386.1 PREDICTED: Maylandia zebra AFG3-like protein 1-like (LOC101471502), transcript variant X2, mRNA	0,0344	0,0026	up	up	up	down	up	up
MPF_LOC101481574.1.1	XM_004538898.1 PREDICTED: Maylandia zebra nuclear factor interleukin-3-regulated protein-like (LOC101481574), mRNA	0,0354	0,0029	down	up	up	up	up	up
MPF_LOC100691083.1.3	XM_003444020.1 PREDICTED: Oreochromis niloticus diacylglycerol O-acyltransferase 1-like (LOC100691083), mRNA	0,0131	0,0001	up	up	up	down	up	up
MPF_contig_009512	NA	0,0195	0,0005	down	up	up	up	up	up
MPF_contig_009550	NA	0,0210	0,0006	down	up	up	up	up	up
MPF_LOC101061379.1.2	XP_003976891.1 PREDICTED: sushi, von Willebrand factor type A, EGF and pentraxin domaincontaining protein 1-like, partial [Takifugu rubripes]	0,0401	0,0042	down	down	down	down	down	down
MPF_LOC100689854.6.17	XP_003448732.1 PREDICTED: zinc finger protein 250-like [Oreochromis niloticus]	0,0275	0,0014	down	up	up	up	up	up

MPF_contig_009588	NA	0,0371	0,0034	down	up	up	up	up	up
MPF_contig_009617	NA	0,0154	0,0002	down	up	up	up	up	up
MPF_LOC101481552.5.41	XM_004575656.1 PREDICTED: Maylandia zebra protein NLRC3-like (LOC101481552), mRNA	0,0262	0,0012	down	down	up	up	up	up
MPF_ZNF84.5.14	ZNF84_HUMAN (sp|P51523) Zinc finger protein 84 OS=Homo sapiens GN=ZNF84 PE=1 SV=2	0,0435	0,0052	up	up	up	up	up	up
MPF_contig_009685	NA	0,0231	0,0008	up	up	up	up	up	up
MPF_contig_009706	NA	0,0230	0,0008	down	down	down	up	down	down
MPF_LOC101466459.8.29	XM_004554283.1 PREDICTED: Maylandia zebra semaphorin-3G-like (LOC101466459), mRNA	0,0287	0,0016	down	up	up	up	up	up
MPF_LOC101064585.2.2	XM_003975501.1 PREDICTED: Takifugu rubripes DEP domain-containing protein 5-like (LOC101064585), mRNA	0,0194	0,0005	up	up	up	up	up	up
MPF_contig_009735	NA	0,0367	0,0033	up	up	up	down	up	up
MPF_LOC100694557.5.24	XM_003458536.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100694557), mRNA	0,0224	0,0007	down	down	up	up	up	up
MPF_contig_009768	NA	0,0160	0,0002	down	down	down	down	down	down
MPF_LOC101470485.1.3	XM_004545890.1 PREDICTED: Maylandia zebra uncharacterized LOC101470485 (LOC101470485), mRNA	0,0288	0,0016	down	up	up	up	up	up
MPF_LOC101484672.2.6	XM_004548379.1 PREDICTED: Maylandia zebra lysine-specific demethylase 7A-like (LOC101484672), transcript variant X2, mRNA	0,0401	0,0042	down	down	up	down	up	up
MPF_LOC101487549.3.9	XM_004574260.1 PREDICTED: Maylandia zebra uncharacterized LOC101487549 (LOC101487549), mRNA	0,0171	0,0003	down	up	up	up	up	up
MPF_contig_009844	NA	0,0220	0,0007	down	down	up	down	up	up
MPF_LOC100698625.10.22	XM_003456694.1 PREDICTED: Oreochromis niloticus protein NLRC3-like (LOC100698625), mRNA	0,0148	0,0002	down	down	down	up	down	down
MPF_LOC101477603.1.4	XM_004564201.1 PREDICTED: Maylandia zebra mast/stem cell growth factor receptor kita-like (LOC101477603), transcript variant X1, mRNA	0,0488	0,0073	down	up	up	up	up	up
MPF_contig_009872	NA	0,0131	0,0001	down	up	down	up	down	down
MPF_contig_009909	NA	0,0354	0,0029	down	down	down	down	down	down
MPF_contig_009977	NA	0,0143	0,0002	down	down	down	down	down	down
MPF_contig_009982	NA	0,0364	0,0032	down	down	up	up	up	up
MPF_contig_009983	NA	0,0143	0,0002	up	up	down	down	down	down
MPF_LOC100692844.2.8	XM_003458212.1 PREDICTED: Oreochromis niloticus tripartite motif-containing protein 16-like (LOC100692844), mRNA	0,0418	0,0047	down	down	up	down	up	up

MPF_contig_010014	NA	0,0224	0,0007	down	up	up	up	up	up

5. Supplementary table 11

Gene position in Figure 29A	PhyloFish gene ID
1	MPF_contig_041411
2	MPF_contig_028987
3	MPF_LOC100933241.11.24
4	MPF_contig_026589
5	MPF_LOC101466982.2.2
6	MPF_LOC101466982.1.2
7	MPF_contig_007520
8	MPF_contig_005437
9	MPF_CCDC57.2.2
10	MPF_CCDC57.1.2
11	MPF_LOC100698539.1.1
12	MPF_contig_026772
13	MPF_LOC101467026.1.1
14	MPF_LOC101073532.1.2
15	MPF_contig_049067
16	MPF_contig_006673
17	MPF_contig_032700
18	MPF_LOC101475525.4.5
19	MPF_contig_036627
20	MPF_LOC101483148.1.1
21	MPF_LOC101475777.3.3
22	MPF_LOC101469709.1.2
23	MPF_contig_042113
24	MPF_contig_005296
25	MPF_LOC101471516.1.1
26	MPF_contig_036844
27	MPF_contig_047310
28	MPF_contig_004690
29	MPF_contig_027257
30	MPF_LOC101481611.1.2
31	MPF_LOC101475192.1.1
32	MPF_LOC100692490.4.4

33	MPF_LOC100695404.1.1
34	MPF_LOC101477465.2.3
35	MPF_contig_033809
36	MPF_contig_044670
37	MPF_contig_037677
38	MPF_LOC101482458.3.3
39	MPF_contig_001047
40	MPF_contig_000130
41	MPF_contig_005684
42	MPF_LOC101470901.6.10
43	MPF_LOC101470901.4.10
44	MPF_LOC101468504.2.2
45	MPF_LOC101167235.2.2
46	MPF_SC4AB.3.3
47	MPF_LOC101160029.2.2
48	MPF_LOC101474701.1.2
49	MPF_LOC101169532.11.45
50	MPF_LOC101463719.6.12
51	MPF_contig_025802
52	MPF_LOC101474183.2.2
53	MPF_LIN1.6.14
54	MPF_LOC101474742.1.1
55	MPF_contig_046848
56	MPF_LOC100709771.1.1
57	MPF_LOC101158032.1.2
58	MPF_contig_003893
59	MPF_LOC100705728.13.17
60	MPF_RU17.1.1
61	MPF_LOC100712073.1.1
62	MPF_contig_017105
63	MPF_IFIT5.4.9
64	MPF_LOC100706439.1.2
65	MPF_LOC101481352.2.3
66	MPF_contig_002474

67	MPF_LOC101471998.1.1
68	MPF_LOC100699959.1.1
69	MPF_LOC101463599.2.2
70	MPF_contig_043409
71	MPF_contig_034467
72	MPF_REST.2.2
73	MPF_contig_002686
74	MPF_LOC101467899.2.2
75	MPF_LOC101480481.1.1
76	MPF_LOC101476322.2.2
77	MPF_ZC3HD.1.3
78	MPF_MUC14A.1.1
79	MPF_LOC101473264.2.2
80	MPF_contig_038890
81	MPF_contig_019268
82	MPF_contig_038149
83	MPF_LOC101076067.1.1
84	MPF_LOC100699424.5.7
85	MPF_LOC101476997.1.2
86	MPF_LOC100693266.1.1
87	MPF_LOC101474771.1.1
88	MPF_LOC101465583.5.7
89	MPF_LOC100690779.1.2
90	MPF_contig_005001
91	MPF_contig_026051
92	MPF_G6PCA.2.1.1
93	MPF_LOC101161312.2.4
94	MPF_LOC100703705.5.14
95	MPF_LOC101479129.2.2
96	MPF_LOC101485836.2.2
97	MPF_LOC101485836.1.2
98	MPF_LOC100690589.3.3
99	MPF_LOC100701791.2.9
100	MPF_LOC100702327.1.1
101	MPF_LOC101482128.1.2

102	MPF_LOC101481486.1.2
103	MPF_LOC100698021.1.1
104	MPF_LOC101469041.3.4
105	MPF_contig_045124
106	MPF_LOC101464019.2.2
107	MPF_LOC101463583.1.1
108	MPF_contig_044426
109	MPF_LOC100696573.2.4
110	MPF_LOC101078877.1.1
111	MPF_contig_014987
112	MPF_contig_037127
113	MPF_LOC101472023.1.2
114	MPF_LOC101469710.1.2
115	MPF_contig_014481
116	MPF_contig_024773
117	MPF_contig_008498
118	MPF_contig_027614
119	MPF_LOC101483197.6.8
120	MPF_LOC100701598.3.6
121	MPF_LOC100693306.12.13
122	MPF_LOC100693306.3.13
123	MPF_LOC101483197.2.8
124	MPF_LOC101482434.3.5
125	MPF_contig_034129
126	MPF_LOC100697331.4.4
127	MPF_contig_036824
128	MPF_contig_038580
129	MPF_contig_024444
130	MPF_contig_019111
131	MPF_LOC101482619.1.3
132	MPF_LOC101077981.1.2
133	MPF_LOC101477400.4.4
134	MPF_BTNL2.1.7
135	MPF_LOC100694829.1.1

136	MPF_LOC100703514.1.1
137	MPF_LOC101484158.1.1
138	MPF_SELMODRAFT_443953.1.1
139	MPF_LOC101486920.1.1
140	MPF_PTPRT.1.1
141	MPF_LOC101472409.2.3
142	MPF_contig_037687
143	MPF_LOC100705145.1.1
144	MPF_LOC101485591.1.2
145	MPF_LOC100706791.1.1
146	MPF_BT3A2.1.1
147	MPF_LOC100707240.2.2
148	MPF_ATAD2.2.2
149	MPF_LOC101476812.1.3
150	MPF_LOC101468599.1.1
151	MPF_LOC100702771.1.1
152	MPF_LOC100699383.1.6
153	MPF_LOC101167402.1.2
154	MPF_LOC101472196.3.3
155	MPF_LOC101472196.2.3
156	MPF_contig_045852
157	MPF_LOC100705413.1.1
158	MPF_LOC100698929.2.2
159	MPF_LOC101484059.1.1
160	MPF_LOC100693188.1.1
161	MPF_AHNK.15.22
162	MPF_LOC101482877.1.1
163	MPF_LOC101470765.1.1
164	MPF_LOC101475558.1.3
165	MPF_contig_044256
166	MPF_LOC101479656.2.2
167	MPF_NIBL1.1.1
168	MPF_LOC101167377.1.1
169	MPF_LOC101477437.2.3
170	MPF_LOC101471584.1.1

171	MPF_contig_032727
172	MPF_contig_035430
173	MPF_contig_002641
174	MPF_contig_029749
175	MPF_LOC101073761.1.2
176	MPF_contig_028308

177	MPF_LOC100692784.3.3
178	MPF_LOC101476648.1.1
179	MPF_LOC100712218.1.1
180	MPF_LOC101468524.2.2
181	MPF_LOC101465566.2.2
182	MPF_LOC101463763.2.2
183	MPF_CXAR.1.5
184	MPF_LOC100700049.1.1
185	MPF_LOC101479727.6.6
186	MPF_THAP1.2.4
187	MPF_contig_016535
188	MPF_LOC100704882.1.2
189	MPF_LOC101465489.1.1
190	MPF_LOC100694761.1.2
191	MPF_LOC101160526.1.1
192	MPF_LOC101476898.4.4
193	MPF_LOC100710617.1.3
194	MPF_LOC100689966.1.1
195	MPF_LOC101169978.1.1
196	MPF_LOC101479843.1.1
197	MPF_LOC101175636.1.1
198	MPF_LOC100711789.3.22
199	MPF_contig_018475
200	MPF_contig_030303
201	MPF_LOC100689895.10.13
202	MPF_LOC100704735.1.2
203	MPF_contig_049139
204	MPF_LOC100698511.1.1

205	MPF_NEMVEDRAFT_V1G245263.1.1
206	MPF_LOC101075011.1.5
207	MPF_LOC100711789.8.22
208	MPF_LOC100712501.1.3
209	MPF_LOC101174554.1.1
210	MPF_LOC101161271.4.4
211	MPF_LOC100705304.1.1
212	MPF_LOC100709038.4.4
213	MPF_LOC100709038.2.4
214	MPF_LOC100704613.1.1
215	MPF_contig_036778
216	MPF_BT2A3.1.1
217	MPF_LOC101483625.1.2
218	MPF_LOC100708882.1.1
219	MPF_TEAD1.1.1
220	MPF_contig_047563
221	MPF_LOC100698625.6.22
222	MPF_LOC101155681.1.1
223	MPF_LOC100558617.2.2
224	MPF_contig_036321
225	MPF_LOC101471273.1.2
226	MPF_contig_044938
227	MPF_LOC100689895.12.13
228	MPF_LOC100689895.9.13
229	MPF_LOC101075011.4.5
230	MPF_TITIN.2.4
231	MPF_LOC100711789.5.22
232	MPF_LOC100711789.9.22
233	MPF_LOC101468624.1.1
234	MPF_UNC89.3.3
235	MPF_LOC100711789.2.22
236	MPF_TITIN.3.4
237	MPF_contig_044649
238	MPF_contig_009643

239	MPF_LOC101071192.1.1
240	MPF_LOC100709659.1.5
241	MPF_LOC101473204.1.1
242	MPF_LOC101476111.3.3
243	MPF_contig_022063
244	MPF_LSS.1.1
245	MPF_contig_002956
246	MPF_LOC100702553.2.4
247	MPF_LOC101480422.1.1
248	MPF_TBB7.1.1
249	MPF_LOC101481610.1.4
250	MPF_LOC100706345.1.1
251	MPF_LOC100710673.7.7
252	MPF_LOC101479341.5.9
253	MPF_contig_000405
254	MPF_contig_038164
255	MPF_LOC101466800.1.1
256	MPF_LOC101468190.1.2
257	MPF_LOC101155645.2.2
258	MPF_LOC100696573.1.4
259	MPF_contig_022452
260	MPF_LOC101471603.2.2
261	MPF_LOC100698039.1.1
262	MPF_LOC100704617.1.1
263	MPF_LOC101469943.2.2
264	MPF_LOC100537015.1.4
265	MPF_contig_016692
266	MPF_LOC101473661.1.1
267	MPF_contig_035679
268	MPF_LOC101468018.7.7
269	MPF_RS17.23.23
270	MPF_LOC101475031.1.1
271	MPF_ATF1A.1.1
272	MPF_contig_036939
273	MPF_contig_008939

274	MPF_LOC101482845.4.5
275	MPF_LOC100690684.1.1
276	MPF_LOC101465583.1.7
277	MPF_LOC101465583.2.7
278	MPF_PDE1A.1.1
279	MPF_LOC100707046.6.12
280	MPF_contig_048609
281	MPF_contig_042909
282	MPF_contig_005144
283	MPF_LOC101465885.1.2
284	MPF_LOC101162073.1.1
285	MPF_LOC101480816.1.2
286	MPF_LOC101482296.2.3
287	MPF_contig_028528
288	MPF_contig_043816
289	MPF_contig_016233
290	MPF_contig_020169
291	MPF_LOC101478741.2.2
292	MPF_LOC101480464.2.2
293	MPF_CSL2.1.2
294	MPF_LOC100692711.1.1
295	MPF_LOC100711031.2.4
296	MPF_LOC100705178.1.2
297	MPF_LOC101467334.2.2
298	MPF_contig_018509
299	MPF_contig_022012
300	MPF_LOC100701098.1.1
301	MPF_LOC101487341.2.3
302	MPF_contig_037497
303	MPF_LOC101079355.1.1
304	MPF_LOC101062260.2.2
305	MPF_contig_028781
306	MPF_PCGF1.2.2
307	MPF_LOC101472577.1.1

308	MPF_contig_041682
309	MPF_HACE1.3.3
310	MPF_LOC101470955.1.1
311	MPF_contig_033424
312	MPF_HACE1.1.3
313	MPF_NEMVEDRAFT_V1G131035.1.1
314	MPF_BRAFLDRAFT_92923.9.11
315	MPF_LOC101472722.1.1
316	MPF_LOC100697304.1.3
317	MPF_LOC101469089.4.8
318	MPF_contig_012824
319	MPF_LOC101487985.1.1
320	MPF_contig_012766
321	MPF_contig_010528
322	MPF_LOC101076755.1.1
323	MPF_LOC100706422.1.5
324	MPF_contig_004526
325	MPF_LOC101075645.1.1
326	MPF_LOC100692526.3.4
327	MPF_LOC100692526.1.4
328	MPF_PTPRF.1.1
329	MPF_LOC100710945.1.1
330	MPF_contig_012534
331	MPF_contig_036137
332	MPF_EIF4A1.2.3
333	MPF_LOC101477102.1.1
334	MPF_LOC100709351.7.10
335	MPF_LOC101474632.2.2
336	MPF_LOC100692372.1.1
337	MPF_LOC100711616.1.1
338	MPF_CYYR1.8.19
339	MPF_contig_037954
340	MPF_LOC100693306.9.13
341	MPF_LOC100694351.1.1
342	MPF_LOC101158586.1.1

343	MPF_LOC101477479.1.1
344	MPF_LOC101465736.1.3
345	MPF_LOC101464981.1.1
346	MPF_LOC100707856.1.1
347	MPF_LOC101476415.1.1
348	MPF_MUC18.1.2
349	MPF_MUC18.2.2
350	MPF_LOC101482280.1.1
351	MPF_contig_030312
352	MPF_LOC101474967.2.3
353	MPF_contig_014271
354	MPF_LOC100695025.1.1
355	MPF_LOC101476898.1.4
356	MPF_LOC101471138.1.1
357	MPF_LOC101464890.4.8
358	MPF_LOC101479311.1.1

6. Supplementary table 12

F7+ Gene Ontology list. PhyloFish gene ID, gene description, Gene Ontology Category, ID and Terms represented in the eggs transcriptome of the F7+ population. GO Categories are: P = Biological Process, F = Molecular Function and C = Cellular Component.

Sequence Name	Sequence Description	GO Category	GO ID	GO Term
MPF_ATF1A.1.1	ATPase inhibitor mitochondrial-like	P	GO:0009790	embryo development
MPF_ATF1A.1.1	ATPase inhibitor mitochondrial-like	C	GO:0005739	mitochondrion
MPF_ATF1A.1.1	ATPase inhibitor mitochondrial-like	F	GO:0030234	enzyme regulator activity
MPF_contig_008939	rho guanine nucleotide exchange factor 9 isoform X2	P	GO:0007165	signal transduction
MPF_contig_008939	rho guanine nucleotide exchange factor 9 isoform X2	F	GO:0003674	molecular_function
MPF_contig_016233	reticulon-4 isoform X1	C	GO:0005737	cytoplasm
MPF_contig_016233	reticulon-4 isoform X1	C	GO:0005783	endoplasmic reticulum
MPF_contig_041682	metal transporter CNNM2	P	GO:0042592	homeostatic process
MPF_contig_041682	metal transporter CNNM2	P	GO:0048856	anatomical structure development
MPF_contig_041682	metal transporter CNNM2	C	GO:0005575	cellular_component
MPF_CYYR1.8.19	Transposable element Tcb1	P	GO:0008150	biological_process

MPF_EIF4A1.2.3	eukaryotic initiation factor 4A-I	F	GO:0016887	ATPase activity
MPF_EIF4A1.2.3	eukaryotic initiation factor 4A-I	F	GO:0043167	ion binding
MPF_EIF4A1.2.3	eukaryotic initiation factor 4A-I	F	GO:0008135	translation factor activity, RNA binding
MPF_EIF4A1.2.3	eukaryotic initiation factor 4A-I	F	GO:0004386	helicase activity
MPF_EIF4A1.2.3	eukaryotic initiation factor 4A-I	C	GO:0005840	ribosome
MPF_HACE1.1.3	E3 ubiquitin- ligase HACE1 isoform X1	P	GO:0006464	cellular protein modification process
MPF_HACE1.1.3	E3 ubiquitin- ligase HACE1 isoform X1	F	GO:0016874	ligase activity
MPF_HACE1.3.3	E3 ubiquitin- ligase HACE1 isoform X1	P	GO:0006464	cellular protein modification process
MPF_HACE1.3.3	E3 ubiquitin- ligase HACE1 isoform X1	F	GO:0016874	ligase activity
MPF_LOC100558617.2.2	Transposon TX1 uncharacterized 149 kDa	P	GO:0006810	transport
MPF_LOC100558617.2.2	Transposon TX1 uncharacterized 149 kDa	C	GO:0005886	plasma membrane
MPF_LOC100558617.2.2	Transposon TX1 uncharacterized 149 kDa	F	GO:0003674	molecular_function
MPF_LOC100690684.1.1	FAM173B-like	C	GO:0005575	cellular_component
MPF_LOC100692372.1.1	serine threonine tyrosine-interacting 1	F	GO:0016791	phosphatase activity
MPF_LOC100692372.1.1	serine threonine tyrosine-interacting 1	P	GO:0006464	cellular protein modification process

MPF_LOC100692526.1.4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1	C	GO:0005575	cellular_component
MPF_LOC100692526.3.4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1	C	GO:0005575	cellular_component
MPF_LOC100692711.1.1	NAD(P)H-hydrate epimerase	C	GO:0005739	mitochondrion
MPF_LOC100692711.1.1	NAD(P)H-hydrate epimerase	F	GO:0016853	isomerase activity
MPF_LOC100693306.9.13	NLRC3-like isoform X3	F	GO:0043167	ion binding
MPF_LOC100694761.1.2	red long wavelength sensitive opsin	P	GO:0006464	cellular protein modification process
MPF_LOC100694761.1.2	red long wavelength sensitive opsin	C	GO:0005575	cellular_component
MPF_LOC100694761.1.2	red long wavelength sensitive opsin	F	GO:0004871	signal transducer activity
MPF_LOC100694761.1.2	red long wavelength sensitive opsin	P	GO:0050877	neurological system process
MPF_LOC100695025.1.1	CTD small phosphatase 2-A	F	GO:0016791	phosphatase activity
MPF_LOC100698039.1.1	cleavage and polyadenylation specificity factor subunit 4	F	GO:0043167	ion binding
MPF_LOC100698039.1.1	cleavage and polyadenylation specificity factor subunit 4	P	GO:0048856	anatomical structure development
MPF_LOC100698039.1.1	cleavage and polyadenylation specificity factor subunit 4	P	GO:0030154	cell differentiation

MPF_LOC100698625.6.22	NLRC3-like	F	GO:0043167	ion binding
MPF_LOC100701098.1.1	superoxide dismutase [Cu-Zn]	C	GO:0005623	cell
MPF_LOC100701098.1.1	superoxide dismutase [Cu-Zn]	F	GO:0016491	oxidoreductase activity
MPF_LOC100701098.1.1	superoxide dismutase [Cu-Zn]	P	GO:0042592	homeostatic process
MPF_LOC100701098.1.1	superoxide dismutase [Cu-Zn]	F	GO:0043167	ion binding
MPF_LOC100701098.1.1	superoxide dismutase [Cu-Zn]	P	GO:0006950	response to stress
MPF_LOC100704613.1.1	transmembrane 170B	C	GO:0005575	cellular_component
MPF_LOC100704617.1.1	transmembrane 9	C	GO:0005575	cellular_component
MPF_LOC100705178.1.2	Iron-sulfur cluster assembly enzyme mitochondrial	P	GO:0006790	sulfur compound metabolic process
MPF_LOC100705178.1.2	Iron-sulfur cluster assembly enzyme mitochondrial	P	GO:0042592	homeostatic process
MPF_LOC100705178.1.2	Iron-sulfur cluster assembly enzyme mitochondrial	C	GO:0005739	mitochondrion
MPF_LOC100705178.1.2	Iron-sulfur cluster assembly enzyme mitochondrial	P	GO:0051186	cofactor metabolic process
MPF_LOC100705178.1.2	Iron-sulfur cluster assembly enzyme mitochondrial	P	GO:0022607	cellular component assembly

MPF_LOC100705178.1.2	Iron-sulfur cluster assembly enzyme mitochondrial	F	GO:0043167	ion binding
MPF_LOC100705178.1.2	Iron-sulfur cluster assembly enzyme mitochondrial	P	GO:0051604	protein maturation
MPF_LOC100705178.1.2	Iron-sulfur cluster assembly enzyme mitochondrial	P	GO:0009058	biosynthetic process
MPF_LOC100705304.1.1	monoacylglycerol lipase ABHD12-like	C	GO:0005575	cellular_component
MPF_LOC100706345.1.1	nephrocystin-1 isoform X1	C	GO:0005929	cilium
MPF_LOC100706345.1.1	nephrocystin-1 isoform X1	P	GO:0048856	anatomical structure development
MPF_LOC100706422.1.5	trifunctional purine biosynthetic adenosine-3	P	GO:0044281	small molecule metabolic process
MPF_LOC100706422.1.5	trifunctional purine biosynthetic adenosine-3	C	GO:0005737	cytoplasm
MPF_LOC100706422.1.5	trifunctional purine biosynthetic adenosine-3	P	GO:0051186	cofactor metabolic process
MPF_LOC100706422.1.5	trifunctional purine biosynthetic adenosine-3	F	GO:0043167	ion binding
MPF_LOC100706422.1.5	trifunctional purine biosynthetic adenosine-3	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC100706422.1.5	trifunctional purine biosynthetic adenosine-3	P	GO:0009058	biosynthetic process

MPF_LOC100706422.1.5	trifunctional purine biosynthetic adenosine-3	P	GO:0044711	single-organism biosynthetic process
MPF_LOC100706422.1.5	trifunctional purine biosynthetic adenosine-3	F	GO:0016874	ligase activity
MPF_LOC100707046.6.12	NLRC3-like	F	GO:0003674	molecular_function
MPF_LOC100707856.1.1	transforming growth factor beta-2	P	GO:0008283	cell proliferation
MPF_LOC100707856.1.1	transforming growth factor beta-2	C	GO:0005615	extracellular space
MPF_LOC100707856.1.1	transforming growth factor beta-2	P	GO:0007165	signal transduction
MPF_LOC100707856.1.1	transforming growth factor beta-2	P	GO:0048856	anatomical structure development
MPF_LOC100707856.1.1	transforming growth factor beta-2	F	GO:0003674	molecular_function
MPF_LOC100707856.1.1	transforming growth factor beta-2	P	GO:0040007	growth
MPF_LOC100708882.1.1	transcriptional enhancer factor TEF-3-like	F	GO:0003677	DNA binding
MPF_LOC100708882.1.1	transcriptional enhancer factor TEF-3-like	F	GO:0003700	transcription factor activity, sequence-specific DNA binding
MPF_LOC100708882.1.1	transcriptional enhancer factor TEF-3-like	P	GO:0007165	signal transduction
MPF_LOC100708882.1.1	transcriptional enhancer factor TEF-3-like	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC100708882.1.1	transcriptional enhancer factor TEF-3-like	P	GO:0009058	biosynthetic process

MPF_LOC100708882.1.1	transcriptional enhancer factor TEF-3-like	C	GO:0043234	protein complex
MPF_LOC100708882.1.1	transcriptional enhancer factor TEF-3-like	C	GO:0005622	intracellular
MPF_LOC100709351.7.10	integral membrane 2B isoform X1	C	GO:0005575	cellular_component
MPF_LOC100710617.1.3	biogenesis of lysosome-related organelles complex 1 subunit 1	C	GO:0005829	cytosol
MPF_LOC100710617.1.3	biogenesis of lysosome-related organelles complex 1 subunit 1	C	GO:0043234	protein complex
MPF_LOC100710673.7.7	60S ribosomal L22	F	GO:0003723	RNA binding
MPF_LOC100710673.7.7	60S ribosomal L22	F	GO:0003735	structural constituent of ribosome
MPF_LOC100710673.7.7	60S ribosomal L22	P	GO:0048856	anatomical structure development
MPF_LOC100710673.7.7	60S ribosomal L22	P	GO:0030154	cell differentiation
MPF_LOC100710673.7.7	60S ribosomal L22	C	GO:0005829	cytosol
MPF_LOC100710673.7.7	60S ribosomal L22	P	GO:0042254	ribosome biogenesis
MPF_LOC100710673.7.7	60S ribosomal L22	C	GO:0005840	ribosome
MPF_LOC100710673.7.7	60S ribosomal L22	P	GO:0002376	immune system process
MPF_LOC100710673.7.7	60S ribosomal L22	P	GO:0006412	translation
MPF_LOC100710945.1.1	interferon-induced 44-like	F	GO:0043167	ion binding

MPF_LOC100711031.2.4	BCL2 adenovirus E1B 19 kDa -interacting 3-like	P	GO:0008219	cell death
MPF_LOC100711031.2.4	BCL2 adenovirus E1B 19 kDa -interacting 3-like	C	GO:0005739	mitochondrion
MPF_LOC100711616.1.1	rho guanine nucleotide exchange factor 2-like	P	GO:0007165	signal transduction
MPF_LOC100711616.1.1	rho guanine nucleotide exchange factor 2-like	F	GO:0043167	ion binding
MPF_LOC100711616.1.1	rho guanine nucleotide exchange factor 2-like	C	GO:0005622	intracellular
MPF_LOC101062260.2.2	calcium calmodulin-dependent kinase type II subunit alpha	P	GO:0009790	embryo development
MPF_LOC101062260.2.2	calcium calmodulin-dependent kinase type II subunit alpha	F	GO:0043167	ion binding
MPF_LOC101062260.2.2	calcium calmodulin-dependent kinase type II subunit alpha	P	GO:0006464	cellular protein modification process
MPF_LOC101062260.2.2	calcium calmodulin-dependent kinase type II subunit alpha	P	GO:0006520	cellular amino acid metabolic process
MPF_LOC101062260.2.2	calcium calmodulin-dependent kinase type II subunit alpha	F	GO:0016301	kinase activity
MPF_LOC101071192.1.1	grainyhead 3 homolog	P	GO:0009790	embryo development
MPF_LOC101071192.1.1	grainyhead 3 homolog	F	GO:0003677	DNA binding
MPF_LOC101071192.1.1	grainyhead 3 homolog	C	GO:0005694	chromosome

MPF_LOC101075011.4.5	collagen alpha-5(IV) chain	F	GO:0005198	structural molecule activity
MPF_LOC101075011.4.5	collagen alpha-5(IV) chain	C	GO:0043234	protein complex
MPF_LOC101075011.4.5	collagen alpha-5(IV) chain	C	GO:0005578	proteinaceous extracellular matrix
MPF_LOC101155645.2.2	villin isoform X1	P	GO:0007010	cytoskeleton organization
MPF_LOC101155645.2.2	villin isoform X1	F	GO:0008092	cytoskeletal protein binding
MPF_LOC101155681.1.1	myb SANT-like DNA-binding domain-containing 4	C	GO:0005634	nucleus
MPF_LOC101155681.1.1	myb SANT-like DNA-binding domain-containing 4	F	GO:0003677	DNA binding
MPF_LOC101155681.1.1	myb SANT-like DNA-binding domain-containing 4	P	GO:0008219	cell death
MPF_LOC101160526.1.1	zinc finger 395 isoform X1	F	GO:0003674	molecular_function
MPF_LOC101162073.1.1	C21orf2	P	GO:0006397	mRNA processing
MPF_LOC101169978.1.1	Y+L amino acid transporter 1	F	GO:0022891	substrate-specific transmembrane transporter activity
MPF_LOC101169978.1.1	Y+L amino acid transporter 1	F	GO:0022892	substrate-specific transporter activity
MPF_LOC101169978.1.1	Y+L amino acid transporter 1	F	GO:0022857	transmembrane transporter activity

MPF_LOC101169978.1.1	Y+L amino acid transporter 1	P	GO:0048856	anatomical structure development
MPF_LOC101169978.1.1	Y+L amino acid transporter 1	P	GO:0030154	cell differentiation
MPF_LOC101169978.1.1	Y+L amino acid transporter 1	C	GO:0005575	cellular_component
MPF_LOC101169978.1.1	Y+L amino acid transporter 1	P	GO:0002376	immune system process
MPF_LOC101175636.1.1	leucine-rich repeat-containing 24-like isoform X1	C	GO:0005575	cellular_component
MPF_LOC101464981.1.1	LRR and PYD domains-containing 12-like	C	GO:0005634	nucleus
MPF_LOC101464981.1.1	LRR and PYD domains-containing 12-like	F	GO:0003677	DNA binding
MPF_LOC101464981.1.1	LRR and PYD domains-containing 12-like	F	GO:0003700	transcription factor activity, sequence-specific DNA binding
MPF_LOC101464981.1.1	LRR and PYD domains-containing 12-like	C	GO:0005737	cytoplasm
MPF_LOC101464981.1.1	LRR and PYD domains-containing 12-like	F	GO:0043167	ion binding
MPF_LOC101464981.1.1	LRR and PYD domains-containing 12-like	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC101464981.1.1	LRR and PYD domains-containing 12-like	P	GO:0009058	biosynthetic process
MPF_LOC101464981.1.1	LRR and PYD domains-containing 12-like	C	GO:0043234	protein complex
MPF_LOC101465583.1.7	Histone	P	GO:0008283	cell proliferation

MPF_LOC101465583.1.7	Histone	F	GO:0043167	ion binding
MPF_LOC101465583.1.7	Histone	P	GO:0007155	cell adhesion
MPF_LOC101465583.1.7	Histone	P	GO:0009058	biosynthetic process
MPF_LOC101465583.1.7	Histone	C	GO:0005576	extracellular region
MPF_LOC101465583.1.7	Histone	C	GO:0005654	nucleoplasm
MPF_LOC101465583.1.7	Histone	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC101465583.1.7	Histone	P	GO:0065003	macromolecular complex assembly
MPF_LOC101465583.1.7	Histone	P	GO:0000902	cell morphogenesis
MPF_LOC101465583.1.7	Histone	C	GO:0000228	nuclear chromosome
MPF_LOC101465583.1.7	Histone	C	GO:0043234	protein complex
MPF_LOC101465583.1.7	Histone	P	GO:0007049	cell cycle
MPF_LOC101465583.1.7	Histone	P	GO:0000003	reproduction
MPF_LOC101465583.1.7	Histone	P	GO:0006950	response to stress
MPF_LOC101465583.1.7	Histone	P	GO:0040007	growth
MPF_LOC101465583.1.7	Histone	F	GO:0003677	DNA binding
MPF_LOC101465583.1.7	Histone	F	GO:0042393	histone binding

MPF_LOC101465583.1.7	Histone	P	GO:0051276	chromosome organization
MPF_LOC101465583.1.7	Histone	P	GO:0030154	cell differentiation
MPF_LOC101465583.2.7	histone	P	GO:0008283	cell proliferation
MPF_LOC101465583.2.7	histone	F	GO:0043167	ion binding
MPF_LOC101465583.2.7	histone	P	GO:0007155	cell adhesion
MPF_LOC101465583.2.7	histone	P	GO:0009058	biosynthetic process
MPF_LOC101465583.2.7	histone	C	GO:0005576	extracellular region
MPF_LOC101465583.2.7	histone	C	GO:0005654	nucleoplasm
MPF_LOC101465583.2.7	histone	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC101465583.2.7	histone	P	GO:0065003	macromolecular complex assembly
MPF_LOC101465583.2.7	histone	P	GO:0000902	cell morphogenesis
MPF_LOC101465583.2.7	histone	C	GO:0000228	nuclear chromosome
MPF_LOC101465583.2.7	histone	C	GO:0043234	protein complex
MPF_LOC101465583.2.7	histone	P	GO:0007049	cell cycle
MPF_LOC101465583.2.7	histone	P	GO:0000003	reproduction

MPF_LOC101465583.2.7	histone	P	GO:0006950	response to stress
MPF_LOC101465583.2.7	histone	P	GO:0040007	growth
MPF_LOC101465583.2.7	histone	F	GO:0003677	DNA binding
MPF_LOC101465583.2.7	histone	F	GO:0042393	histone binding
MPF_LOC101465583.2.7	histone	P	GO:0051276	chromosome organization
MPF_LOC101465583.2.7	histone	P	GO:0030154	cell differentiation
MPF_LOC101466800.1.1	kynurenine--oxoglutarate transaminase 1	F	GO:0043167	ion binding
MPF_LOC101466800.1.1	kynurenine--oxoglutarate transaminase 1	P	GO:0009058	biosynthetic process
MPF_LOC101467334.2.2	endophilin-A3-like isoform X1	C	GO:0005737	cytoplasm
MPF_LOC101467334.2.2	endophilin-A3-like isoform X1	P	GO:0048856	anatomical structure development
MPF_LOC101467334.2.2	endophilin-A3-like isoform X1	P	GO:0007267	cell-cell signaling
MPF_LOC101467334.2.2	endophilin-A3-like isoform X1	F	GO:0004871	signal transducer activity
MPF_LOC101468190.1.2	cell adhesion molecule 4 isoform X1	P	GO:0048646	anatomical structure formation involved in morphogenesis
MPF_LOC101468190.1.2	cell adhesion molecule 4 isoform X1	C	GO:0005575	cellular_component
MPF_LOC101468624.1.1	charged multivesicular body 1a	C	GO:0005634	nucleus

MPF_LOC101468624.1.1	charged multivesicular body 1a	C	GO:0005768	endosome
MPF_LOC101468624.1.1	charged multivesicular body 1a	P	GO:0016192	vesicle-mediated transport
MPF_LOC101468624.1.1	charged multivesicular body 1a	P	GO:0051276	chromosome organization
MPF_LOC101468624.1.1	charged multivesicular body 1a	P	GO:0048856	anatomical structure development
MPF_LOC101468624.1.1	charged multivesicular body 1a	P	GO:0007059	chromosome segregation
MPF_LOC101468624.1.1	charged multivesicular body 1a	P	GO:0007034	vacuolar transport
MPF_LOC101468624.1.1	charged multivesicular body 1a	P	GO:0007067	mitotic nuclear division
MPF_LOC101468624.1.1	charged multivesicular body 1a	C	GO:0043234	protein complex
MPF_LOC101468624.1.1	charged multivesicular body 1a	P	GO:0000278	mitotic cell cycle
MPF_LOC101470955.1.1	RNA-binding MEX3B	F	GO:0003723	RNA binding
MPF_LOC101470955.1.1	RNA-binding MEX3B	F	GO:0043167	ion binding
MPF_LOC101471138.1.1	zinc finger E-box-binding homeobox 1-like isoform X2	F	GO:0003677	DNA binding
MPF_LOC101471138.1.1	zinc finger E-box-binding homeobox 1-like isoform X2	F	GO:0043167	ion binding
MPF_LOC101472577.1.1	metal transporter CNNM2	P	GO:0042592	homeostatic process
MPF_LOC101472577.1.1	metal transporter CNNM2	P	GO:0048856	anatomical structure development

MPF_LOC101472577.1.1	metal transporter CNNM2	C	GO:0005575	cellular_component
MPF_LOC101472722.1.1	zinc finger 703-like	F	GO:0043167	ion binding
MPF_LOC101474632.2.2	integral membrane 2B isoform X2	C	GO:0005575	cellular_component
MPF_LOC101476111.3.3	serine threonine- kinase OSR1 isoform X3	F	GO:0043167	ion binding
MPF_LOC101476111.3.3	serine threonine- kinase OSR1 isoform X3	P	GO:0006464	cellular protein modification process
MPF_LOC101476111.3.3	serine threonine- kinase OSR1 isoform X3	P	GO:0006520	cellular amino acid metabolic process
MPF_LOC101476111.3.3	serine threonine- kinase OSR1 isoform X3	F	GO:0016301	kinase activity
MPF_LOC101476415.1.1	prostacyclin synthase-like	C	GO:0005737	cytoplasm
MPF_LOC101476415.1.1	prostacyclin synthase-like	F	GO:0016491	oxidoreductase activity
MPF_LOC101476415.1.1	prostacyclin synthase-like	F	GO:0043167	ion binding
MPF_LOC101476415.1.1	prostacyclin synthase-like	C	GO:0005783	endoplasmic reticulum
MPF_LOC101476898.1.4	microsomal glutathione S-transferase 1	C	GO:0005575	cellular_component
MPF_LOC101476898.4.4	Microsomal glutathione S-transferase 1	C	GO:0005575	cellular_component
MPF_LOC101476898.4.4	Microsomal glutathione S-transferase 1	F	GO:0003674	molecular_function
MPF_LOC101477102.1.1	eukaryotic initiation factor 4A-I	F	GO:0016887	ATPase activity

MPF_LOC101477102.1.1	eukaryotic initiation factor 4A-I	F	GO:0043167	ion binding
MPF_LOC101477102.1.1	eukaryotic initiation factor 4A-I	F	GO:0008135	translation factor activity, RNA binding
MPF_LOC101477102.1.1	eukaryotic initiation factor 4A-I	F	GO:0004386	helicase activity
MPF_LOC101477102.1.1	eukaryotic initiation factor 4A-I	C	GO:0005840	ribosome
MPF_LOC101479341.5.9	Fc receptor 5	C	GO:0005575	cellular_component
MPF_LOC101479843.1.1	mitochondrial dicarboxylate carrier	C	GO:0005739	mitochondrion
MPF_LOC101479843.1.1	mitochondrial dicarboxylate carrier	P	GO:0006810	transport
MPF_LOC101480422.1.1	tubulin beta-4B chain-like	P	GO:0008150	biological_process
MPF_LOC101480422.1.1	tubulin beta-4B chain-like	C	GO:0005856	cytoskeleton
MPF_LOC101480422.1.1	tubulin beta-4B chain-like	C	GO:0005737	cytoplasm
MPF_LOC101480422.1.1	tubulin beta-4B chain-like	F	GO:0003924	GTPase activity
MPF_LOC101480422.1.1	tubulin beta-4B chain-like	F	GO:0005198	structural molecule activity
MPF_LOC101480422.1.1	tubulin beta-4B chain-like	F	GO:0043167	ion binding
MPF_LOC101482296.2.3	transmembrane 56-B-like	C	GO:0005575	cellular_component
MPF_LOC101482845.4.5	ragulator complex LAMTOR5	C	GO:0005768	endosome
MPF_LOC101482845.4.5	ragulator complex LAMTOR5	P	GO:0008219	cell death

MPF_LOC101482845.4.5	ragulator complex LAMTOR5	C	GO:0043234	protein complex
MPF_LOC101482845.4.5	ragulator complex LAMTOR5	P	GO:0044403	symbiosis, encompassing mutualism through parasitism
MPF_LOC101483625.1.2	transcriptional enhancer factor TEF-1 isoform X3	P	GO:0009790	embryo development
MPF_LOC101483625.1.2	transcriptional enhancer factor TEF-1 isoform X3	F	GO:0003677	DNA binding
MPF_LOC101483625.1.2	transcriptional enhancer factor TEF-1 isoform X3	F	GO:0003700	transcription factor activity, sequence-specific DNA binding
MPF_LOC101483625.1.2	transcriptional enhancer factor TEF-1 isoform X3	P	GO:0007165	signal transduction
MPF_LOC101483625.1.2	transcriptional enhancer factor TEF-1 isoform X3	F	GO:0001071	nucleic acid binding transcription factor activity
MPF_LOC101483625.1.2	transcriptional enhancer factor TEF-1 isoform X3	C	GO:0043234	protein complex
MPF_LOC101483625.1.2	transcriptional enhancer factor TEF-1 isoform X3	F	GO:0008134	transcription factor binding
MPF_LOC101483625.1.2	transcriptional enhancer factor TEF-1 isoform X3	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC101483625.1.2	transcriptional enhancer factor TEF-1 isoform X3	P	GO:0009058	biosynthetic process
MPF_LOC101483625.1.2	transcriptional enhancer factor TEF-1 isoform X3	C	GO:0005654	nucleoplasm
MPF_LOC101487985.1.1	E3 ubiquitin- ligase NEDD4 isoform X1	P	GO:0006464	cellular protein modification process

MPF_LOC101487985.1.1	E3 ubiquitin- ligase NEDD4 isoform X1	F	GO:0016874	ligase activity
MPF_LSS.1.1	lanosterol synthase	F	GO:0016853	isomerase activity
MPF_MUC18.1.2	cell surface glyco MUC18 isoform X1	C	GO:0005575	cellular_component
MPF_PCGF1.2.2	serine threonine- kinase Chk2	F	GO:0043167	ion binding
MPF_PCGF1.2.2	serine threonine- kinase Chk2	P	GO:0006464	cellular protein modification process
MPF_PCGF1.2.2	serine threonine- kinase Chk2	P	GO:0006520	cellular amino acid metabolic process
MPF_PCGF1.2.2	serine threonine- kinase Chk2	F	GO:0016301	kinase activity
MPF_PCGF1.2.2	serine threonine- kinase Chk2	P	GO:0006950	response to stress
MPF_RS17.23.23	40S ribosomal S17	F	GO:0003735	structural constituent of ribosome
MPF_RS17.23.23	40S ribosomal S17	P	GO:0022618	ribonucleoprotein complex assembly
MPF_RS17.23.23	40S ribosomal S17	C	GO:0005829	cytosol
MPF_RS17.23.23	40S ribosomal S17	P	GO:0042254	ribosome biogenesis
MPF_RS17.23.23	40S ribosomal S17	C	GO:0005840	ribosome
MPF_RS17.23.23	40S ribosomal S17	P	GO:0006412	translation
MPF_TBB7.1.1	tubulin beta chain	P	GO:0007010	cytoskeleton organization

MPF_TBB7.1.1	tubulin beta chain	P	GO:0007165	signal transduction
MPF_TBB7.1.1	tubulin beta chain	P	GO:0022607	cellular component assembly
MPF_TBB7.1.1	tubulin beta chain	F	GO:0005198	structural molecule activity
MPF_TBB7.1.1	tubulin beta chain	F	GO:0043167	ion binding
MPF_TBB7.1.1	tubulin beta chain	C	GO:0043234	protein complex
MPF_TBB7.1.1	tubulin beta chain	C	GO:0005576	extracellular region
MPF_TBB7.1.1	tubulin beta chain	P	GO:0000278	mitotic cell cycle
MPF_TBB7.1.1	tubulin beta chain	P	GO:0006950	response to stress

MPF_TBB7.1.1	tubulin beta chain	P	GO:0002376	immune system process
MPF_TBB7.1.1	tubulin beta chain	C	GO:0005886	plasma membrane
MPF_TBB7.1.1	tubulin beta chain	C	GO:0005635	nuclear envelope
MPF_TBB7.1.1	tubulin beta chain	P	GO:0051301	cell division
MPF_TBB7.1.1	tubulin beta chain	C	GO:0005856	cytoskeleton
MPF_TBB7.1.1	tubulin beta chain	P	GO:0030705	cytoskeleton-dependent intracellular transport
MPF_TBB7.1.1	tubulin beta chain	C	GO:0005737	cytoplasm

MPF_TBB7.1.1	tubulin beta chain	F	GO:0003924	GTPase activity
MPF_TBB7.1.1	tubulin beta chain	F	GO:0019899	enzyme binding

7. Supplementary table 13

F1 Gene Ontology list. PhyloFish gene ID, gene description, Gene Ontology Category, ID and Terms represented in the eggs transcriptome of the F1 population. GO Categories are: P = Biological Process, F = Molecular Function and C = Cellular Component.

PhyloFish gene ID	Gene description	GO Category	GO ID	GO Term
MPF_BT3A2.1.1	butyrophilin subfamily 3 member A2-like	C	GO:0005575	cellular_component
MPF_contig_001047	vitrin isoform X1	C	GO:0005578	proteinaceous extracellular matrix
MPF_contig_019268	nuclease-sensitive element-binding 1 isoform X1	F	GO:0003677	DNA binding
MPF_contig_019268	nuclease-sensitive element-binding 1 isoform X1	F	GO:0003723	RNA binding
MPF_contig_019268	nuclease-sensitive element-binding 1 isoform X1	P	GO:0006397	mRNA processing
MPF_contig_019268	nuclease-sensitive element-binding 1 isoform X1	P	GO:0006412	translation
MPF_contig_034467	CAP-Gly domain-containing linker 1 isoform X4	P	GO:0007010	cytoskeleton organization

MPF_contig_034467	CAP-Gly domain-containing linker 1 isoform X4	P	GO:0006461	protein complex assembly
MPF_contig_038149	nuclease-sensitive element-binding 1 isoform X4	F	GO:0003677	DNA binding
MPF_contig_038149	nuclease-sensitive element-binding 1 isoform X4	F	GO:0003723	RNA binding
MPF_contig_038149	nuclease-sensitive element-binding 1 isoform X4	P	GO:0006397	mRNA processing
MPF_contig_038149	nuclease-sensitive element-binding 1 isoform X4	P	GO:0006412	translation
MPF_contig_042113	eyes absent homolog 3 isoform X1	F	GO:0016791	phosphatase activity
MPF_contig_042113	eyes absent homolog 3 isoform X1	F	GO:0043167	ion binding
MPF_contig_042113	eyes absent homolog 3 isoform X1	P	GO:0048856	anatomical structure development
MPF_contig_042113	eyes absent homolog 3 isoform X1	P	GO:0006464	cellular protein modification process
MPF_contig_042113	eyes absent homolog 3 isoform X1	C	GO:0043234	protein complex
MPF_contig_042113	eyes absent homolog 3 isoform X1	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_contig_042113	eyes absent homolog 3 isoform X1	P	GO:0009058	biosynthetic process
MPF_contig_042113	eyes absent homolog 3 isoform X1	C	GO:0005622	intracellular

MPF_contig_043409	CAP-Gly domain-containing linker 1 isoform X1	P	GO:0007010	cytoskeleton organization
MPF_contig_043409	CAP-Gly domain-containing linker 1 isoform X1	P	GO:0006461	protein complex assembly
MPF_contig_045852	ral GTPase-activating subunit alpha-2 isoform X5	C	GO:0005737	cytoplasm
MPF_contig_045852	ral GTPase-activating subunit alpha-2 isoform X5	P	GO:0007165	signal transduction
MPF_contig_045852	ral GTPase-activating subunit alpha-2 isoform X5	F	GO:0030234	enzyme regulator activity
MPF_CXAR.1.5	coxsackievirus and adenovirus receptor homolog	C	GO:0005575	cellular_component
MPF_G6PCA.2.1.1	glucose-6-phosphatase-like	P	GO:0044281	small molecule metabolic process
MPF_G6PCA.2.1.1	glucose-6-phosphatase-like	P	GO:0005975	carbohydrate metabolic process

MPF_G6PCA.2.1.1	glucose-6-phosphatase-like	C	GO:0005737	cytoplasm
MPF_G6PCA.2.1.1	glucose-6-phosphatase-like	F	GO:0016791	phosphatase activity
MPF_G6PCA.2.1.1	glucose-6-phosphatase-like	C	GO:0005783	endoplasmic reticulum
MPF_G6PCA.2.1.1	glucose-6-phosphatase-like	P	GO:0009058	biosynthetic process

MPF_G6PCA.2.1.1	glucose-6-phosphatase-like	P	GO:0044711	single-organism biosynthetic process
MPF_G6PCA.2.1.1	glucose-6-phosphatase-like	P	GO:0044723	single-organism carbohydrate metabolic process
MPF_IFIT5.4.9	Transposable element Tcb1 transposase	F	GO:0003677	DNA binding
MPF_IFIT5.4.9	Transposable element Tcb1 transposase	P	GO:0032196	transposition
MPF_IFIT5.4.9	Transposable element Tcb1 transposase	P	GO:0006259	DNA metabolic process
MPF_LOC100690589.3.3	major histocompatibility complex class I-related gene -like	C	GO:0043234	protein complex
MPF_LOC100690589.3.3	major histocompatibility complex class I-related gene -like	C	GO:0005886	plasma membrane
MPF_LOC100690589.3.3	major histocompatibility complex class I-related gene -like	F	GO:0003674	molecular_function
MPF_LOC100690589.3.3	major histocompatibility complex class I-related gene -like	P	GO:0002376	immune system process
MPF_LOC100690779.1.2	formimidoyltransferase-cyclodeaminase	P	GO:0008150	biological_process
MPF_LOC100690779.1.2	formimidoyltransferase-cyclodeaminase	F	GO:0043167	ion binding
MPF_LOC100690779.1.2	formimidoyltransferase-cyclodeaminase	C	GO:0005794	Golgi apparatus
MPF_LOC100692490.4.4	60S ribosomal L37a	C	GO:0005634	nucleus

MPF_LOC100692490.4.4	60S ribosomal L37a	F	GO:0003735	structural constituent of ribosome
MPF_LOC100692490.4.4	60S ribosomal L37a	C	GO:0005829	cytosol
MPF_LOC100692490.4.4	60S ribosomal L37a	C	GO:0005840	ribosome
MPF_LOC100692490.4.4	60S ribosomal L37a	C	GO:0005576	extracellular region
MPF_LOC100692490.4.4	60S ribosomal L37a	P	GO:0006412	translation
MPF_LOC100692784.3.3	iodotyrosine deiodinase 1	F	GO:0016491	oxidoreductase activity
MPF_LOC100692784.3.3	iodotyrosine deiodinase 1	C	GO:0005575	cellular_component
MPF_LOC100693188.1.1	ADP-ribosylation factor-binding GGA1-like	P	GO:0016192	vesicle-mediated transport
MPF_LOC100693188.1.1	ADP-ribosylation factor-binding GGA1-like	C	GO:0005737	cytoplasm
MPF_LOC100693188.1.1	ADP-ribosylation factor-binding GGA1-like	F	GO:0043167	ion binding
MPF_LOC100693188.1.1	ADP-ribosylation factor-binding GGA1-like	C	GO:0043234	protein complex
MPF_LOC100693188.1.1	ADP-ribosylation factor-binding GGA1-like	F	GO:0019899	enzyme binding
MPF_LOC100693266.1.1	N-lysine methyltransferase SMYD2	F	GO:0043167	ion binding
MPF_LOC100693266.1.1	N-lysine methyltransferase SMYD2	P	GO:0048856	anatomical structure development

MPF_LOC100693266.1.1	N-lysine methyltransferase SMYD2	F	GO:0008168	methyltransferase activity
MPF_LOC100693266.1.1	N-lysine methyltransferase SMYD2	P	GO:0003013	circulatory system process
MPF_LOC100693306.3.13	NLRC3-like isoform X1	F	GO:0043167	ion binding
MPF_LOC100698021.1.1	chymotrypsin-like elastase family member 3B	F	GO:0008233	peptidase activity
MPF_LOC100698929.2.2	E3 ubiquitin- ligase RNF25	F	GO:0043167	ion binding
MPF_LOC100699383.1.6	translationally-controlled tumor	P	GO:0007165	signal transduction
MPF_LOC100699383.1.6	translationally-controlled tumor	F	GO:0043167	ion binding
MPF_LOC100699383.1.6	translationally-controlled tumor	P	GO:0048856	anatomical structure development
MPF_LOC100699383.1.6	translationally-controlled tumor	C	GO:0043234	protein complex
MPF_LOC100699383.1.6	translationally-controlled tumor	F	GO:0008134	transcription factor binding
MPF_LOC100699383.1.6	translationally-controlled tumor	P	GO:0006810	transport
MPF_LOC100699383.1.6	translationally-controlled tumor	P	GO:0006950	response to stress
MPF_LOC100699383.1.6	translationally-controlled tumor	C	GO:0005654	nucleoplasm
MPF_LOC100699383.1.6	translationally-controlled tumor	C	GO:0005615	extracellular space
MPF_LOC100699383.1.6	translationally-controlled tumor	C	GO:0005768	endosome
MPF_LOC100699383.1.6	translationally-controlled tumor	C	GO:0005856	cytoskeleton

MPF_LOC100699383.1.6	translationally-controlled tumor	P	GO:0008219	cell death
MPF_LOC100699383.1.6	translationally-controlled tumor	P	GO:0042592	homeostatic process
MPF_LOC100699959.1.1	noelin-like	P	GO:0048856	anatomical structure development
MPF_LOC100700049.1.1	phosphatidylinositol-glycan biosynthesis class W	F	GO:0016746	transferase activity, transferring acyl groups
MPF_LOC100700049.1.1	phosphatidylinositol-glycan biosynthesis class W	C	GO:0005737	cytoplasm
MPF_LOC100700049.1.1	phosphatidylinositol-glycan biosynthesis class W	P	GO:0006629	lipid metabolic process
MPF_LOC100700049.1.1	phosphatidylinositol-glycan biosynthesis class W	P	GO:0006464	cellular protein modification process
MPF_LOC100700049.1.1	phosphatidylinositol-glycan biosynthesis class W	C	GO:0005783	endoplasmic reticulum
MPF_LOC100700049.1.1	phosphatidylinositol-glycan biosynthesis class W	P	GO:0009058	biosynthetic process
MPF_LOC100700049.1.1	phosphatidylinositol-glycan biosynthesis class W	P	GO:0044711	single-organism biosynthetic process
MPF_LOC100701791.2.9	MHC class I alpha antigen	C	GO:0043234	protein complex
MPF_LOC100701791.2.9	MHC class I alpha antigen	C	GO:0005886	plasma membrane

MPF_LOC100701791.2.9	MHC class I alpha antigen	F	GO:0003674	molecular_function
MPF_LOC100701791.2.9	MHC class I alpha antigen	P	GO:0002376	immune system process
MPF_LOC100702327.1.1	MHC class I antigen	C	GO:0043234	protein complex
MPF_LOC100702327.1.1	MHC class I antigen	C	GO:0005886	plasma membrane
MPF_LOC100702327.1.1	MHC class I antigen	F	GO:0003674	molecular_function
MPF_LOC100702327.1.1	MHC class I antigen	P	GO:0002376	immune system process
MPF_LOC100703514.1.1	bifunctional coenzyme A synthase	P	GO:0044281	small molecule metabolic process
MPF_LOC100703514.1.1	bifunctional coenzyme A synthase	P	GO:0051186	cofactor metabolic process
MPF_LOC100703514.1.1	bifunctional coenzyme A synthase	F	GO:0043167	ion binding
MPF_LOC100703514.1.1	bifunctional coenzyme A synthase	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC100703514.1.1	bifunctional coenzyme A synthase	P	GO:0009058	biosynthetic process
MPF_LOC100703514.1.1	bifunctional coenzyme A synthase	P	GO:0044711	single-organism biosynthetic process
MPF_LOC100703514.1.1	bifunctional coenzyme A synthase	F	GO:0016301	kinase activity
MPF_LOC100705145.1.1	phenylserine dehydratase-like isoform X2	F	GO:0043167	ion binding

MPF_LOC100705145.1.1	phenylserine dehydratase-like isoform X2	P	GO:0006520	cellular amino acid metabolic process
MPF_LOC100705413.1.1	piccolo-like isoform X4	F	GO:0043167	ion binding
MPF_LOC100705413.1.1	piccolo-like isoform X4	C	GO:0005575	cellular_component
MPF_LOC100705728.13.17	E3 ubiquitin- ligase TRIM21-like	F	GO:0043167	ion binding
MPF_LOC100705728.13.17	E3 ubiquitin- ligase TRIM21-like	C	GO:0005622	intracellular
MPF_LOC100706439.1.2	kinesin KIF1C	P	GO:0008150	biological_process
MPF_LOC100706439.1.2	kinesin KIF1C	F	GO:0043167	ion binding
MPF_LOC100706439.1.2	kinesin KIF1C	F	GO:0008092	cytoskeletal protein binding
MPF_LOC100706439.1.2	kinesin KIF1C	P	GO:0044699	single-organism process
MPF_LOC100709771.1.1	insulin-like growth factor-binding 2-B	C	GO:0005576	extracellular region
MPF_LOC100709771.1.1	insulin-like growth factor-binding 2-B	F	GO:0003674	molecular_function
MPF_LOC100709771.1.1	insulin-like growth factor-binding 2-B	P	GO:0040007	growth
MPF_LOC100712073.1.1	39S ribosomal mitochondrial	F	GO:0003735	structural constituent of ribosome
MPF_LOC100712073.1.1	39S ribosomal mitochondrial	C	GO:0005840	ribosome
MPF_LOC100712073.1.1	39S ribosomal mitochondrial	P	GO:0006412	translation

MPF_LOC101073761.1.2	malate cytoplasmic isoform X1	P	GO:0044281	small molecule metabolic process
MPF_LOC101073761.1.2	malate cytoplasmic isoform X1	P	GO:0005975	carbohydrate metabolic process
MPF_LOC101073761.1.2	malate cytoplasmic isoform X1	P	GO:0006091	generation of precursor metabolites and energy
MPF_LOC101073761.1.2	malate cytoplasmic isoform X1	F	GO:0016491	oxidoreductase activity
MPF_LOC101077981.1.2	MHC class II	C	GO:0043234	protein complex
MPF_LOC101077981.1.2	MHC class II	C	GO:0005886	plasma membrane
MPF_LOC101077981.1.2	MHC class II	P	GO:0002376	immune system process
MPF_LOC101078877.1.1	mitochondrial 2-oxoglutarate malate carrier	F	GO:0003735	structural constituent of ribosome
MPF_LOC101078877.1.1	mitochondrial 2-oxoglutarate malate carrier	C	GO:0005739	mitochondrion
MPF_LOC101078877.1.1	mitochondrial 2-oxoglutarate malate carrier	F	GO:0008092	cytoskeletal protein binding
MPF_LOC101078877.1.1	mitochondrial 2-oxoglutarate malate carrier	P	GO:0006810	transport
MPF_LOC101078877.1.1	mitochondrial 2-oxoglutarate malate carrier	P	GO:0006412	translation
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	F	GO:0032182	ubiquitin-like protein binding

MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	P	GO:0009790	embryo development
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	P	GO:0008283	cell proliferation
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	P	GO:0009056	catabolic process
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	F	GO:0043167	ion binding
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	P	GO:0006464	cellular protein modification process
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	C	GO:0000228	nuclear chromosome
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	C	GO:0043234	protein complex
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	P	GO:0006259	DNA metabolic process
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	P	GO:0006950	response to stress
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	P	GO:0000003	reproduction
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	P	GO:0051276	chromosome organization
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	C	GO:0005829	cytosol
MPF_LOC101158032.1.2	Ubiquitin-conjugating enzyme E2 A	F	GO:0019899	enzyme binding
MPF_LOC101167377.1.1	snRNA-activating complex subunit 1-like	C	GO:0005634	nucleus
MPF_LOC101167377.1.1	snRNA-activating complex subunit 1-like	F	GO:0003677	DNA binding
MPF_LOC101167377.1.1	snRNA-activating complex subunit 1-like	C	GO:0043234	protein complex

MPF_LOC101167377.1.1	snRNA-activating complex subunit 1-like	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC101167377.1.1	snRNA-activating complex subunit 1-like	P	GO:0009058	biosynthetic process
MPF_LOC101167402.1.2	tumor necrosis factor receptor superfamily member 12A	C	GO:0005575	cellular_component
MPF_LOC101463599.2.2	CAP-Gly domain-containing linker 1 isoform X5	P	GO:0007010	cytoskeleton organization
MPF_LOC101463599.2.2	CAP-Gly domain-containing linker 1 isoform X5	P	GO:0006461	protein complex assembly
MPF_LOC101463719.6.12	40S ribosomal S3a	P	GO:0009790	embryo development
MPF_LOC101463719.6.12	40S ribosomal S3a	C	GO:0005737	cytoplasm
MPF_LOC101463763.2.2	U2 small nuclear ribonucleo B	C	GO:0005634	nucleus
MPF_LOC101463763.2.2	U2 small nuclear ribonucleo B	F	GO:0003723	RNA binding
MPF_LOC101463763.2.2	U2 small nuclear ribonucleo B	P	GO:0006397	mRNA processing
MPF_LOC101464019.2.2	protocadherin-16-like	F	GO:0043167	ion binding
MPF_LOC101464019.2.2	protocadherin-16-like	P	GO:0007155	cell adhesion
MPF_LOC101464019.2.2	protocadherin-16-like	C	GO:0005886	plasma membrane

MPF_LOC101465583.5.7	histone	P	GO:0008283	cell proliferation
MPF_LOC101465583.5.7	histone	F	GO:0043167	ion binding
MPF_LOC101465583.5.7	histone	P	GO:0007155	cell adhesion
MPF_LOC101465583.5.7	histone	P	GO:0009058	biosynthetic process
MPF_LOC101465583.5.7	histone	C	GO:0005576	extracellular region
MPF_LOC101465583.5.7	histone	C	GO:0005654	nucleoplasm
MPF_LOC101465583.5.7	histone	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC101465583.5.7	histone	P	GO:0065003	macromolecular complex assembly
MPF_LOC101465583.5.7	histone	P	GO:0000902	cell morphogenesis
MPF_LOC101465583.5.7	histone	C	GO:0000228	nuclear chromosome
MPF_LOC101465583.5.7	histone	C	GO:0043234	protein complex
MPF_LOC101465583.5.7	histone	P	GO:0007049	cell cycle
MPF_LOC101465583.5.7	histone	P	GO:0000003	reproduction
MPF_LOC101465583.5.7	histone	P	GO:0006950	response to stress
MPF_LOC101465583.5.7	histone	P	GO:0040007	growth

MPF_LOC101465583.5.7	histone	F	GO:0003677	DNA binding
MPF_LOC101465583.5.7	histone	F	GO:0042393	histone binding
MPF_LOC101465583.5.7	histone	P	GO:0051276	chromosome organization
MPF_LOC101465583.5.7	histone	P	GO:0030154	cell differentiation
MPF_LOC101466982.1.2	pyruvate dehydrogenase E1 component subunit somatic mitochondrial isoform X2	P	GO:0044281	small molecule metabolic process
MPF_LOC101466982.1.2	pyruvate dehydrogenase E1 component subunit somatic mitochondrial isoform X2	P	GO:0006790	sulfur compound metabolic process
MPF_LOC101466982.1.2	pyruvate dehydrogenase E1 component subunit somatic mitochondrial isoform X2	F	GO:0016491	oxidoreductase activity
MPF_LOC101466982.1.2	pyruvate dehydrogenase E1 component subunit somatic mitochondrial isoform X2	P	GO:0051186	cofactor metabolic process
MPF_LOC101466982.1.2	pyruvate dehydrogenase E1 component subunit somatic mitochondrial isoform X2	P	GO:0009058	biosynthetic process
MPF_LOC101466982.1.2	pyruvate dehydrogenase E1 component subunit somatic mitochondrial isoform X2	C	GO:0043226	organelle
MPF_LOC101466982.1.2	pyruvate dehydrogenase E1 component subunit somatic mitochondrial isoform X2	P	GO:0044711	single-organism biosynthetic process

MPF_LOC101466982.1.2	pyruvate dehydrogenase E1 component subunit somatic mitochondrial isoform X2	C	GO:0005622	intracellular
MPF_LOC101467026.1.1	X-linked interleukin-1 receptor accessory -like 2	F	GO:0016757	transferase activity, transferring glycosyl groups
MPF_LOC101467026.1.1	X-linked interleukin-1 receptor accessory -like 2	P	GO:0007165	signal transduction
MPF_LOC101467026.1.1	X-linked interleukin-1 receptor accessory -like 2	P	GO:0006464	cellular protein modification process
MPF_LOC101467026.1.1	X-linked interleukin-1 receptor accessory -like 2	P	GO:0009058	biosynthetic process
MPF_LOC101467026.1.1	X-linked interleukin-1 receptor accessory -like 2	C	GO:0005575	cellular_component
MPF_LOC101468524.2.2	transcription factor Sp3-like isoform X2	F	GO:0043167	ion binding
MPF_LOC101469709.1.2	eyes absent homolog 3 isoform X1	F	GO:0016791	phosphatase activity
MPF_LOC101469709.1.2	eyes absent homolog 3 isoform X1	F	GO:0043167	ion binding
MPF_LOC101469709.1.2	eyes absent homolog 3 isoform X1	P	GO:0048856	anatomical structure development
MPF_LOC101469709.1.2	eyes absent homolog 3 isoform X1	P	GO:0006464	cellular protein modification process
MPF_LOC101469709.1.2	eyes absent homolog 3 isoform X1	C	GO:0043234	protein complex

MPF_LOC101469709.1.2	eyes absent homolog 3 isoform X1	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC101469709.1.2	eyes absent homolog 3 isoform X1	P	GO:0009058	biosynthetic process
MPF_LOC101469709.1.2	eyes absent homolog 3 isoform X1	C	GO:0005622	intracellular
MPF_LOC101470901.4.10	40S ribosomal S3	P	GO:0009790	embryo development
MPF_LOC101470901.4.10	40S ribosomal S3	F	GO:0016829	lyase activity
MPF_LOC101470901.4.10	40S ribosomal S3	C	GO:0005840	ribosome
MPF_LOC101470901.4.10	40S ribosomal S3	P	GO:0006259	DNA metabolic process
MPF_LOC101470901.4.10	40S ribosomal S3	P	GO:0006950	response to stress
MPF_LOC101470901.4.10	40S ribosomal S3	P	GO:0002376	immune system process
MPF_LOC101470901.4.10	40S ribosomal S3	P	GO:0006412	translation
MPF_LOC101470901.4.10	40S ribosomal S3	C	GO:0005634	nucleus
MPF_LOC101470901.4.10	40S ribosomal S3	F	GO:0003677	DNA binding
MPF_LOC101470901.4.10	40S ribosomal S3	F	GO:0003723	RNA binding
MPF_LOC101470901.4.10	40S ribosomal S3	F	GO:0003735	structural constituent of ribosome
MPF_LOC101470901.4.10	40S ribosomal S3	P	GO:0042592	homeostatic process

MPF_LOC101470901.4.10	40S ribosomal S3	F	GO:0004518	nuclease activity
MPF_LOC101470901.4.10	40S ribosomal S3	P	GO:0030154	cell differentiation
MPF_LOC101470901.4.10	40S ribosomal S3	C	GO:0005829	cytosol
MPF_LOC101470901.4.10	40S ribosomal S3	F	GO:0016798	hydrolase activity, acting on glycosyl bonds
MPF_LOC101470901.6.10	40S ribosomal S3	P	GO:0009790	embryo development
MPF_LOC101470901.6.10	40S ribosomal S3	F	GO:0016829	lyase activity
MPF_LOC101470901.6.10	40S ribosomal S3	C	GO:0005840	ribosome
MPF_LOC101470901.6.10	40S ribosomal S3	P	GO:0006259	DNA metabolic process
MPF_LOC101470901.6.10	40S ribosomal S3	P	GO:0006950	response to stress
MPF_LOC101470901.6.10	40S ribosomal S3	P	GO:0002376	immune system process
MPF_LOC101470901.6.10	40S ribosomal S3	P	GO:0006412	translation
MPF_LOC101470901.6.10	40S ribosomal S3	C	GO:0005634	nucleus
MPF_LOC101470901.6.10	40S ribosomal S3	F	GO:0003677	DNA binding
MPF_LOC101470901.6.10	40S ribosomal S3	F	GO:0003723	RNA binding

MPF_LOC101470901.6.10	40S ribosomal S3	F	GO:0003735	structural constituent of ribosome
MPF_LOC101470901.6.10	40S ribosomal S3	P	GO:0042592	homeostatic process
MPF_LOC101470901.6.10	40S ribosomal S3	F	GO:0004518	nuclease activity
MPF_LOC101470901.6.10	40S ribosomal S3	P	GO:0030154	cell differentiation
MPF_LOC101470901.6.10	40S ribosomal S3	C	GO:0005829	cytosol
MPF_LOC101470901.6.10	40S ribosomal S3	F	GO:0016798	hydrolase activity, acting on glycosyl bonds
MPF_LOC101471516.1.1	serine threonine- kinase OSR1-like	F	GO:0043167	ion binding
MPF_LOC101471516.1.1	serine threonine- kinase OSR1-like	P	GO:0006464	cellular protein modification process
MPF_LOC101471516.1.1	serine threonine- kinase OSR1-like	F	GO:0004871	signal transducer activity
MPF_LOC101471516.1.1	serine threonine- kinase OSR1-like	F	GO:0016301	kinase activity
MPF_LOC101471516.1.1	serine threonine- kinase OSR1-like	C	GO:0005622	intracellular
MPF_LOC101471584.1.1	cytosolic carboxypeptidase 4-like	F	GO:0008233	peptidase activity
MPF_LOC101471998.1.1	MFS-type transporter SLC18B1	P	GO:0055085	transmembrane transport
MPF_LOC101471998.1.1	MFS-type transporter SLC18B1	C	GO:0005575	cellular_component

MPF_LOC101472023.1.2	Mitochondrial import inner membrane translocase subunit Tim17-B	F	GO:0022891	substrate-specific transmembrane transporter activity
MPF_LOC101472023.1.2	Mitochondrial import inner membrane translocase subunit Tim17-B	F	GO:0022892	substrate-specific transporter activity
MPF_LOC101472023.1.2	Mitochondrial import inner membrane translocase subunit Tim17-B	F	GO:0022857	transmembrane transporter activity
MPF_LOC101472023.1.2	Mitochondrial import inner membrane translocase subunit Tim17-B	C	GO:0005739	mitochondrion
MPF_LOC101472023.1.2	Mitochondrial import inner membrane translocase subunit Tim17-B	F	GO:0008565	protein transporter activity
MPF_LOC101472023.1.2	Mitochondrial import inner membrane translocase subunit Tim17-B	C	GO:0043234	protein complex

MPF_LOC101472409.2.3	Formin-2	C	GO:0005856	cytoskeleton
MPF_LOC101472409.2.3	Formin-2	P	GO:0007010	cytoskeleton organization
MPF_LOC101472409.2.3	Formin-2	P	GO:0006461	protein complex assembly
MPF_LOC101472409.2.3	Formin-2	F	GO:0008092	cytoskeletal protein binding
MPF_LOC101473264.2.2	casein kinase II subunit alpha	F	GO:0043167	ion binding

MPF_LOC101473264.2.2	casein kinase II subunit alpha	P	GO:0006464	cellular protein modification process
MPF_LOC101473264.2.2	casein kinase II subunit alpha	F	GO:0016301	kinase activity
MPF_LOC101474701.1.2	histone	F	GO:0003677	DNA binding
MPF_LOC101474701.1.2	histone	P	GO:0008150	biological_process
MPF_LOC101474701.1.2	histone	C	GO:0000228	nuclear chromosome
MPF_LOC101475192.1.1	probable palmitoyltransferase ZDHHC11	F	GO:0016746	transferase activity, transferring acyl groups
MPF_LOC101475192.1.1	probable palmitoyltransferase ZDHHC11	F	GO:0043167	ion binding
MPF_LOC101475192.1.1	probable palmitoyltransferase ZDHHC11	C	GO:0005575	cellular_component
MPF_LOC101475777.3.3	dual specificity mitogen-activated kinase kinase 7 isoform X2	P	GO:0009790	embryo development
MPF_LOC101475777.3.3	dual specificity mitogen-activated kinase kinase 7 isoform X2	F	GO:0043167	ion binding
MPF_LOC101475777.3.3	dual specificity mitogen-activated kinase kinase 7 isoform X2	P	GO:0006464	cellular protein modification process
MPF_LOC101475777.3.3	dual specificity mitogen-activated kinase kinase 7 isoform X2	P	GO:0048646	anatomical structure formation involved in morphogenesis
MPF_LOC101475777.3.3	dual specificity mitogen-activated kinase kinase 7 isoform X2	F	GO:0016301	kinase activity

MPF_LOC101476322.2.2	ETS domain-containing transcription factor ERF	C	GO:0005634	nucleus
MPF_LOC101476322.2.2	ETS domain-containing transcription factor ERF	F	GO:0003677	DNA binding
MPF_LOC101476322.2.2	ETS domain-containing transcription factor ERF	F	GO:0003700	transcription factor activity, sequence-specific DNA binding
MPF_LOC101476322.2.2	ETS domain-containing transcription factor ERF	F	GO:0000988	transcription factor activity, protein binding
MPF_LOC101476322.2.2	ETS domain-containing transcription factor ERF	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC101476322.2.2	ETS domain-containing transcription factor ERF	P	GO:0009058	biosynthetic process
MPF_LOC101476812.1.3	DNA-directed RNA polymerase III subunit RPC8	F	GO:0003677	DNA binding
MPF_LOC101476812.1.3	DNA-directed RNA polymerase III subunit RPC8	F	GO:0016779	nucleotidyltransferase activity
MPF_LOC101476812.1.3	DNA-directed RNA polymerase III subunit RPC8	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC101476812.1.3	DNA-directed RNA polymerase III subunit RPC8	P	GO:0009058	biosynthetic process
MPF_LOC101477400.4.4	cyclin-G2-like	P	GO:0007049	cell cycle

MPF_LOC101477465.2.3	ribonuclease inhibitor-like	F	GO:0003700	transcription factor activity, sequence-specific DNA binding
MPF_LOC101477465.2.3	ribonuclease inhibitor-like	F	GO:0043167	ion binding
MPF_LOC101477465.2.3	ribonuclease inhibitor-like	P	GO:0034641	cellular nitrogen compound metabolic process
MPF_LOC101477465.2.3	ribonuclease inhibitor-like	P	GO:0009058	biosynthetic process
MPF_LOC101479129.2.2	collagen alpha-6(VI) chain isoform X1	C	GO:0043234	protein complex
MPF_LOC101479129.2.2	collagen alpha-6(VI) chain isoform X1	F	GO:0030234	enzyme regulator activity
MPF_LOC101479129.2.2	collagen alpha-6(VI) chain isoform X1	C	GO:0005578	proteinaceous extracellular matrix
MPF_LOC101479656.2.2	beta-taxilin-like	F	GO:0003674	molecular_function
MPF_LOC101480481.1.1	DNA repair XRCC3 isoform X2	F	GO:0016887	ATPase activity
MPF_LOC101480481.1.1	DNA repair XRCC3 isoform X2	F	GO:0003677	DNA binding
MPF_LOC101480481.1.1	DNA repair XRCC3 isoform X2	F	GO:0043167	ion binding
MPF_LOC101480481.1.1	DNA repair XRCC3 isoform X2	P	GO:0006259	DNA metabolic process
MPF_LOC101480481.1.1	DNA repair XRCC3 isoform X2	P	GO:0006950	response to stress
MPF_LOC101481352.2.3	kinesin KIF1C	P	GO:0008150	biological_process

MPF_LOC101481352.2.3	kinesin KIF1C	F	GO:0043167	ion binding
MPF_LOC101481352.2.3	kinesin KIF1C	F	GO:0008092	cytoskeletal protein binding
MPF_LOC101481352.2.3	kinesin KIF1C	P	GO:0044699	single-organism process
MPF_LOC101481486.1.2	MARCKS-related -like	F	GO:0016301	kinase activity
MPF_LOC101481611.1.2	elongation factor mitochondrial	C	GO:0005739	mitochondrion
MPF_LOC101481611.1.2	elongation factor mitochondrial	F	GO:0008135	translation factor activity, RNA binding
MPF_LOC101482128.1.2	MARCKS-related -like	F	GO:0016301	kinase activity
MPF_LOC101482434.3.5	NLRC3-like isoform X2	F	GO:0043167	ion binding
MPF_LOC101483197.2.8	NLRC3-like isoform X2	F	GO:0043167	ion binding
MPF_LOC101483197.6.8	NLRC3-like isoform X2	F	GO:0043167	ion binding
MPF_LOC101484059.1.1	spermatogenesis-associated 5	F	GO:0043167	ion binding
MPF_LOC101484158.1.1	E3 ubiquitin- ligase TRIM32	P	GO:0009790	embryo development
MPF_LOC101484158.1.1	E3 ubiquitin- ligase TRIM32	P	GO:0043473	pigmentation
MPF_LOC101484158.1.1	E3 ubiquitin- ligase TRIM32	F	GO:0043167	ion binding
MPF_LOC101484158.1.1	E3 ubiquitin- ligase TRIM32	P	GO:0006810	transport
MPF_LOC101484158.1.1	E3 ubiquitin- ligase TRIM32	P	GO:0044765	single-organism transport

MPF_LOC101484158.1.1	E3 ubiquitin- ligase TRIM32	C	GO:0005622	intracellular
MPF_LOC101484158.1.1	E3 ubiquitin- ligase TRIM32	F	GO:0016874	ligase activity
MPF_LOC101486920.1.1	LRR and PYD domains-containing 12-like	F	GO:0043167	ion binding

MPF_SC4AB.3.3	sodium channel type 2 subunit alpha	F	GO:0022891	substrate-specific transmembrane transporter activity
MPF_SC4AB.3.3	sodium channel type 2 subunit alpha	F	GO:0022892	substrate-specific transporter activity
MPF_SC4AB.3.3	sodium channel type 2 subunit alpha	F	GO:0022857	transmembrane transporter activity
MPF_SC4AB.3.3	sodium channel type 2 subunit alpha	P	GO:0050877	neurological system process
MPF_SC4AB.3.3	sodium channel type 2 subunit alpha	C	GO:0005886	plasma membrane

ABSTRACT/RÉSUMÉ

Study of the gene expression patterns in Eurasian perch (Perca fluviatilis Linnaeus, 1758) eggs related to their quality and to the domestication process

In the aquaculture context, increase on production are expected for the next years and yet, many reproductive issues are reported, including high mortality during early life stages. It concerns mostly species for which the domestication process is at the very beginning. My PhD work aimed at better understanding and potentially helping improving reproductive performance by investigating the transcriptomic content of the Eurasian perch (*Perca fluviatilis*) eggs in association with their quality which may constitute one of the sources for embryonic mortality. Eurasian perch is a species, in process of domestication, with strong importance for aquaculture diversification in inland Europe.

We employed microarray and RT-qPCR analyses to characterize gene expression patterns of Eurasian perch eggs presenting different potential to develop properly after fertilization. The experiments were conducted in two scientific contexts. In the first one, different methods to access egg quality were employed and their potential impacts on the transcriptomic results were evaluated. Therefore, when eggs were classified into the respective quality groups (high or low) using early embryonic survival as criteria, we were always able to identify distinct patterns of gene expression between quality groups. However, the number and nature of the differentially expressed genes (DEG) were variable and only one gene was commonly differentially expressed no matter the methods employed. This shows how transcriptomic results are sensitive to methods and should be deeply considered for intra- and inter-species comparisons. The second context consisted of investigating whether females presenting different histories of domestication would differ in their eggs mRNA content, and how it affects egg quality. In this study, females closest to wild populations presented better egg quality. In addition, two distinct patterns of gene expression were observed and more than 300 DEG were identified between populations. Because not much is known about the causes of high variability in reproductive performance in species in process of domestication, these findings could open new hypothesis of investigation. Finally, it became important to determine the moment until which the gene identified in the previous approaches were exclusively supporting embryonic early development. With this purpose, a preliminary study allowed making a first evaluation of the zygotic genome activation (ZGA) in this species.

As a whole, this study identified numerous maternal-effect genes which implication in embryos early development should be further investigated. In addition, these results suggest that more comparable methods to investigate egg quality in Eurasian perch could be established. These methods will make possible more precise studies in the variation of the development success under the influence of distinct factors, such the domestication process. Similar methods could also be established in other species considering their own common or divergent characters. It would help understanding molecular mechanisms species specific or widely found in finfish species.

Keywords: microarray, egg content, gene ontology, mRNA, fish populations, reproductive cycle, oogenesis

Etude du pattern d'expression des gènes dans les ovocytes de la perche commune (Perca fluviatilis Linnaeus, 1758) en fonction de leur qualité et du processus de domestication

Avec le déclin grandissant des prises de pêches, une augmentation de la production piscicole est attendue pour les prochaines années. Cependant, de nombreux problèmes de reproduction sont observés dans les élevages, principalement une mortalité élevée au début de la vie. Cela concerne principalement des espèces piscicoles pour lesquelles le processus de domestication commence. Mon travail de thèse a visé à mieux comprendre et potentiellement aider à améliorer les performances de reproduction en étudiant le contenu transcriptomique des œufs de perche commune (*Perca fluviatilis*) en lien avec leur qualité. Ces résultats participent à la compréhension des mécanismes moléculaires impliqués dans la mortalité embryonnaire précoce. Cette espèce, en cours de domestication, revêt une grande importance dans le contexte de la diversification des espèces d'intérêt aquacole en Europe continentale.

J'ai utilisé des analyses par puce à ADN et RT-qPCR pour caractériser les profils d'expression génique dans les œufs de perche de qualité variables. Les expériences ont été menées dans deux contextes scientifiques. Dans un premier temps, j'ai comparé l'effet des méthodes d'évaluation de la qualité des œufs sur les résultats transcriptomiques obtenus. Ainsi, les œufs ont été classés dans des groupes de qualité (bonne ou mauvaise) en utilisant divers critères liés au développement embryonnaire (taux de survie, taux de malformation) et divers seuils limites pour borner ces groupes. L'utilisation de critères de survie embryonnaire précoces a permis d'identifier des profils d'expression génique distincts entre les groupes de qualité. Cependant, le nombre et la nature des gènes exprimés de manière différentielle (DEG) étaient variables. Un seul gène était exprimé de manière différentielle dans toutes les analyses, quelles que soient les conditions. Cela montre à quel point les résultats transcriptomiques sont sensibles aux méthodes d'évaluation qui doivent être sérieusement pris en compte en amont de comparaisons intra et inter-espèces. Dans un deuxième temps, j'ai comparé le contenu transcriptomique d'œufs de femelles avec des histoires de domestication différentes. Dans cette étude, les femelles les plus proches des populations sauvages présentaient une meilleure qualité d'œufs. En outre, deux modèles distincts d'expression génique ont été observés et plus de 300 DEG ont été identifiés entre les populations. Étant donné que les causes de la variabilité élevée des performances de reproduction des espèces en cours de domestication sont mal connues, cette découverte pourrait ouvrir de nouvelles hypothèses d'investigation. Enfin, il devenait important de déterminer le moment où le gène identifié dans les approches précédentes soutiendrait exclusivement le développement embryonnaire précoce. Dans ce but, une étude préliminaire a permis de faire une première évaluation de l'activation du génome zygotique (ZGA) chez cette espèce.

L'ensemble de ces résultats ouvre la voie vers l'établissement de nouvelles méthodes d'investigation de la qualité des gamètes chez la perche commune. Ces méthodes permettront de faire des études précises de l'évolution du succès de développement à chaque génération au cours d'un processus de domestication. Des méthodes similaires pourraient être établies chez d'autres espèces en prenant en compte leurs particularités. Il serait alors intéressant de tenter d'étudier des espèces présentant des caractères communs ou divergents. Nous pourrons alors tenter de comprendre les régulations propres à chaque espèce ou au contraire largement retrouvés chez plusieurs espèces de poisson.

Mots clés : puces à ADN, contenu de l'ovocyte, ontologie des gènes, ARNm, populations de poissons, cycle de reproduction, oogenèse