



**HAL**  
open science

## Scrambled eggs: Proteomic portraits and novel biomarkers of egg quality in zebrafish (*Danio rerio*)

Ozlem Yilmaz, Amélie Patinote, Thuy Thao Vi Nguyen, Emmanuelle Com, Regis Lavigne, Charles Pineau, Craig V. Sullivan, Julien Bobe

### ► To cite this version:

Ozlem Yilmaz, Amélie Patinote, Thuy Thao Vi Nguyen, Emmanuelle Com, Regis Lavigne, et al.. Scrambled eggs: Proteomic portraits and novel biomarkers of egg quality in zebrafish (*Danio rerio*). PLoS ONE, 2017, 12 (11), pp.1-24. 10.1371/journal.pone.0188084 . hal-01640969

**HAL Id: hal-01640969**

**<https://hal.science/hal-01640969v1>**

Submitted on 20 Nov 2017

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License

RESEARCH ARTICLE

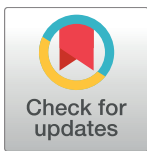
# Scrambled eggs: Proteomic portraits and novel biomarkers of egg quality in zebrafish (*Danio rerio*)

Ozlem Yilmaz<sup>1‡</sup>, Amélie Patinote<sup>1</sup>, Thao Vi Nguyen<sup>1</sup>, Emmanuelle Com<sup>2</sup>, Regis Lavigne<sup>2</sup>, Charles Pineau<sup>2</sup>, Craig V. Sullivan<sup>3</sup>, Julien Bobe<sup>1\*</sup>

**1** Laboratory of Fish Physiology and Genomics, INRA UR1037, Rennes Cedex, France, **2** Protim, Inserm U1085, Irset, Rennes Cedex, France, **3** Carolina AquaGyn, Raleigh, North Carolina, United States of America

‡ Current address: Department of Biology, University of Bergen, Bergen, Norway

\* [julien.bobe@inra.fr](mailto:julien.bobe@inra.fr)



**OPEN ACCESS**

**Citation:** Yilmaz O, Patinote A, Nguyen TV, Com E, Lavigne R, Pineau C, et al. (2017) Scrambled eggs: Proteomic portraits and novel biomarkers of egg quality in zebrafish (*Danio rerio*). PLoS ONE 12 (11): e0188084. <https://doi.org/10.1371/journal.pone.0188084>

**Editor:** Jon M. Jacobs, Pacific Northwest National Laboratory, UNITED STATES

**Received:** February 19, 2017

**Accepted:** October 31, 2017

**Published:** November 16, 2017

**Copyright:** © 2017 Yilmaz et al. This is an open access article distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

**Data Availability Statement:** The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository under the project name "Proteomic portraits of egg quality in zebrafish (*Danio rerio*)" with the Pooled Samples Experiment dataset accession number PXD005137 and project DOI number [10.6019/PXD005137](https://doi.org/10.6019/PXD005137), and the Multiple Samples Experiment dataset accession number PXD005129 and project DOI number [10.6019/PXD005129](https://doi.org/10.6019/PXD005129).

## Abstract

Egg quality is a complex biological trait and a major determinant of reproductive fitness in all animals. This study delivered the first proteomic portraits of egg quality in zebrafish, a leading biomedical model for early development. Egg batches of good and poor quality, evidenced by embryo survival for 24 h, were sampled immediately after spawning and used to create pooled or replicated sample sets whose protein extracts were subjected to different levels of fractionation before liquid chromatography and tandem mass spectrometry. Obtained spectra were searched against a zebrafish proteome database and detected proteins were annotated, categorized and quantified based on normalized spectral counts. Manually curated and automated enrichment analyses revealed poor quality eggs to be deficient of proteins involved in protein synthesis and energy and lipid metabolism, and of some vitellogenin products and lectins, and to have a surfeit of proteins involved in endo-lysosomal activities, autophagy, and apoptosis, and of some oncogene products, lectins and egg envelope proteins. Results of pathway and network analyses suggest that this aberrant proteomic profile results from failure of oocytes giving rise to poor quality eggs to properly transit through final maturation, and implicated Wnt signaling in the etiology of this defect. Quantitative comparisons of abundant proteins in good versus poor quality eggs revealed 17 candidate egg quality markers. Thus, the zebrafish egg proteome is clearly linked to embryo developmental potential, a phenomenon that begs further investigation to elucidate the root causes of poor egg quality, presently a serious and intractable problem in livestock and human reproductive medicine.

## Introduction

Poor gamete quality, a major concern in human reproductive medicine and livestock production, is also common in fishes and is an important limiting factor in global aquaculture [1]. Fish egg quality is defined by the ability to be fertilized and support development of normal

**Funding:** This work was supported by: (OY) Marie Skłodowska-Curie actions (MSCA)-FP7-PEOPLE-2013-IEF - 626272, [http://cordis.europa.eu/project/rcn/189931\\_en.html](http://cordis.europa.eu/project/rcn/189931_en.html); (OY) Region Bretagne- SAD (2013)-FISHEGG (8210); (JB) French National Research Agency (ANR-13-BSV7-0015), <http://www.agence-nationale-recherche.fr/?Project=ANR-13-BSV7-0015>; and (CVS) Carolina Aquagyn. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

**Competing interests:** The authors have declared that no competing interests exist.

embryos and larvae [2, 3]. This ‘developmental competence’ can be affected by intrinsic factors such as maternal age and genetics, as well as environmental factors arising from husbandry practices [4, 5, 6]. The mechanisms by which these various factors influence egg quality are generally not well understood. Diverse parameters such as egg diameter, morphology, buoyancy, yolk composition and fertilization rate, blastomere cell symmetry, activity of key enzymes in intermediary metabolism, and hatching rate have been used as fish egg quality criteria [6]. However, we know little about the causes and extent of variation in these parameters within and among females, between populations, and among different species spawning disparate types of eggs. Additionally, all of these parameters identify egg quality *a posteriori*; truly predictive biomarkers that may directly arise from and identify molecular processes determining egg quality remain to be identified.

Fishes exhibit a diverse array of reproductive modes and life histories, but oocytes of all species employ the same fundamental molecular processes to pass through a series of defined stages leading to production of fertilizable ova that can support offspring development [7, 8]. The vast majority of fishes are oviparous; their offspring develop *in ovo* independent of the mother and are totally dependent upon the contents of the yolk to sustain development. Recent investigations have focused on these molecular contents as potential determinants of egg quality that may be widely conserved among fishes and vertebrates in general [9, 3, 10]. Special attention has been paid to the earliest stages of development, during which times most losses are observed in cultured fishes.

Maternal mRNAs deposited in eggs direct vertebrate development until activation of zygotic transcription around mid-blastula stage [11, 12]. Certain maternal transcripts may exhibit differential abundance in fish eggs of varying quality [13]. Egg quality may also be predicted by subtle differences in the pattern of expression of large suites of maternal genes, constituting a ‘transcriptomic fingerprint’ of egg quality [14]. While the nature and abundance of maternal mRNAs appears to be important to fertility and embryo developmental competence, there has been little consistency between studies regarding the identity of relevant transcripts in different species [13]. Additionally, there seems to be little consistency between transcript abundance and product protein expression during development [15], which complicates interpretation of the transcriptomic findings. Furthermore, modification of proteins after their uptake into growing oocytes plays crucial roles in many aspects of oogenesis. These roles cannot be followed by genomic or transcriptomic technologies, necessitating application of proteomics for their elucidation. While proteomic profiling has been widely employed to study the cell biology of oocytes in many species, including humans, mice, pigs, fish and insects [16], it has rarely been applied to studies of fish egg quality. The spectrum of proteins present in eggs was partly evaluated and a few proteins associated with egg quality were identified in studies of rainbow trout (*Oncorhynchus mykiss*) [17], European sea bass (*Dicentrarchus labrax*) [18], Eurasian perch (*Perca fluviatilis*) [19], and hapuku (*Polyprion oxygeneios*) [20].

Zebrafish are an established biomedical model for research on developmental biology and an emerging model for fertility research [21]. They are a promising species for investigating proteomic determinants of egg quality because they are small, easily bred in the laboratory with short generation time, and lay large eggs of various quality every few days, with external fertilization of the transparent eggs in which embryonic development is easily observed [22]. A reference genome sequence is available, providing the needed proteome database for this line of research in zebrafish, which are the only teleost for which any detailed study of the egg proteome has been performed [23]. The proteome of zebrafish ovary has been characterized and compared to mRNA repertoires and transcript abundances [15], and studies have been conducted on proteomics of developing zebrafish embryos [24, 25, 26, 27]. However, no global proteomic analysis of eggs of different quality grades has been undertaken to identify

**Table 1. Spawning performance of females whose eggs were subjected to proteomic analyses.**

Experiment	Egg quality type	Female number	Eggs total(N)	Eggs incubated	% Intact eggs 2–3 hps	% Survival 8 hps	% Survival 24 hps	% Survival 48 hps	% Survival 72 hps
Pooled Samples	Good	1	115	60	100	100 (1.7)	<b>98.3 (0)</b>	98.3 (0)	98.3 (0)
		2	216	60	100	100 (0)	<b>100 (0)</b>	100 (0)	100 (0)
		3	355	60	100	100 (0)	<b>100 (0)</b>	100 (0)	100 (0)
		4	401	60	100	100 (0)	<b>100 (0)</b>	100 (0)	100 (0)
	Poor	5	129	60	96.7*	91.7 (96.4)	<b>3.3 (0)</b>	3.3 (0)	3.3 (0)
		6	224	60	100*	0	<b>0</b>	0	0
		7	165	53	100*	79.2 (76.2)	<b>11.3 (0)</b>	11.3 (0)	11.3 (0)
		8	266	63	100*	17.5 (0)	<b>14.3 (0)</b>	14.3 (0)	14.3 (0)
Multiple Samples	Good	9	401	60	100	100 (0)	<b>100 (0)</b>	100 (0)	100 (0)
		10	355	60	100	100 (0)	<b>100 (0)</b>	100 (0)	100 (0)
		11	216	60	100	100 (0)	<b>100 (0)</b>	100 (0)	100 (0)
		12	124	60	100	100 (0)	<b>100 (0)</b>	100 (0)	100 (0)
	Poor	13	251	60	100*	0	<b>0</b>	0	0
		14	187	60	100*	13.3 (0)	<b>11.7 (0)</b>	11.7 (0)	11.7 (0)
		15	481	60	100*	6.7 (0)	<b>6.7 (0)</b>	6.7 (0)	6.7 (0)
		16	404	61	96.7*	85.2 (67.3)	<b>16.4 (0)</b>	16.4 (0)	16.4 (0)

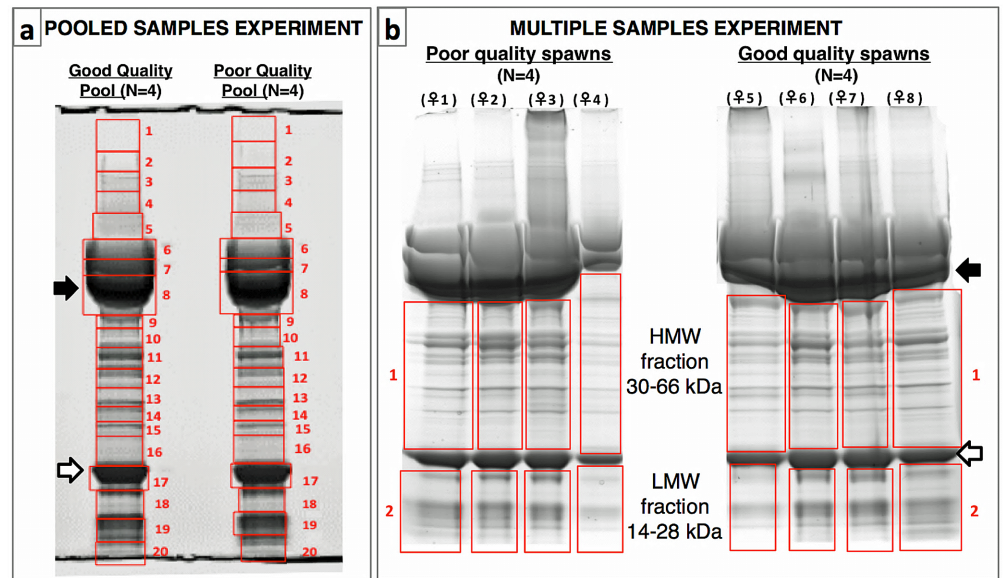
Shown are the experiment, egg quality type, female number, total number of eggs spawned, number of eggs incubated, percentage (%) of eggs intact at 2–3 hours post spawning (hps), and percentage of eggs yielding embryos surviving to 8, 24, 48 and 72 hps with the percentage of these that were abnormal shown in parentheses. For intact eggs at 2–3 hps, asterisks indicate that a high proportion of abnormal embryos showing asymmetric cell cleavage and/or early developmental arrest were observed but not quantified. The percentage of eggs yielding normal embryos surviving to 24 hps (bold text on gray background) was used to assign females to egg quality groups.

<https://doi.org/10.1371/journal.pone.0188084.t001>

physiological processes underpinning egg quality at the molecular level or to discover protein markers predictive of egg quality in this species. Therefore, the objectives of the present study were to compare the proteome profiles of good versus poor quality eggs, to identify potential egg quality marker proteins, and to shed light on the molecular processes by which these profiles and proteins may influence egg quality in zebrafish.

## Results

Zebrafish whose freshly spawned eggs were subjected to proteomic analysis in this study exhibited considerable variance in fecundity and in the proportion of eggs producing embryos surviving to 24 hours post spawning (hps), with no apparent relationship between fecundity and embryo survival (Table 1). For certain spawns, cumulative percent embryo survival decreased to low levels up to 24 hps, but no changes in survival were observed thereafter for up to 72 hps (Table 1). Therefore, survival of normal embryos to 24 hps was utilized as the measure of egg quality in this study. Spawns with a survival rate of normal embryos to 24 hps of >90% were considered to contain good quality eggs and spawns with a survival rate of normal embryos to 24 hps of <30% were considered to contain poor quality eggs. The actual 24 hps survival rates observed were >98% for good quality eggs and <17% for poor quality eggs (Table 1). It was observed that both good and poor quality eggs rapidly underwent cortical reaction and completed chorion hardening by the time they were sampled for proteomics analysis immediately after spawning. However, at 2–3 hps poor quality eggs invariably had a high incidence of abnormal embryos with asymmetric cell cleavage and/or developmental arrest at early cleavage stages; most embryos in poor quality eggs that survived to 8 hps were of this type (Table 1) and none of these survived to 24 hps. At 24 hps and later time points, mean survival of poor quality



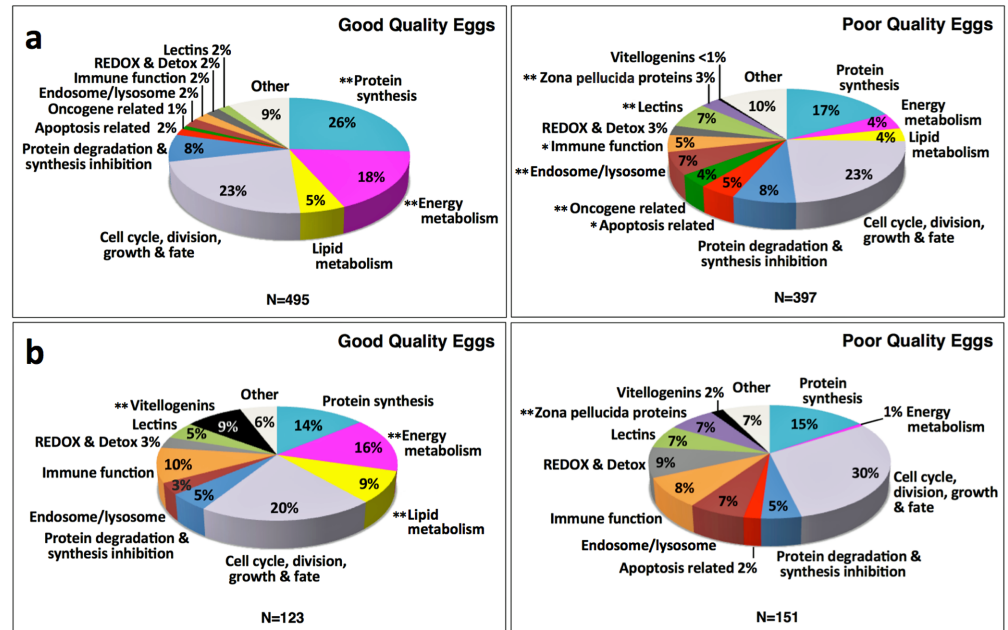
**Fig 1. Sample fractionation prior to LC-MS/MS in the egg quality experiments.** Panel a. Sample fractionation after SDS-PAGE in the Pooled Samples Experiment (N = 4 spawns per egg quality pool). Panel b. Sample fractionation after SDS-PAGE in the Multiple Samples Experiment (N = 4 replicate spawns per egg quality type). For each experiment, numbered frames in red indicate fractions excised from the gel and processed separately before submission to LC-MS/MS. Intact lipovitellin (Lv) heavy chain (closed arrows) and light chain (open arrows) were excluded in the Multiple Samples Experiment to better resolve other proteins. In total, 56 egg protein fractions were individually subjected to LC-MS/MS and downstream proteomic analyses. HMW; High molecular weight, LMW; Low molecular weight.

<https://doi.org/10.1371/journal.pone.0188084.g001>

eggs in the Pooled Samples Experiment ( $7.2 \pm 3.3\%$ ) and the Multiple Samples Experiment ( $8.7 \pm 3.5\%$ ) was significantly less than that of good quality eggs ( $99.6 \pm 0.4\%$  and  $100 \pm 0\%$ , respectively) (Tukey-Duckworth test,  $P < 0.05$ ).

In the Pooled Samples Experiment, proteins extracted from eggs from 4 good quality spawns or from 4 poor quality spawns were pooled before extensive fractionation by SDS-PAGE (20 fractions) prior to LC-MS/MS (Fig 1). Of the 2535 proteins that were identified, 892 (35.2%) showed a  $\geq 2$ -fold difference in normalized spectral counts (N-SC) between egg quality types ( $n = 545$ ), or were unique to an egg quality type (good quality  $n = 136$ , poor quality  $n = 211$ ), and for the purposes of this study were considered to be ‘differentially regulated’. The distribution of these differentially regulated proteins among 13 categories of physiological function chosen to represent most ( $\geq 90\%$ ) of these proteins significantly differed ( $\chi^2$ ,  $p < 0.0001$ ) between egg quality types (Fig 2a). Frequencies of up-regulated proteins related to energy metabolism and protein synthesis were significantly higher in good quality eggs, whereas frequencies of up-regulated zona pellucida proteins (ZPs) and lectins, as well as proteins related to endosome/lysosome function and oncogenes, were significantly higher in poor quality eggs.

An automated *Protein ANalysis THrough Evolutionary Relationships* (PANTHER) over-representation test of the 892 differentially regulated proteins revealed that mostly gene ontology (GO) Biological Process terms related to energy metabolism, including lipid metabolism, and to protein synthesis were preferentially enriched with proteins from good quality eggs (Fig 3). The corresponding GO Molecular Function, Protein Class, and Cellular Component terms enriched by these proteins were also consistent with a proteomic emphasis on energy metabolism and protein synthesis, as well as cell cycle-related activities (S1–S3 Figs). The GO

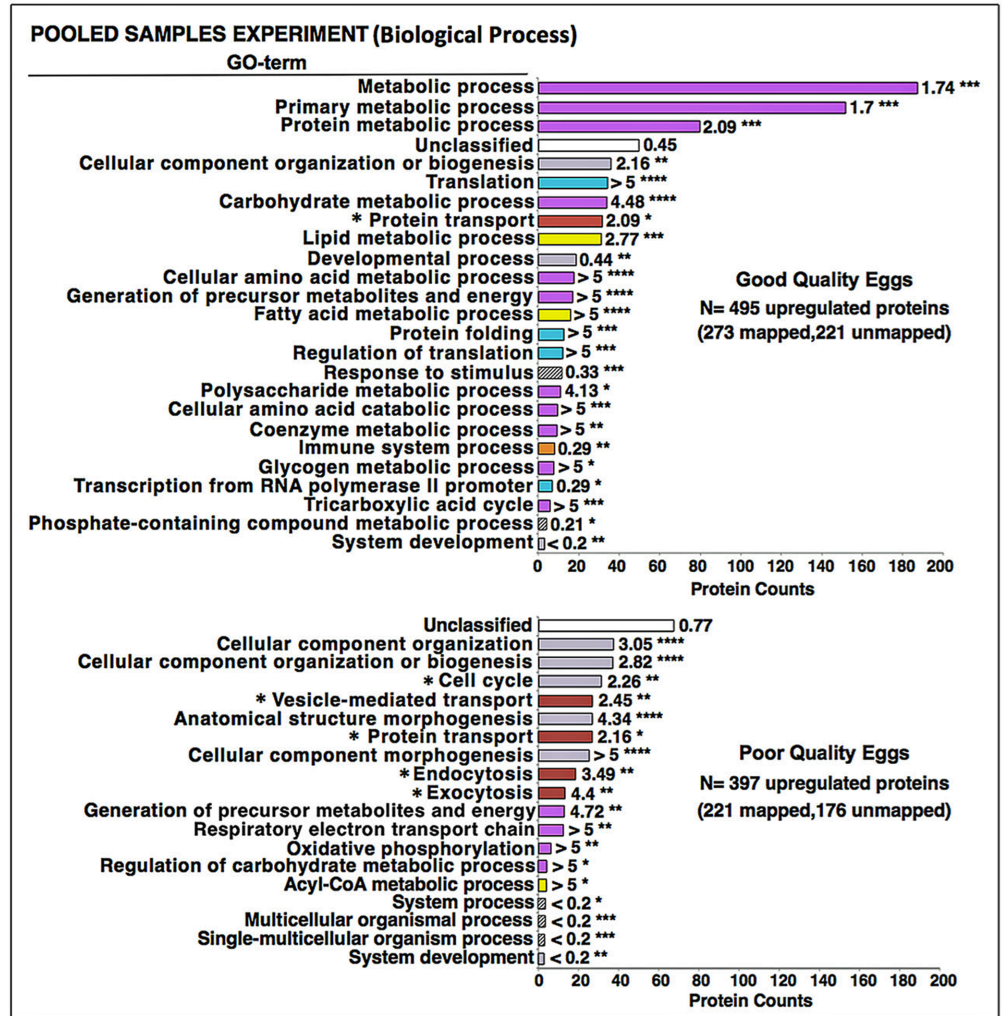


**Fig 2. Distribution of proteins up-regulated in good and poor quality zebrafish eggs among functional categories. Panel a.** Pooled Samples Experiment. **Panel b.** Multiple Samples Experiment. Only proteins common to both egg quality types with a  $\geq 2$ -fold difference in N-SC between egg quality types, or proteins unique to an egg quality type, were considered to be up-regulated for these analyses. In both experiments, the overall distribution of up-regulated proteins among functional categories significantly differed between egg quality types ( $\chi^2$ ,  $p < 0.0001$ ). Double asterisks indicate protein categories whose proportional representation differed significantly between egg quality types ( $\chi^2$ ,  $p < 0.05$ ) after Benjamini Hochberg correction for multiple post-hoc tests. Single asterisks indicate other protein categories with  $p$ -values from the post-hoc  $\chi^2$  analyses  $\leq 0.05$  before Benjamini Hochberg correction. Ensembl Protein IDs and associated gene, transcript and protein names, functional categories, type of regulation (unique or up-regulated), and fold-difference between egg quality types in common protein N-SC values are given in [S1 Table](#) (Pooled Samples Experiment) and [S2 Table](#) (Multiple Samples Experiment).

<https://doi.org/10.1371/journal.pone.0188084.g002>

Biological Process terms Cellular component organization, Cellular component organization or biogenesis, Cell cycle, Vesicle-mediated transport, Anatomical structure morphogenesis, Protein transport, Cellular component morphogenesis, Endocytosis, and Exocytosis were enriched with proteins up-regulated in poor quality eggs (Fig 3). The GO Molecular Function, Protein Class, and Cellular Component terms enriched with these proteins also indicated a proteome tailored to cytoskeletal activities such as vesicle-mediated transport, endocytosis and exocytosis, as well as activities relevant to the cell cycle (e.g. karyokinesis, cytokinesis) (S1–S3 Figs).

Among proteins with a  $\geq 5$ -fold change in N-SC between egg quality types, or unique to an egg quality type (Fig 4), which we considered to be “highly up-regulated”, those highly up-regulated in good quality eggs ( $n = 35$ ) were mainly related to protein synthesis (28.6%), energy metabolism (17.1%) and lipid metabolism (5.7%), and cell cycle, growth and fate regulation (20%), with the remaining categorized proteins being related to protein degradation and synthesis inhibition (8.6%) and apoptosis (2.9%). In this group, only two ribosomal proteins (rpl36-001, rpl36-002) and one tubulin (tubb2-001) were unique to good quality eggs. Corresponding proteins highly up-regulated in poor quality eggs ( $n = 30$ ) were mainly ZPs (23.3%) and lectin family members (20.0%), as well as proteins related to cell cycle, growth and fate regulation (16.7%), with the remaining categorized proteins being related to immune function (10.0%), energy metabolism (6.7%), lipid metabolism (6.7%) and protein synthesis (6.7%).

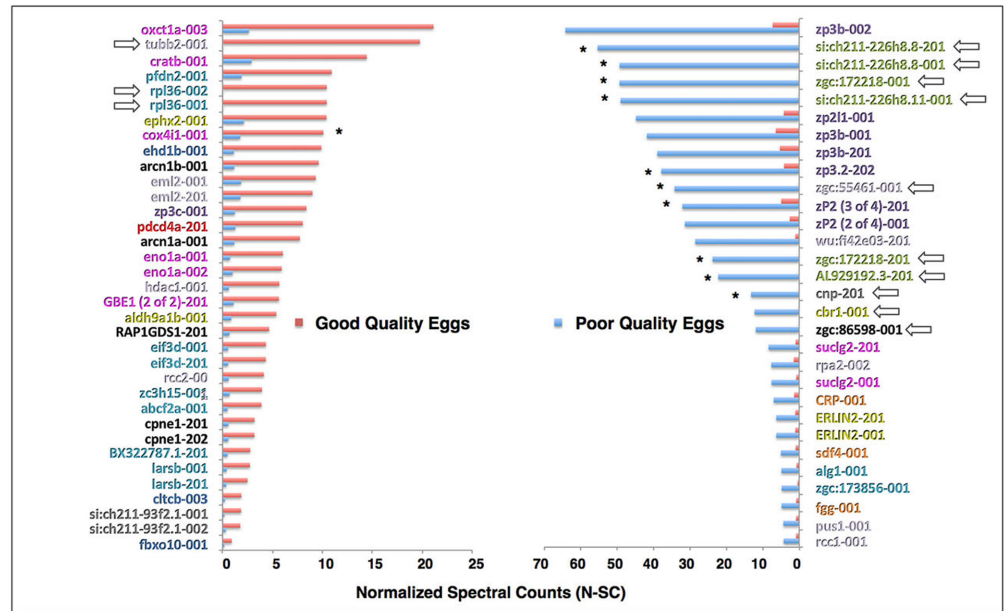


**Fig 3. Enrichment of biological process gene ontology (GO) terms with proteins up-regulated in the Pooled Samples Experiment.** Shown are the results of *Protein Analysis Through Evolutionary Relationships* (PANTHER) over-representation binomial tests [28] for enrichment of Biological Process GO terms with proteins up-regulated in good and poor quality zebrafish eggs in the Pooled Samples Experiment. **Top Panel.** Good quality eggs. **Bottom Panel.** Poor quality eggs. Horizontal bars indicate the number of proteins attributed to each GO term for which statistically significant results ( $p \leq 0.05$  after Bonferroni correction for multiple tests) were observed. Numbers next to the bars indicate the fold-enrichment with proteins attributed to each term and the number of asterisks indicates the significance level of the enrichment, as follows  $p \leq 0.05$  (\*),  $p \leq 0.01$  (\*\*),  $p \leq 0.001$  (\*\*\*), and  $p \leq 0.0001$  (\*\*\*\*). Where possible, horizontal bars are colored to indicate corresponding protein functional categories shown in Fig 2; energy metabolism (magenta), cell cycle, division, growth and fate (lavender), protein synthesis (light blue), endosome/lysosome-related activities (brown), lipid metabolism (yellow), and immune system-related activities (orange). For poor quality eggs, GO terms preceded by an asterisk involve cytoskeletal activities. See text for details.

<https://doi.org/10.1371/journal.pone.0188084.g003>

Aside from the lectins, only 4 of these proteins were unique to poor quality eggs including a tubulin (zgc:55461-001), carbonyl reductase (cbr1-001), casein kinase (zgc:86598-001) and 2', 3'-cyclic nucleotide 3' phosphodiesterase (cnp-201).

In the Multiple Samples Experiment, where protein extracts of eggs from 4 good quality spawns or from 4 poor quality spawns were individually subjected to limited fractionation by SDS-PAGE (2 fractions excluding the major yolk proteins) prior to LC-MS/MS (Fig 1), the 369 proteins identified in the High Molecular Weight (HMW) fraction and 438 proteins



**Fig 4. Proteins highly up-regulated in good or poor quality eggs in the Pooled Samples Experiment.** The proteins are named for the transcript(s) to which spectra were mapped; for full protein names see S1 Table. These proteins were either unique to an egg quality type or they showed a  $\geq 5$ -fold difference in N-SC between egg quality types, placing them in the top 2.3% of proteins showing such differences. **Left Panel.** Proteins highly up-regulated in good quality eggs. **Right Panel.** Proteins highly up-regulated in poor quality eggs. Where possible, protein (transcript) labels are color-coded to indicate functional categories to which the proteins were attributed (Fig 2). Arrows indicate proteins unique to an egg quality type. Asterisks indicate proteins detected and regulated in the same direction in the Multiple Samples Experiment.

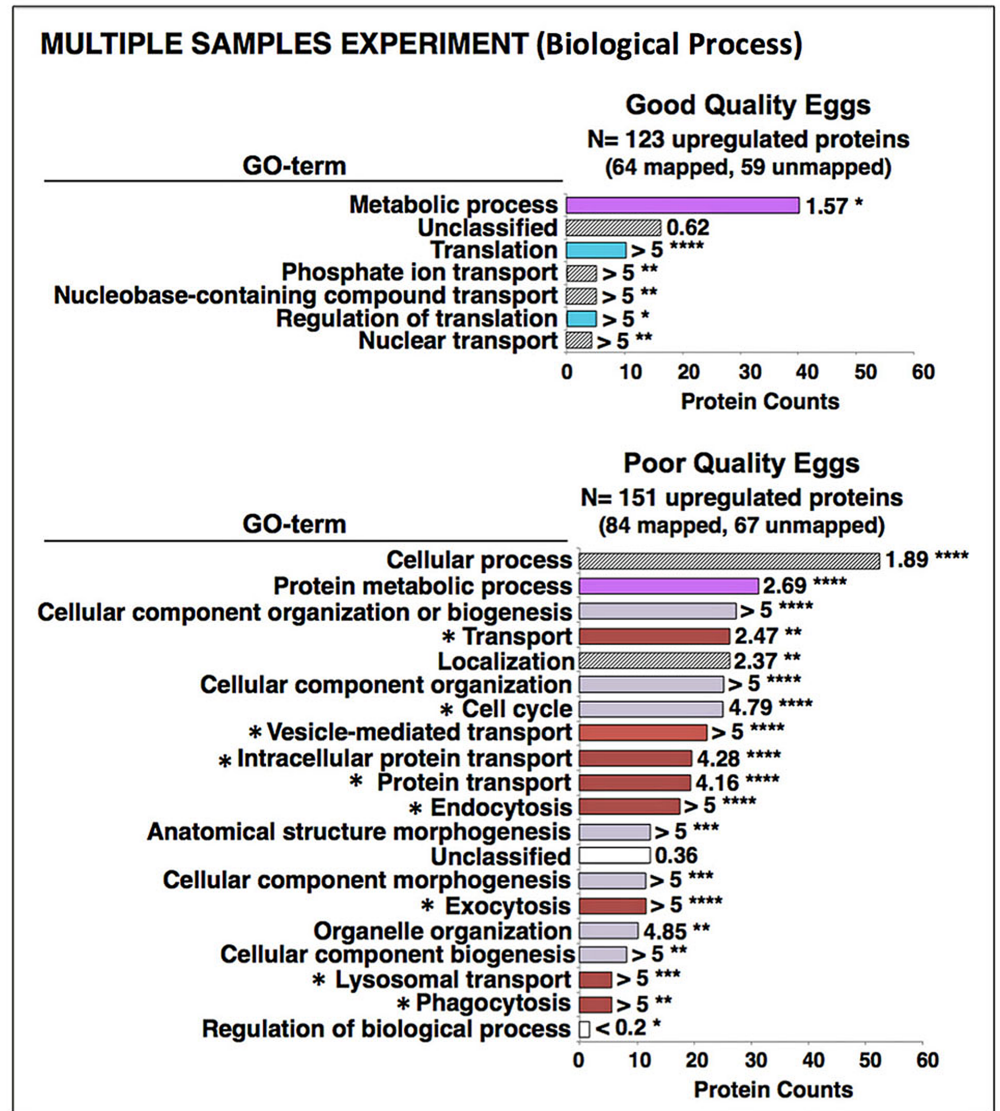
<https://doi.org/10.1371/journal.pone.0188084.g004>

identified in the Low Molecular Weight (LMW) fraction were combined to analyze their distribution among functional categories and for enrichment analyses; however, they were separately submitted to statistical analyses performed to detect significant differences in abundance of individual proteins between egg quality groups.

Considering only proteins with a  $\geq 2$ -fold difference in average N-SC between egg quality groups, or proteins unique to an egg quality group, 123 proteins were up-regulated in good quality eggs and 151 proteins were up-regulated in poor quality eggs in the Multiple Samples Experiment. The distribution of these differentially expressed proteins among functional categories significantly differed between egg quality groups ( $\chi^2$ ,  $p < 0.0001$ ), with frequencies of up-regulated proteins related to energy metabolism and lipid metabolism, and the incidence of vitellogenin (Vtg) products, being significantly higher in good quality eggs, and the frequency of up-regulated ZPs being significantly higher in poor quality eggs (Fig 2). Mapping of the Vtg-products up-regulated in good quality eggs to their parent yolk protein domains in zebrafish Vtgs revealed almost all to be derivatives of the major yolk protein, lipovitellin (arrows in Fig 1).

The PANTHER enrichment analyses revealed that GO Biological Process and Molecular Function terms relevant to metabolism and protein synthesis were enriched with proteins up-regulated in good quality eggs (Fig 5 and S1 Fig). The GO Protein Class and Cellular Component terms enriched with these proteins were also consistent with a proteomic emphasis on energy metabolism and protein synthesis (S2 and S3 Figs). Proteins up-regulated in poor quality eggs mainly enriched the GO Biological Process terms—Cellular process, Protein metabolic process, Cellular component organization or biogenesis, Transport, Localization, Cell cycle,

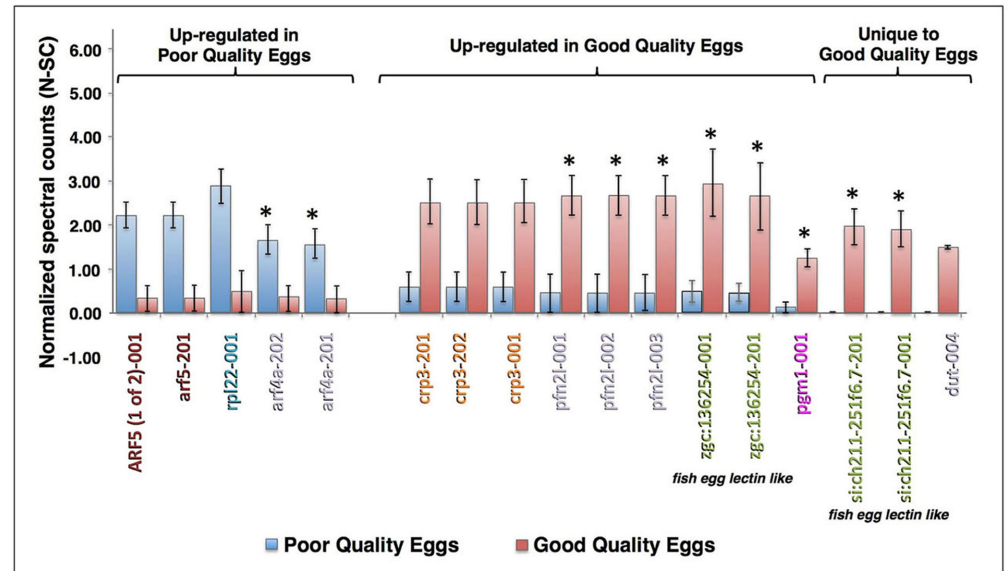




**Fig 5. Enrichment of biological process gene ontology (GO) terms with proteins up-regulated in the Multiple Samples Experiment.** Shown are the results of PANTHER over-representation tests for enrichment of Biological Process GO terms with proteins up-regulated in good and poor quality zebrafish eggs in the Multiple Samples Experiment. **Top Panel.** Good quality eggs. **Bottom Panel.** Poor quality eggs. Horizontal bars indicate the number of proteins attributed to each GO term for which statistically significant results ( $\chi^2$ ,  $p < 0.05$ ) were observed. Numbers next to the bars indicate the fold-enrichment with proteins attributed to each term and the number of asterisks indicates the significance level of the enrichment, as follows  $p \leq 0.05$  (\*),  $p \leq 0.01$  (\*\*),  $p \leq 0.001$  (\*\*\*), and  $p \leq 0.0001$  (\*\*\*\*). Where possible, horizontal bars are colored to indicate corresponding protein functional categories shown in Fig 2; energy metabolism (magenta), protein synthesis (light blue), cell cycle, division, growth and fate (lavender), endosome/lysosome-related activities (brown). For poor quality eggs, GO terms preceded by an asterisk involve cytoskeletal activities. See text for details.

<https://doi.org/10.1371/journal.pone.0188084.g005>

Vesicle mediated transport, Protein- and Intracellular protein-transport, and Endocytosis (Fig 5). The GO Molecular Function, Protein Class and Cellular Component terms enriched by these proteins (S1–S3 Figs) were also in agreement with a proteome tailored to cytoskeletal activities such as vesicle-mediated transport, phagocytosis, endocytosis and exocytosis, and related activities relevant to the cell cycle.



**Fig 6. Proteins significantly differing in abundance between egg quality types in the Multiple Samples Experiment.** The proteins are named for the transcript(s) to which spectra were mapped; for full protein names, see S2 Table. Only proteins common to both egg quality groups with  $\geq 4$ -fold difference in N-SC between groups, placing them in the top 2.3% of proteins showing such differences, or proteins unique to an egg quality group with mean N-SC values  $\geq 0.5$  and a statistically significant difference in N-SC between egg quality groups, are shown (independent samples t-test,  $p \leq 0.05$  after Benjamini Hochberg correction for multiple tests). Vertical bars indicate mean N-SC values ( $n = 4$  per egg quality type) and vertical brackets indicate SEM. Protein (transcript) labels are color-coded to indicate functional categories to which the proteins were attributed (Fig 2). Asterisks indicate proteins that were also detected and regulated in the same direction in the Pooled Samples Experiment.

<https://doi.org/10.1371/journal.pone.0188084.g006>

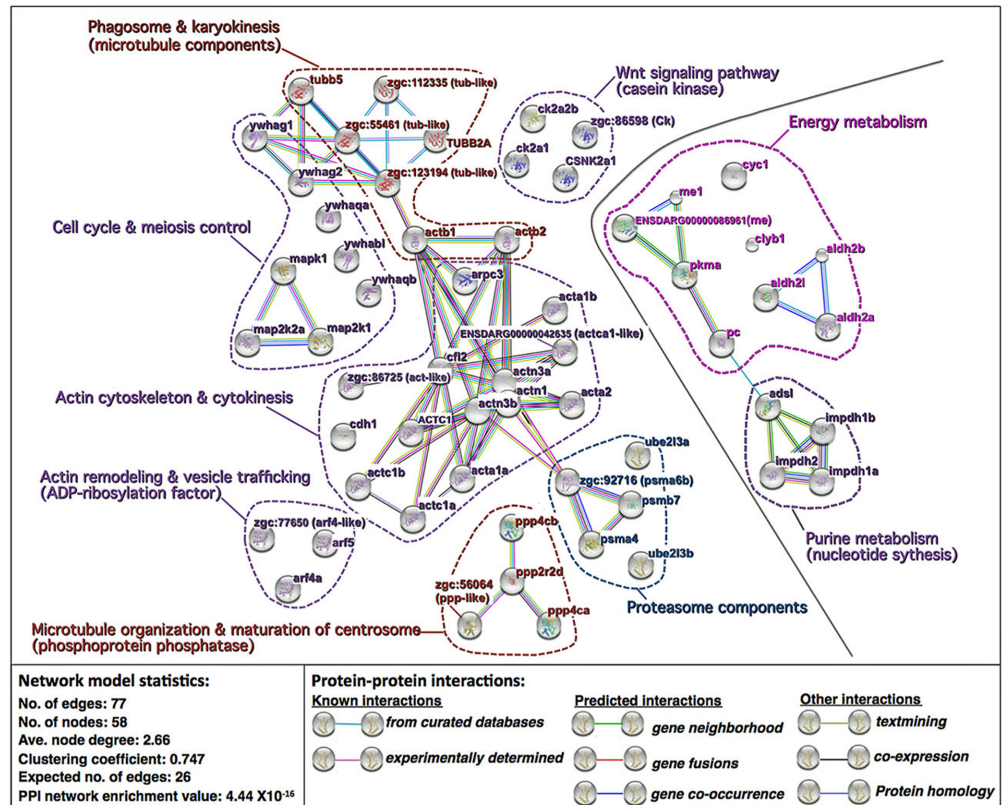
In the Multiple Samples Experiment, 17 proteins displayed a statistically significant difference in N-SC values between egg quality groups (Fig 6). Four forms of ADP-ribosylation factor (Arf) and one form of ribosomal protein L22 (Rpl22) were significantly up-regulated in poor quality eggs. Significantly up-regulated in good quality eggs were three isoforms of c-reactive protein 3 (Crp3), three isoforms of profilin-family member 2-like (Pfn2l), four fish egg lectin-like proteins, one form of phosphoglucomutase 1 (Pgm1), and a variant of deoxyuridine 5'-triphosphate nucleotide-hydrolase (Dut-004). Two of the lectin-like proteins and Dut were considered to be unique to good quality eggs because their mean N-SC values in poor quality eggs did not significantly differ from zero (Fig 6). Discounting isoforms, five proteins significantly up-regulated in good or poor quality eggs in the Replicated Samples Experiment were also up-regulated in the same direction in the Pooled Samples Experiment (i.e. Arf4a, Pfn2l, Zgc:136254, Pgm1, and Si:ch211-251f6.7). Spawns from the present experiment, which represented extremes of egg quality, could be sorted into egg quality groups with 100% accuracy based upon the sum of N-SC values for the four proteins that were up-regulated in good quality eggs both experiments ( $\sum$  Pfn2l N-SC +  $\sum$  Zgc:136254 N-SC + Pgm1 N-SC +  $\sum$  Si:ch211-251f6.7 N-SC); the mean of these summed N-SC values differed between egg quality groups by nearly an order of magnitude (poor quality  $2.33 \pm 1.59$ , good quality  $18.67 \pm 2.63$ ) with no overlap between groups in range (poor quality 0–6.95, good quality 14.72–26.39) or 95% confidence interval (poor quality -2.73–7.39, good quality 10.32–27.03).

When proteins up-regulated in good or poor quality eggs in either experiment were submitted to PANTHER Pathways enrichment analyses, they were found to be significantly

overrepresented in 14 different biological pathways (S3 Table). Proteins up-regulated in good quality eggs were overrepresented in three pathways: Pyruvate metabolism and *De novo* purine biosynthesis (Pooled Samples Experiment), and 5-hydroxytryptamine degradation (Multiple Samples Experiment). Proteins up-regulated in poor quality eggs were overrepresented in the remaining 11 pathways, 9 of which were significantly enriched in both experiments (S3 Table). Remarkably, when submitted proteins were individually mapped to all 14 pathways (S4 Fig), it was discovered that only 74 non-redundant proteins could account for all pathway enrichment.

Network analysis using the *Search Tool for the Retrieval of Interacting Genes/Proteins* (STRING) and the zebrafish protein database resolved the 74 'pathway' proteins into a network with a significantly greater number of known and predicted interactions between proteins than would be expected of a list of 74 proteins randomly chosen from the zebrafish database (PPI network enrichment value  $P \leq .44 \times 10^{-16}$ ) (Fig 7). Proteins up-regulated in good quality eggs formed a subnetwork made up of two protein clusters, one involved in energy metabolism and containing two forms of malic enzyme (Me), pyruvate kinase (Pkma), pyruvate carboxylase (Pc), cytochrome c-1 (Cyc1), citrate lyase (Cly), and three forms of aldehyde dehydrogenase (Aldh), and the other involved in purine (nucleotide) biosynthesis and containing adenylosuccinate lyase (Adsl) and three forms of inosine monophosphate dehydrogenase (Impdh) (Fig 7, right side). Proteins up-regulated in poor quality eggs formed a subnetwork made up of 7 clusters, two of which are made up of proteasome components, including three 20S proteasome subunits (Psm) and 2 forms of ubiquitin-conjugating enzyme E2 (Ube2), or Wnt signaling pathway components, including 4 forms of casein kinase (Csk, Csnk) (Fig 7, left side). The remaining 5 clusters are directly or indirectly involved in cytoskeletal functioning including cell cycle activities and regulation of mitosis and meiosis, vesicle trafficking, and phagocytosis. These include clusters made up of 4 forms of phosphoprotein phosphatase (Ppp), or 3 forms of ADP-ribosylation factor (Arf), a cluster of cell cycle- and meiosis-regulating proteins including mitogen activated protein kinase (Mapk), two forms of Mapk kinase (Map2K), and 5 forms of 14-3-3 (Ywha) protein (i.e. 3-monooxygenase/ tryptophan 5-monooxygenase activation protein), a cluster of microtubule-related components including 5 forms of tubulin (Tub) and 2 forms of beta actin (Actb), and a large cluster consisting of actin cytoskeletal components including 8 forms of actin or actin-like protein, 3 forms of actinin (Actn), actin-related protein 2/3 complex subunit 2 (Arpc2), cadherin 1 (Cdh1) and cofilin 2 (Cfl2).

A STRING enrichment analysis of these 74 'pathway proteins' included Kyoto Encyclopedia of Genes and Genomes (KEGG) Pathways, Protein Families Database (PFAM) Protein Domains, and Interpro Protein Families Database (INTERPRO) Protein Domains and Features (Table 2). Proteins in the good quality egg subnetwork significantly enriched pathways for Pyruvate metabolism, Purine metabolism and Metabolic pathways (KEGG), and also enriched Aldehyde dehydrogenase family domains, IMP dehydrogenase/GMP reductase domain, and Malic enzyme N-terminal and NAD-binding domains (PFAM). Proteins in the poor quality egg subnetwork significantly enriched the pathways Regulation of actin cytoskeleton, Adherens junction, Tight junction, Gap junction, Focal adhesion, Phagosome, and Cell cycle and Oocyte meiosis, among others (KEGG), and also enriched protein domains and features including Actin, Actin and Actin-like conserved site, Actin family, Spectrin repeat, Tubulin GTPase domain and C-terminal domain, 14-3-3 (ywha) protein, conserved site, and domain, Serine/threonine dual specificity protein kinase (e.g. Map2K) catalytic domain, and Adp-ribosylation factor family, among others (PFAM and INTERPRO) (Table 2).



**Fig 7. Network of differentially expressed proteins overexpressed in specific biological pathways.** Shown are the results of Search Tool for the Retrieval of Interacting Genes/Proteins (STRING) network analysis of the 74 non-redundant proteins that were differentially regulated in good versus poor quality eggs and were over-represented in specific biological pathways in the PANTHER Pathways enrichment analyses (S3 Table). Proteins up-regulated in good quality eggs are shown to the right of the solid grey line and proteins up-regulated in poor quality eggs are shown to the left of the line. Each network node (sphere) represents all proteins produced by a single, protein-coding gene locus (splice isoforms and post-translational modifications collapsed). Only nodes representing query proteins are shown. Nodes are named for the transcript(s) to which spectra were mapped, with the text colored according to the processes shown in Fig 2; for full protein names, see S1 and S2 Tables. Small nodes represent proteins of unknown 3D structure. Large nodes represent proteins for which some 3D structure is known or predicted. Edges (lines) represent protein-protein associations meant to be specific and meaningful, i.e. proteins jointly contribute to a shared function but do not necessarily physically interact. Model statistics are presented at the lower left. Explanation of edge colors is given on the lower right. Dashed lines encircle groups of transcripts involved in the named biochemical pathways or physiological processes. See text for details.

<https://doi.org/10.1371/journal.pone.0188084.g007>

## Discussion

The present study revealed the disparate proteomic profiles of good and poor quality zebrafish eggs in two separate experiments with different levels of sample replication and fractionation before mass spectrometry. In spite of the methodological differences, both experiments demonstrated that good and poor quality zebrafish eggs have distinct proteomic profiles. The percentage of up-regulated proteins related to energy metabolism was significantly greater in good quality eggs in both experiments (Fig 2). In the higher resolution Pooled Samples Experiment, the percentage of up-regulated proteins related to protein synthesis was also significantly higher in good quality eggs (Fig 2). For both experiments, the GO-Biological Process enrichment analysis attributed a far greater proportion of up-regulated proteins to terms relevant to energy metabolism (e.g. Metabolic process, Primary metabolic process, Protein metabolic

**Table 2. Enrichment analysis of differentially expressed proteins overexpressed in specific biological pathways.**

Kegg Pathways Enriched in Network			
Pathway ID	Pathway description	Protein count	FDR
4520	Adherins junction	10	1.80E-12
4530	Tight junction	10	2.06E-10
4810	Regulation of actin cytoskeleton	10	1.13E-08
4114	Oocyte meiosis	8	1.38E-08
4540	Gap junction	7	2.28E-07
4145	Phagosome	6	1.84E-05
4510	Focal adhesion	7	2.23E-05
620	<i>Pyruvate metabolism</i>	4	4.66E-05
4110	Cell cycle	5	0.000252
230	<i>Purine metabolism</i>	5	0.000714
5132	Salmonella infection	4	0.000714
4270	Vascular smooth muscle contraction	4	0.00241
1120	Microbial metabolism in diverse environments	4	0.00492
4261	Adrenergic signaling in cardiomyocytes	4	0.00598
1100	Metabolic pathways	9	0.00901
PFAM Protein Domains Enriched in Network			
Pathway ID	Domain description	Protein count	FDR
PF00022	Actin	10	6.07E-18
PF00244	14-3-3 protein	5	2.41E-08
PF00091	Tubulin/FtsZ family, GTPase domain	4	0.000166
PF03953	Tubulin C-terminal domain	4	0.000166
PF08726	Ca2+ insensitive EF hand	3	0.000177
PF00171	<i>Aldehyde dehydrogenase family</i>	3	0.007
PF00227	Proteasome subunit	3	0.0124
PF00478	<i>IMP dehydrogenase / GMP reductase domain</i>	3	0.0155
PF00390	<i>Malic enzyme, N-terminal domain</i>	2	0.0188
PF00435	Spectrin repeat	3	0.0188
PF03949	<i>Malic enzyme, NAD binding domain</i>	2	0.0188
PF00025	ADP-ribosylation factor family	3	0.04
INTERPRO Protein Domains and Features Enriched in Network			
Pathway ID	Domain or feature description	Protein count	FDR
IPR004001	Actin, conserved site	10	1.18E-20
IPR020902	Actin/actin-like conserved site	10	4.69E-20
IPR004000	Actin family	10	4.41E-18
IPR000308	14-3-3 protein	5	1.75E-08
IPR023409	14-3-3 protein, conserved site	5	1.75E-08
IPR023410	14-3-3 domain	5	1.75E-08
IPR002290	Ser/thr/dual spec. protein kinase, cat. domain	7	0.00219

Results of a STRING enrichment analysis of the protein network shown in Fig 7 for proteins that were differentially regulated in good versus poor quality eggs and were over-represented in specific biological pathways in the PANTHER Pathways enrichment analyses (S3 Table). Shown are KEGG pathways and INTERPRO protein domains represented by  $\geq 4$  or  $\geq 5$  genes, respectively, with a false discovery rate (FDR)  $< 0.01$ , and PFAM Protein Domains represented by  $\geq 2$  genes, with a FDR  $< 0.05$ . Entries for proteins only found in good quality eggs are set in italics type.

<https://doi.org/10.1371/journal.pone.0188084.t002>

process, Carbohydrate metabolic process, others) and protein synthesis (e.g. Translation, Regulation of translation, Protein folding, others) for good quality eggs than for poor quality eggs (Figs 3 and 5), as did the GO-Molecular Function enrichment analysis (S1 Fig), and the GO-Protein Class enrichment analysis (S2 Fig). Also in both experiments, the percentage of up-regulated proteins related to lipid metabolism was higher in good quality eggs, significantly so in the Multiple Samples Experiment where such proteins were not detected in poor quality eggs (Fig 2). Collectively, these findings suggest some failure of poor quality eggs to maintain regular cellular activities involving energy metabolism, lipid metabolism and protein synthesis relative to normally functioning eggs with high embryo developmental potential.

In the Multiple Samples Experiment, polypeptide derivatives of the Vtg-derived major yolk protein, lipovitellin (Lv), were strongly up-regulated in good quality eggs relative to poor quality eggs (Fig 2). These derivatives were mainly proteolytic products of the intact Lv heavy chain (LvHc) and Lv light chain (LvLc), which we deliberately excluded from the HMW and LMW fractions to better resolve smaller and less abundant proteins (see Fig 1). In the Pooled Samples Experiment, contribution of these small Lv derivatives to overall Vtg N-SC values would have been masked by the dominant contribution of proteins in the major Lv bands. Evidence for a dearth of Lv proteolysis products in poor quality eggs was also obtained when proteomic profiles of eggs from Eurasian perch (*Perca fluviatilis*) of varying reproductive performance were revealed by 2D-DIGE followed by MS/MS by Castets et al. [19]. These authors found ~42 kDa Vtg products mapping to *Perca flavescens* Vtg C, which contains only Lv domains, in three spots characterized by low expression in poor quality eggs. Proteolysis of Lvs normally occurs during final oocyte maturation in zebrafish and possibly all teleosts [29] as a mechanism for generation of free amino acids (FAA), which act as osmolytes to promote oocyte hydration and which are a critical energy source for early embryos. Most energy metabolism in early embryos is based on utilization of these FAA whose carbon skeletons are fed into the tricarboxylic acid cycle to fuel intermediary metabolism [30]. This cycle may be more active in high quality ova as the pyruvate metabolism pathway was overrepresented by proteins up-regulated in good quality eggs (S3 Table, see also S4 Fig Panel I). FAA are also utilized to support gluconeogenesis; glucose is an important substrate for synthesis of nucleic acids and polysaccharides in embryonic development [6]. Thus, the apparent deficiency of proteolytic products of Vtgs in poor quality zebrafish eggs may indicate a failure of the oocytes to properly transition from oocyte growth into final maturation antecedent to spawning, which would compromise water balance, energy metabolism and anabolic activities in any developing embryos.

Impairment of a proper transition of oocytes into final maturation is also suggested by the greater representation of up-regulated proteins related to endosome/lysosome activity in poor quality eggs in both experiments, which was significantly greater than seen in good quality eggs in the Pooled Samples Experiment (Fig 2). In both experiments, the GO-Biological Process enrichment analysis attributed a high proportion of up-regulated proteins to terms relevant to endosome/lysosome activity (e.g. Vesicle-mediated transport, Endocytosis, Exocytosis, Phagocytosis, Lysosomal transport) for poor quality eggs but not good quality eggs (Figs 3 and 5), as did the GO-Molecular Function, Protein Class, and Cellular Component enrichment analyses (S1–S3 Figs). The network comprised of proteins up-regulated in poor quality eggs that were overrepresented among several biological pathways (S3 Table) is also dominated by cytoskeletal components and clusters of other proteins that regulate these components (Fig 7, see also Table 2). The predominant activities occurring in growing teleost oocytes are the massive uptake of Vtgs from the circulation via receptor-mediated endocytosis, fusion of the endosomes containing Vtgs with lysosomes containing cathepsin D (CtsD) to form multivesicular bodies, and cleavage of Vtgs by CtsD into their constituent yolk proteins, which are stored in

yolk granules or globules until they undergo the maturational proteolysis associated with oocyte hydration [29, 30]. These bulk endocytotic activities are terminated at initiation of oocyte maturation with cessation of Vtg uptake [31] and deactivation of much of the extensive cellular endo-lysosomal machinery [32], events that may be disrupted in poor quality zebrafish oocytes/eggs. Indirect evidence supporting this concept comes from results of the PANTHER pathways enrichment analysis showing that the 5-hydroxytryptamine (serotonin) degradation pathway was significantly enriched in good quality eggs versus poor quality eggs (S3 Table), due to overrepresentation with several aldehyde dehydrogenases (S4 Fig Panel n). Serotonin is a potent reversible inhibitor of steroid-mediated resumption of meiosis and final oocyte maturation [33] and its degradation in good quality eggs would promote the transition to final maturation; with the process being inhibited or dysregulated in poor quality eggs with deficient serotonin degradation. Enrichment of the epidermal growth factor (EGF) receptor signaling pathway with several key proteins in poor quality eggs (S3 Table, see also S4 Fig Panel g) provides further opportunity for dysregulation of oocyte maturation, which is mediated by luteinizing hormone (LH). EGF is expressed in the zebrafish oocyte and its receptor (EGFR) is expressed in the follicle cell layer; paracrine actions of EGF in zebrafish include down-regulation of the LH receptor and of follicle responsiveness to LH, and upregulation of follicle stimulating hormone (FSH) receptor [34]. In the present study, the exact same suite of proteins enriched the fibroblast growth factor (FGF) signaling pathway; however, little is known about ovarian actions of FGF in zebrafish or other teleosts.

An alternative, but not mutually exclusive, explanation for the enrichment of poor quality eggs with proteins relevant to endo-lysosomal processes could be a higher level of autophagy (autophagy), a normal process in oocytes/eggs and embryos of fishes, including zebrafish [35]. The most common trigger of autophagy is nutrient restriction, which could result from limitation of FAA available to early embryos. Autophagy is normally a cytoprotective process that facilitates cell survival by ensuring adequate energy levels via recycling of damaged macromolecules and cellular components. However, dysregulation of autophagy can be cytotoxic, resulting in the accumulation of abnormal proteins and/or damaged organelles that is commonly observed in human neurodegenerative diseases, such as Alzheimer's, Huntington's, and Parkinson's diseases [36]. Notably, pathways for all three of these diseases were enriched with proteins up-regulated in poor quality eggs in the present study (S3 Table). While we did not detect any definitive protein markers of autophagy signaling in poor quality eggs, the process shares much of the same cellular protein machinery involved in other endo-lysosomal and vesicle trafficking activities that appear to be up-regulated in poor quality eggs, including the majority of proteins in the network shown in Fig 7. In zebrafish as in other vertebrates, autophagy opposes and is intimately linked to apoptosis via proteins playing a regulatory role in both events [37], and poor quality eggs exhibited a greater proportion of up-regulated proteins related to apoptosis in both experiments, significantly so in the Pooled Samples Experiment (Fig 2). Apoptosis is programmed cell death promoted by processes leading to mitochondrial dysfunction (loss of membrane potential) and downstream activation of the caspase pathway. Some examples of apoptosis-related proteins upregulated in or unique to poor quality eggs in this study include several variants of caspase 3a (Casp3a) and mitogen-activated protein kinase 1 (MapK1) (S1 Table), and also death-associated protein 1b (Dap1b) (S2 Table). The increased representation of up-regulated oncogene-related proteins in poor quality eggs may also be related to a struggle to offset apoptosis. This increase was almost entirely due to up regulation of multiple variants of tumor protein D52-like (S1 Table); D52 is known to inhibit apoptosis and promote cell proliferation in human cancer cells [38]. Thus, the up-regulation of endo-lysosome-, autophagy-, apoptosis- and oncogene-related proteins in poor quality eggs could be functionally (or dysfunctionally) interrelated.

Wnt signaling, which plays critical roles in cell proliferation and fate determination, axis patterning and morphogenetic movements [39], probably also influences egg quality in zebrafish. Canonical Wnt signaling is mediated by intracellular free  $\beta$ -catenin, normally kept at low levels via its tethering by cadherin to the inner surface of the plasma membrane, or phosphorylation on its N-terminus by Ck1 and glycogen synthase kinase-3 $\beta$ , targeting it for ubiquitination and proteasome-mediated degradation [40]. Casein kinase 2 (Ck2) acts at several levels in these pathways to promote Wnt signaling and rescue  $\beta$ -catenin from destruction. Non-canonical Wnt signaling, which is independent of  $\beta$ -catenin, affects release of intracellular  $\text{Ca}^{2+}$ , activates JNK signaling and the Rho family of small GTPases, and regulates cadherin recycling, signals ultimately affecting cytoskeletal architecture, the establishment and modulation of cell polarity, and cell movements [41]. In the present study, the presence of Ck2 and proteasome component (Psm and Ube) clusters among the network of 'pathway proteins' up-regulated in poor quality zebrafish eggs (Fig 7), coupled with enrichment of Wnt signaling, Cadherin signaling, and Cytoskeletal regulation by Rho GTPase pathways by these proteins (S3 Table), implicates dysregulation of Wnt signaling in the etiology of poor egg quality in zebrafish.

Lectins were elevated in poor quality zebrafish eggs in both experiments, substantially so in the Pooled Samples Experiment (Fig 2). These were mainly sea urchin egg lectin (SUEL)-type and L-rhamnose-binding lectins (L-RBLs) including some fish egg lectin (FEL)-like proteins (70–75%), and also  $\text{Ca}^{2+}$ -dependent (C-type) lectins (25–30%). C-type lectins have been localized to the cortical granules of fish eggs from whence they are discharged at fertilization into the perivitelline space, where they function in chorion hardening of the egg and establishing the block to polyspermy [42]. The other lectin types are known to play roles in innate immunity by binding to carbohydrate molecules on the surface of pathogens and enhancing their clearance via opsonization and phagocytosis [43]. In the Pooled Samples Experiment, 3 SUEL-type and one L-RBL were amongst the most highly up-regulated proteins in poor quality eggs (Fig 4). Conversely, 4 novel FEL-like proteins with predicted rhamnose-binding properties were significantly up-regulated in good quality eggs in the Multiple Samples Experiment (Fig 6). Although the exact relation of the different types of lectin to egg quality remains to be verified, disparate expression of these proteins in zebrafish eggs of different quality grades suggests that they may impact embryo development. Carp FEL shows broad binding specificity for Gram-positive and Gram-negative bacteria, and injection of purified native FEL into zebrafish embryos markedly promoted embryo resistance to pathogenic *Aeromonas hydrophila* [43], indicating that the FELs are immunocompetent to defend developing embryos/larvae from pathogenic attack.

Zona pellucida proteins with  $\geq 2$ -fold differential expression between good and poor quality eggs and nominal intact molecular weights ranging from 12 to 93.5 kDa, and from 16.5 to 104.8 kDa were detected in fractions covering the 30–60 kDa range in SDS-PAGE in the Multiple Samples Experiment and the 25–55 kDa range in the Pooled Samples Experiment (Fig 1), respectively. The high abundance of ZPs among proteins up-regulated in poor quality eggs, and the detection of some HMW ZP (i.e. 93.5 and 104.8 kDa) products in LMW fractions, may indicate premature disintegration of the egg envelope. Other possibilities are that the crosslinking of ZPs by transglutaminase to form a robust chorion following fertilization [44] is somehow impaired, or that the synthesis and deposition in the egg envelope of high molecular weight ZPs is disturbed in poor quality oocytes/eggs. As the disparate types of ZPs have considerable promise as biomarkers of egg quality, these possibilities should be evaluated in future research.

In spite of limited replication, substantial variation in N-SC values between fish, and the need to correct false discovery rate for large numbers of tests, 17 differentially expressed proteins exhibited statistically significant differences in N-SC between egg quality groups in our



Multiple Samples Experiment and are, therefore, potential biomarkers of egg quality (Fig 6). Up-regulated in poor quality eggs were four variants of Arf4a or 5; the two Arf4a proteins were also up-regulated in the Pooled Samples Experiment. These Arfs are small GTPases that regulate vesicle trafficking and actin skeletal dynamics [45], including modulation of cytoskeletal regulation by Rho GTPase, a pathway enriched by proteins up-regulated in poor quality eggs in both experiments (S3 Table, see also S4 Fig Panel a). Three of these Arfs also contribute to the molecular phenotype of poor quality eggs partially illustrated in Fig 7. The other protein significantly up-regulated in poor quality eggs was ribosomal protein L22 (Rpl22), which to date has not been implicated in any specific developmental pathway, mechanism, or disease.

Significantly elevated in good quality eggs were 3 variants of Crp3, which is classically involved in recognition (opsinization) of pathogens and cell damage during the acute phase response of innate immunity. C-reactive protein also engages in complex, mutually-stimulating interactions with autophagy and it promotes proliferation and inhibits apoptosis of certain tumor cells [46]. We speculate that maternal Crp3 is also engaged in these latter functions in early zebrafish embryos. Three variants of Pfn2l were significantly up-regulated in good quality eggs. Profilins regulate cytoskeletal dynamics, including actin polymerization and its coordination with microtubule dynamics [47], and they are also involved in regulation of small GTPase signaling and vesicle trafficking [48]. The glucose metabolizing enzyme, Pgm1 was also significantly elevated in good quality eggs (Fig 6). The earliest stages of embryogenesis are dependent upon cytosolic glycogen as an energy source, later switching to free amino acids [30], and maternally supplied Pgm1 may assist in glycogen utilization during this time. There are multiple beneficial and long-lasting effects of hepatic Pgm1 expression in later stage rainbow trout embryos and larvae on their subsequent development, growth and maturation that probably arise from increased flux through glycolysis [49]. Thus, Pgm1 may be an especially promising egg quality marker.

In the present study, a spectral counting procedure was employed to assess the relative abundance of proteins by virtue of the applicability of this 'label-free' technique to multiple highly complex biological samples, and in consideration of the higher degree of quantitative proteome coverage and linear dynamic range expected using this approach versus common stable isotope labeling techniques, features that are advantageous when large and global protein changes are observed [50]. The high consistency of results between our Pooled and Multiple Samples experiments with respect to differences between egg quality groups in representation of proteins among different functional (and GO) categories and pathways, and our detection of statistically significant differences in abundance of numerous proteins (N = 17 including isoforms) between egg quality groups in the latter experiment, as well as the ability of selected protein abundances to accurately predict egg quality in the same fish, confirm the existence of proteomic profiles related to egg quality. Future investigations of the proteomics of egg quality may benefit from the additional employment of some form of absolute protein quantification using internal standards in order to confirm protein abundance assessments with increased accuracy [20, 50], albeit at the potential expense of some of the advantageous features of spectral counting procedures noted above.

A dearth of developing embryos at 2–3 hps, potentially resulting from low fertility, was a common but not universal manifestation of poor egg quality in both of our experiments (Table 1). Although actual insemination of ova was not empirically assessed, based on the enormous disparity in size between the male and female gametes, proteomic differences between good and poor quality eggs collected immediately after spawning were considered to be unrelated to paternal contribution. Our ability to accurately sort spawns representing extremes of egg quality into the 'correct' egg quality groups based on the relative abundances of a few proteins up-regulated in good quality eggs in both experiments also indicates that,

under the present experimental conditions, variation in the fertility or reproductive performance of male zebrafish did not influence our egg quality assessments. Further investigations will be required to confirm whether eggs that fail to give rise to developing embryos are fertilized, perhaps by employing males of a transgenic line expressing a fusion of a histone variant to green fluorescent protein [51], or some other marker protein amenable to live imaging. Failure of eggs to be fertilized, and/or failure of fertilized eggs to undergo early cell cleavage, may also be hallmarks of poor egg quality, in which case it may be necessary to partition out male effects on fertility using classical 'nested' mating designs.

## Conclusions

Female zebrafish bred at weekly intervals are an opportune model to investigate molecular determinants of egg quality because they exhibit considerable variation in egg quality associated with clear changes in proteomic profiles. The poor quality zebrafish eggs are characterized by a proportional deficiency of proteins involved in protein synthesis, energy metabolism and lipid metabolism, and a dearth of proteolytic products of the major Lv yolk proteins, with a corresponding surfeit of proteins involved in endo-lysosomal activities, including autophagy, apoptosis and oncogenes. We propose that these differences are interrelated and arise from failure of oocytes giving rise to poor quality eggs to properly transit from growth through final maturation, limiting the liberation of critical energy substrates (FAA) from Lvs and, thus, necessitating autophagy and impairing the normal maturational attenuation of mass endocytotic processes, developments that collectively disrupt the normal composition and functions of the cytoskeleton. Results of pathway enrichment analyses and network modeling implicate dysregulation of the Wnt signaling pathway as a contributing factor in poor egg quality. Several novel egg quality marker proteins were identified for careful validation in future studies; these include lectins, egg envelope proteins (ZPs), and 9 additional proteins (excluding isoforms) exhibiting significant differences in relative abundance between egg quality types. Collectively, these observations indicate that the proteomic profiles of zebrafish eggs are strongly linked to, and possibly determine, egg quality.

## Methods

### Animal care, spawning and egg quality assessment

Zebrafish (*Danio rerio*) of the AB strain originally emanating from Tübingen (Germany) were obtained from our zebrafish facility (INRA UR1037 LPGP, Rennes, France) where they had been bred for 7–8 generations. The fish were ~1 year of age at the start of experiments and of average length ~5.0 cm and average weight ~1.4g. The zebrafish were housed under standard conditions of photoperiod (14 hours light and 10 hours dark) and temperature (28°C) in 10 L aquaria, and were fed three times a day *ad libitum* with a commercial diet (GEMMA, Skretting, Wincham, Northwich, UK). Females were bred at weekly intervals. The night before spawning, paired males and females bred from different parents were separated by an opaque divider in individual aquaria equipped with marbles at the bottom as the spawning substrate. The divider was removed in the morning, with the fish left undisturbed to spawn. Approximately sixty eggs per female were collected at the 1-cell stage immediately after spawning and incubated in 100 mm Petri dishes filled with embryo medium (17.1 mM NaCl, 0.4 mM KCl, 0.65 mM MgSO<sub>4</sub>, 0.27 mM CaCl<sub>2</sub>, 0.01 mg/L methylene blue) to assess egg quality based on embryo development. Prior to assessing developmental competence, groups of 40 eggs per spawn were removed, frozen in liquid nitrogen, and stored at -80°C until being used for proteomics analyses.

Incubated eggs/embryos were serially sampled for observation at the early blastula (~256 cell) stage (~2–3 hps), at the shield to 75% epiboly stages (~8 hps), at the early pharyngula stage (~24 hps), and during the hatching period at 48 and 72 hps (long-pec to protruding-mouth stages) following standard developmental staging [52]. At the time of sampling, the number of surviving eggs/embryos was recorded, those not surviving were removed and, for samples taken at 8 hps and beyond, the number of abnormal embryos was recorded. For samples taken at ~2–3 hps, any incidence of a high proportion (>50%) of abnormal embryos showing asymmetric cell cleavage and or early developmental arrest was also noted.

Egg samples utilized in the present experiments were selected from among  $N = 136$  total spawns for which the mean  $\pm$  SEM percentage of eggs yielding well-formed embryos surviving to 24 hpf was  $74.35 \pm 2.35\%$ . As noted in Results, spawns for which survival of normal embryos to 24 hps was >90% were considered to contain good quality eggs, with those having a survival rate of <30% considered to contain poor quality eggs. By these criteria, 55 of the 136 spawns (40.4%) contained good quality eggs and 15 spawns (11.0%) contained poor quality eggs. From this sample set, good and poor quality spawns were selected for our experiments at random, with the exception that contribution of individual male and female breeders was restricted to a single spawn in this study.

All experiments complied with French & European regulations ensuring 'animal welfare' and that 'Animals will be held in the INRA UR1037 LPGP fish facility (DDCSPP approval # B35-238-6).' Experimental protocols involving animals were approved by the Comité Rennais d'éthique pour l'expérimentation animale (CREEA).

## Experimental design

Two separate experiments with different levels of sample replication and fractionation of samples before LC-MS/MS were conducted to characterize the proteome of good versus poor quality zebrafish eggs and to discover potential markers of egg quality. In the Pooled Samples Experiment, intended to maximize resolution of both rare and abundant proteins, egg protein extracts from 4 spawns (40 eggs/spawn) of good quality or of poor quality were pooled separately and were subjected to extensive fractionation by SDS-PAGE ( $n = 20$  fractions) prior to LC-MS/MS (Fig 1). The Multiple Samples Experiment, intended to detect differential expression of the more abundant proteins, involved collection of a HMW fraction (30–66kDa) and a LMW fraction (14–28 kDa) of proteins (exclusive of intact Lv subunits) after SDS-PAGE prior to submitting the excised fractions LC-MS/MS, the entire procedure being repeated for 8 samples arising from 4 spawns of each egg quality type (Fig 1).

## Protein extraction and SDS-PAGE

Samples were subjected to sonication in 20 mM, pH 7.4, HEPES Buffer containing 200 mM EDTA, 100 mM DTT, 200 mM 4-(2-aminoethyl)-benzenesulfonyl fluoride, and 2 mM trans epoxysuccinyl-L-leucylamido-(4-guanidino) butane, on ice. Soluble protein extracts were recovered after centrifugation ( $15\,000 \times g$ ) at  $\sim 4^\circ\text{C}$  for 30 minutes. The remaining pellet was treated with 30 mM Tris/8M Urea/ 4% CHAPS buffer, re-sonicated on ice, pooled with soluble protein extracts from the same sample and ultracentrifuged ( $105,000 \times g$ ) for 1h at  $\sim 4^\circ\text{C}$  followed by supernatant recovery and determination of the protein concentration by Bradford Assay [53] (Bio-Rad, Marnes-la-Coquette, France). Samples of extracts were then mixed with sample buffer (NuPAGE<sup>®</sup> LDS Sample Buffer 4x) and DTT (NuPAGE<sup>®</sup> Sample Reducing Agent) and incubated at  $70^\circ\text{C}$  for 10 min before being subjected to SDS-PAGE (80  $\mu\text{g}$  protein/sample lane) on a 4–12% Bis-Tris precast gel (NuPAGE<sup>™</sup> Novex<sup>™</sup> 4–12% Bis-Tris Protein Gels) run in MOPS buffer (NuPAGE<sup>®</sup> MOPS SDS Running Buffer) mixed

with antioxidant (NuPAGE<sup>®</sup> Antioxidant) at 200V-400mA (~23W) for 1h. After electrophoresis, gels were briefly rinsed in MilliQ ultrapure water (Millipore S.A.S., Alsace, France) and incubated in fixation solution containing 30% EtOH / 10% acetic acid / 60% MilliQ water for 15 min in order to fix proteins on the gel, and were then washed in MilliQ water three times for 5 min each. Gels were then incubated in EZBlue<sup>™</sup> Gel Staining Reagent (Sigma-Aldrich, Saint-Quentin Fallavier, France) at room temperature with slight agitation for 2h, and de-stained in MilliQ water at room temperature overnight. For the Pooled Samples Experiment, each gel lane was fractionated into 20 pieces, which were excised from the gel and processed separately thereafter (Fig 1). In the Multiple Samples Experiment, the HMW and LMW fractions were excised from the gel and processed separately thereafter (Fig 1).

### In-gel tryptic digestion and LC-MS/MS

Gel pieces (fractions) were repeatedly washed in MilliQ water followed by incubation in ammonium bicarbonate (Ambic) 100mM: acetonitrile (ACN) 100% (1:1, v:v) until complete de-coloration and were then dried at 37°C for 20 min before reduction and alkylation. The dried fractions were incubated in 65 mM DTT at 37°C for 15 min followed by incubation at room temperature in the dark for 15 min after addition of 135 mM iodoacetamide, after which they were subjected to several washes in 100 mM Ambic: 100% ACN (1:1, v:v) and dried at 37°C for 20 min. Dried gel pieces were rehydrated in 50 mM Ambic containing sequencing grade modified trypsin (Promega, Charbonnières-les-Bains, France) at a final concentration of 12.5 ng/μl and incubated overnight at 37°C. Liquid containing protein digests was recovered by pipette and the remaining gel pieces were treated with 70% ACN: 0.1% formic acid with agitation at room temperature for 20 min. Liquid containing protein digests was collected and pooled with the previously collected digest and this elution step was repeated once again before the pooled digests were evaporated to dryness in a vacuum centrifuge. Pellets containing digested peptides were then resolubilized in 20 μl of 95% H<sub>2</sub>O: 5% formic acid by vortex mixing for 10 min before being subjected to LC-MS/MS.

Peptide mixtures were analyzed with a nanoflow high-performance liquid chromatography (HPLC) system (LC Packings Ultimate 3000, Thermo Fisher Scientific, Courtaboeuf, France) connected to a hybrid LTQ-Orbitrap XL spectrometer (Thermo Fisher Scientific) equipped with a nanoelectrospray ion source (New Objective), as previously described [54]. The mass spectrometer was operated in the data-dependent mode by automatic switching between full-survey scan MS and consecutive MS/MS acquisition. Survey full scan MS spectra (mass range 400–2000) were acquired in the Orbitrap section of the instrument with a resolution of  $r = 60,000$  at  $m/z$  400; ion injection times are calculated for each spectrum to allow for accumulation of  $10^6$  ions in the Orbitrap. The ten most intense peptide ions in each survey scan with an intensity above 2000 were sequentially isolated and fragmented in the linear ion trap by collision-induced dissociation. For Orbitrap measurements, an external calibration was used before each injection series ensuring an overall error mass accuracy below 5 ppm for the detected peptides. MS data were saved in RAW file format (Thermo Fisher Scientific) using XCalibur 2.0.7 with tune 2.4.

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium [55] via the PRIDE [56] partner repository under the project name “Proteomic portraits of egg quality in zebrafish (*Danio rerio*)” with the Pooled Samples Experiment dataset accession number PXD005137 and project DOI number 10.6019/PXD005137, and the Multiple Samples Experiment dataset accession number PXD005129 and project DOI number 10.6019/PXD005129.

## Protein identification, quantification, annotation and statistics

The spectra search was performed with the Proteome Discoverer 1.2 software supported by Mascot (Mascot server v2.2.07; <http://www.matrixscience.com>). Obtained MS/MS spectra were searched against a target-decoy concatenated database created from the zebrafish Ensembl proteome database (Danio rerio\_Zv9, March 2015) using Mascot (Matrix Science). Mass tolerance was set to 10 ppm and 0.5 Daltons for MS and MS/MS, respectively. Enzyme selectivity was set to full trypsin, with one miscleavage allowed. The allowed protein modifications were fixed carbamidomethylation of cysteines and variable oxidation of methionine. Attributed spectra were then analyzed using ProteoIQ 2.8 (Premier Biosoft, Palo Alto, CA, USA) at < 1% FDR, 0.5% minimum protein group probability, and 6 aa minimum peptide length, in order to identify egg quality group-specific and common proteins and quantify them based on their N-SC values. For each protein, obtained spectral counts were normalized in three sequential steps; a) normalization by apportion of shared peptides based on the number of unique peptides each protein group possessed, b) normalization by the total spectral counts between replicates and biological samples, and c) normalization by the size of each protein (amino acid residues).

Protein annotations were performed using the GO, KEGG and Database for Annotation, Visualization and Integrated Discovery (DAVID [57, 58]) functional annotation tools. Only proteins exhibiting a  $\geq 2$ -fold difference in N-SC between egg quality groups, or proteins unique to an egg quality group, were considered to be differentially expressed between groups and subjected to further analyses. Differentially expressed proteins detected in the HMW and LMW fractions in the Multiple Samples Experiment were combined for classifications by functional category and for enrichment analyses; however they were submitted individually to statistical analyses conducted to detect significant differences in mean N-SC values between egg quality groups.

Differentially expressed proteins were classified into thirteen arbitrarily chosen functional categories that would account for  $\geq 90\%$  of the proteins. These functional categories are: protein synthesis (PS), energy metabolism (EM), lipid metabolism (LM), cell cycle, division, growth and fate (CC), protein degradation and synthesis inhibition (PD), apoptosis-related (AP), oncogene-related (OG), endosome/lysosome-related (EL), immune function-related (IF), oxidoreductase (REDOX)- and detoxification (Detox)-related (RD), lectins, ZPs, and Vtgs. Up-regulated proteins that could not be attributed to any of these categories and were placed in the category "other". For simplicity, proteins were attributed to only one category considered as the 'best' fit. Presented results are based on consensus annotations of two independent observers made before any other analyses categorizing the proteins (i.e. observations made 'blind'). Chi square analysis with significance level of ( $p \leq 0.05$ ) after Benjamini Hochberg correction for multiple tests was used to detect differences between egg quality groups in the distribution of up-regulated proteins among functional categories.

Enrichment analyses were conducted separately for each experiment using the PANTHER-GO Slim enrichment tool from GO Consortium [59] available online at <http://geneontology.org/> for Biological Process, Molecular Function, Protein Class and Cellular Component. Up-regulated proteins from both experiments were subjected to a PANTHER Pathway [60] analysis and proteins attributed to enriched pathways ( $n = 74$ ) were pooled before being submitted to analysis using the STRING search tool for retrieval of protein-protein interaction networks [61] available from the STRING Consortium online at <http://string-db.org/>, with the data settings Confidence: High (0.70), Max Number of Interactions to Show: None/query proteins only. For all PANTHER analyses, only statistically significant enrichment results ( $p < 0.05$  after Bonferroni correction for multiple tests) are shown.

To detect significant differences between egg quality groups in mean N-SC values for differentially expressed proteins from the HMW and LMW fractions (Multiple Samples Experiment) an independent t-test ( $p < 0.05$ ) followed by Benjamini Hochberg correction for multiple tests ( $p < 0.1$ ) was used (IBM SPSS Statistics Version 19.0.0, Armonk, NY).

## Supporting information

**S1 Table. Proteins differentially regulated in the Pooled Samples Experiment.**  
(PDF)

**S2 Table. Proteins differentially regulated in the Multiple Samples Experiment.**  
(PDF)

**S3 Table. Enrichment of PANTHER pathways with differentially regulated proteins.**  
(PDF)

**S1 Fig. Enrichment of Molecular Function GO terms with differentially regulated proteins.**  
(PDF)

**S2 Fig. Enrichment of Protein Class GO terms with differentially regulated proteins.**  
(PDF)

**S3 Fig. Enrichment of Cellular Component GO terms with differentially regulated proteins.**  
(PDF)

**S4 Fig. Diagrams of PANTHER pathways enriched with differentially regulated proteins.**  
(PDF)

## Acknowledgments

We thank an anonymous reviewer of this article in draft for helpful suggestions on data analysis and representation.

## Author Contributions

**Conceptualization:** Ozlem Yilmaz, Julien Bobe.

**Data curation:** Ozlem Yilmaz.

**Formal analysis:** Ozlem Yilmaz, Craig V. Sullivan.

**Funding acquisition:** Ozlem Yilmaz, Julien Bobe.

**Investigation:** Ozlem Yilmaz.

**Methodology:** Ozlem Yilmaz, Amélie Patinote, Thao Vi Nguyen, Emmanuelle Com, Regis Lavigne, Charles Pineau, Craig V. Sullivan, Julien Bobe.

**Project administration:** Julien Bobe.

**Resources:** Ozlem Yilmaz, Amélie Patinote, Thao Vi Nguyen, Emmanuelle Com, Regis Lavigne, Charles Pineau, Craig V. Sullivan, Julien Bobe.

**Software:** Ozlem Yilmaz, Emmanuelle Com, Regis Lavigne, Charles Pineau.

**Supervision:** Ozlem Yilmaz, Charles Pineau, Julien Bobe.

**Validation:** Ozlem Yilmaz.

**Visualization:** Ozlem Yilmaz, Craig V. Sullivan.

**Writing – original draft:** Ozlem Yilmaz.

**Writing – review & editing:** Ozlem Yilmaz, Craig V. Sullivan, Julien Bobe.

## References

1. Migaud H, Bell G, Cabrera E, McAndrew B, Davie A, Bobe J, et al. Gamete quality and broodstock management in temperate fish. *Rev. in Aquaculture*. 2013; 5: S194–S223.
2. Bobe J, Labbé C. Egg and sperm quality in fish. *Gen. Comp. Endocrinol.* 2010; 165: 535–548. <https://doi.org/10.1016/j.ygcen.2009.02.011> PMID: 19272390
3. Bobe J. Egg quality in fish: Present and future challenges. *Animal Front.* 2015; 5: 66–72.
4. Kjorsvik E, Mangorjensen A, Holmefjord I. Egg quality in Fishes. *Adv. Mar. Biol.* 1990; 26:71–113.
5. Brooks S, Tyler CR, Sumpter JP. Egg quality in Fish: what makes a good egg? *Rev. in Fish Biol. & Fish.* 1997; 7: 387–416.
6. Lahnsteiner F, Soares F, Ribeiro L, Dinis MT. Egg quality determination in teleost fish. In: Cabrera E, Robles V, Herraes P, editors. *Methods in Reproductive Aquaculture, Marine and Freshwater Species*. 2009. pp. 149–173.
7. Babin PJ, Carnevali O, Lubzens E, Schenider WJ. Molecular aspects of oocyte vitellogenesis. In: Babin PJ, Cerdà J, Lubzens E, editors. *The Fish Oocyte: From Basic Studies to Biotechnological Applications*. 2007. pp. 39–76.
8. Lubzens E, Young G, Bobe J, Cerdà J. Oogenesis in teleosts: How fish eggs are formed. *Gen. Comp. Endocrinol.* 2010; 165: 367–389. <https://doi.org/10.1016/j.ygcen.2009.05.022> PMID: 19505465
9. Cerdà J, Bobe J, Babin PJ, Admon A, Lubzens E. Functional genomics and proteomic approaches for the study of gamete formation and viability in farmed finfish. *Rev. Fish. Sci.* 2008; 16: (S1), 54–70.
10. Lubzens E, Bobe J, Young G, Sullivan CV. Maternal investment in fish oocytes and eggs: the molecular cargo and its contributions to fertility and early development. *Aquaculture*. 2017; 472: 107–143
11. Stitzel ML, Seydoux G. Regulation of the oocyte-to-zygote transition. *Science*. 2007; 316: 407–408. <https://doi.org/10.1126/science.1138236> PMID: 17446393
12. Tadros W, Lipshitz HD. The maternal-to-zygotic transition: a play in two acts. *Development*. 2009; 136: 3033–3042. <https://doi.org/10.1242/dev.033183> PMID: 19700615
13. Sullivan CV, Chapman RW, Reading BJ, Anderson PE. Transcriptomics of mRNA and egg quality in farmed fish: Some recent developments and future directions. *Gen. Comp. Endocrinol.* 2015; 221: 23–30. <https://doi.org/10.1016/j.ygcen.2015.02.012> PMID: 25725305
14. Chapman RW, Reading BJ, Sullivan CV. Ovary transcriptome via artificial intelligence reveals a transcriptomic fingerprint predicting egg quality in striped bass, *Morone saxatilis*. *PLoS ONE*. 2014; 9(5): e96818. <https://doi.org/10.1371/journal.pone.0096818> PMID: 24820964
15. Groh K, Nesatyy VJ, Segner H, Eggen RIL, Suter MJ-F. Global proteomics analysis of testis and ovary in adult zebrafish (*Danio rerio*). *Fish Physiol. Biochem.* 2011; 37: 619–647. <https://doi.org/10.1007/s10695-010-9464-x> PMID: 21229308
16. Chapovetsky V, Gattegno T, Admon A. Proteomics analysis of the developing fish oocyte. In: Babin PJ, Cerdà J, Lubzens E, editors. *The Fish Oocyte: From Basic Studies to Biotechnological Applications*. 2007. pp. 99–111.
17. Rime H, Guitton N, Pineau C, Bonnet E, Bobe J, Jalabert B. Post-ovulatory ageing and egg quality: a proteomic analysis of rainbow trout coelomic fluid. *Reprod. Biol. Endocrinol.* 2004; 2: 26. <https://doi.org/10.1186/1477-7827-2-26> PMID: 15180895
18. Crespel A, Rime H, Fraboulet E, Bobe J, Fauvel C. Egg quality in domesticated and wild seabass (*Dicentrarchus labrax*): a proteomic analysis. *Cybio*. 2008; 32: 205.
19. Castets MD, Shaerlinger B, Silvestre F, Gardeur JN, Dieu M, Corbier C, et al. Combined analysis of *Perca fluviatilis* reproductive performance and oocyte proteomic profile. *Theriogenology*. 2012; 78: 432–442. <https://doi.org/10.1016/j.theriogenology.2012.02.023> PMID: 22578620
20. Kohn YY, Symonds JE, Kleffmann T, Nakagawa S, Lagisz M, Lokman PM. Proteomic analysis of early-stage embryos: implications for egg quality in hapuku (*Polyprion oxygeneios*). *Fish Physiol. Biochem.* 2015; 41:1403–1417. <https://doi.org/10.1007/s10695-015-0095-0> PMID: 26183261
21. Hoo JY, Kumari Y, Shaikh MF, Hue SM, Goh BH. Zebrafish: A Versatile Animal Model for Fertility Research. *Biomed. Res. Int.* 2016; ID 9732780.

22. Ribas L, Piferrer F. The zebrafish (*Danio rerio*) as a model organism, with emphasis on applications for finfish aquaculture research. *Rev. in Aquaculture*. 2013; 5: 1–32.
23. Ziv T, Gattegno T, Chapovetsky V, Wolf H, Barnea E, Lubzens E, et al. Comparative proteomics of the developing fish (zebrafish and gilthead seabream) oocytes. *Comp. Biochem. Physiol. Part D*. 2008; 3: 12–35.
24. Link V, Shevchenko A, Heisenberg CP. Proteomics of early zebrafish embryos. *BMC Dev. Biol.* 2006; 6: 1. <https://doi.org/10.1186/1471-213X-6-1> PMID: 16412219
25. Lucitt MB, Price TS, Pizarro A, Wu W, Yocum AK, Seiler C, et al. Analysis of the Zebrafish Proteome during Embryonic Development. *Mol. & Cel. Proteom.* 2008; 7(5): 981–994.
26. Löbner C, Wee S, Ler SG, Li RH, Carney T, Blackstock W, et al. Expanding the zebrafish embryo proteome using multiple fractionation approaches and tandem mass spectrometry. *Proteomics*. 2012; 12 (11): 1879–1882. <https://doi.org/10.1002/pmic.201100576> PMID: 22653788
27. Van der Plas-Duivesteyn SJ, Mohamed Y, Dalebout H, Meijer A, Botermans A, Hoogendijk JL, et al. Identifying Proteins in Zebrafish Embryos Using Spectral Libraries Generated from Dissected Adult Organs and Tissues. *J. Proteome Res.* 2014; 13: 1537–1544. <https://doi.org/10.1021/pr4010585> PMID: 24460240
28. Chou RJ, Campbell MJ. Transcription, genomes, function. *TIGS 2000*; 16(9):409–415.
29. Carnevali O, Cionna C, Tosti L, Lubzens E, Maradonna F. Role of cathepsins in ovarian follicle growth and maturation. *Gen. Comp. Endocrinol.* 2006; 146: 195–203. <https://doi.org/10.1016/j.ygcen.2005.12.007> PMID: 16430893
30. Finn RN, Fyhn HJ. Requirement for amino acids in ontogeny of fish. *Aquaculture Res.* 2010; 41: 684–716.
31. Sullivan CV, Hiramatsu N, Kennedy AM, Clark RW, Weber GM, Matsubara T, et al. Induced maturation and spawning: opportunities and applications for research on oogenesis. *Fish Physiol. Biochem.* 2003; 28: 481–486.
32. Le Menn F, Cerdà J, Babin PJ. Ultrastructural aspects of the ontogeny and differentiation of ray-finned fish ovarian follicles. In: Babin PJ, Cerdà J, Lubzens E, editors. *The Fish Oocyte: From Basic Studies to Biotechnological Applications*. 2007. pp. 1–37.
33. Cerdà J, Subhedar N, Reich G, Wallace RA, Selman K. Oocyte sensitivity to serotonergic regulation during the follicular cycle of the teleost *Fundulus heteroclitus*. *Biol. Reprod.* 1998; 59: 53–61. PMID: 9674993
34. Liu K-C, Ge W. Differential regulation of gonadotropin receptors (fshr and lhcr) by epidermal growth factor (EGF) in the zebrafish ovary. *Gen. Comp. Endocrinol.* 2012; 181: 288–294. <https://doi.org/10.1016/j.ygcen.2012.07.032> PMID: 23036736
35. Imamura S, Yabu T, Yamashita M. Autophagy-mediated yolk absorption during fish embryogenesis. *Bull. Fish. Res. Agen.* 2008; 26: 29–34.
36. Banerjee R, Beal MF, Thomas B. Autophagy in neurodegenerative disorders: Pathogenic roles and therapeutic implications. *Trends Neurosci.* 2010; 33: 541–549. <https://doi.org/10.1016/j.tins.2010.09.001> PMID: 20947179
37. Gioacchini G, Dalla Valle L, Benato F, Fimia GM, Nardacci R, Ciccocanti F, et al. Interplay between autophagy and apoptosis in the development of *Danio rerio* follicles and the effects of a probiotic. *Reprod. Fertil. Dev.* 2013; 25: 1115–25. <https://doi.org/10.1071/RD12187> PMID: 23195281
38. Ummanni R, Teller S, Junker H, Zimmermann U, Venz S, Scharf C, et al. Altered expression of tumor protein D52 regulates apoptosis and migration of prostate cancer cells. *FEBS J.* 2008; 275: 5703–13. <https://doi.org/10.1111/j.1742-4658.2008.06697.x> PMID: 18959755
39. Clevers H. Wnt/β-catenin signaling in development and disease. *Cell.* 2006; 127: 469–480. <https://doi.org/10.1016/j.cell.2006.10.018> PMID: 17081971
40. Verkade H, Heath JK. Wnt signaling mediates diverse developmental processes in zebrafish. In: Vincan E, editor. *Wnt Signaling, Volume II: Pathway Models*, vol. 469; Humana Press; 2008. pp 225–251.
41. Dominguez I, Soneshein GE, Seldin DC. CK2 and its role in Wnt and NF-κB signaling: linking development and cancer. *Cell. Mol. Life Sci.* 2009; 66: 1850–1857. <https://doi.org/10.1007/s00018-009-9153-z> PMID: 19387549
42. Dong C-H, Yang S-T, Yang Z-A, Zhang L, Gui J-F. A C-type lectin associated and translocated with cortical granules during oocyte maturation and egg fertilization in fish. *Dev. Biol.* 2004; 265: 341–354. PMID: 14732397
43. Wang Y, Bu L, Yang L, Li H, Zhang S. Identification and functional characterization of fish-egg lectin in zebrafish. *Fish & Shellfish Immunol.* 2016; 52: 23–30.



44. Oppen-Berntsen DO, Helvik JV, Walther BT. The major structural proteins of cod (*Gadus morhua*) eggshells and protein crosslinking during teleost egg hardening. *Dev Biol.* 1990; 137: 258–65. PMID: [2303164](https://pubmed.ncbi.nlm.nih.gov/2303164/)
45. Myers KR, Casanova JE. Regulation of actin cytoskeleton dynamics by Arf-family GTPases. *Trends Cell Biol.* 2008; 18:184–192. <https://doi.org/10.1016/j.tcb.2008.02.002> PMID: [18328709](https://pubmed.ncbi.nlm.nih.gov/18328709/)
46. Peisajovich A, Marnell L, Mold C, Du Clos TW. C-reactive protein at the interface between innate immunity and inflammation. *Expert Rev. Immunol.* 2008; 4: 379–390. <https://doi.org/10.1586/1744666X.4.3.379> PMID: [20476927](https://pubmed.ncbi.nlm.nih.gov/20476927/)
47. Sadi S, Sulimenko V, de Almeida FN, Blom H, Draber P, Aspenström P, et al. Profilin connects Actin Assembly with Microtubule dynamics. *Molec. Biol. Cell.* 2016; 27: 2381–2393. <https://doi.org/10.1091/mbc.E15-11-0799> PMID: [27307590](https://pubmed.ncbi.nlm.nih.gov/27307590/)
48. Witke W. The role of profiling complexes in cell motility and other cellular processes. *Trends Cell Biol.* 2004; 14: 461–469. <https://doi.org/10.1016/j.tcb.2004.07.003> PMID: [15308213](https://pubmed.ncbi.nlm.nih.gov/15308213/)
49. Allendorf FW, Knudsen KL, Leary RF. Adaptive significance of differences in the tissue-specific expression of a phosphoglucosylase gene in rainbow trout. *Proc Natl Acad Sci USA.* 1983; 80: 1397–400. PMID: [6219391](https://pubmed.ncbi.nlm.nih.gov/6219391/)
50. Bantscheff M, Schirle M, Sweetman G, Rick J, Kuster B. Quantitative mass spectrometry in proteomics: a critical review. *Anal. Bioanal. Chem.* 2013; 389:1017–1031.
51. Pauls S, Geldmacher-Voss B, Campos-Ortega JA. A zebrafish histone variant H2A.F/Z and a transgenic H2A.F/Z:GFP fusion protein for in vivo studies of embryonic development. *Dev. Genes Evol.* 2011; 211:603–610.
52. Kimmel CB, Ballard WW, Kimmel SR, Ullmann B, Schilling TF. Stages of embryonic development of the zebrafish. *Dev. Dyn.* 1995; 203:253–310. <https://doi.org/10.1002/aja.1002030302> PMID: [8589427](https://pubmed.ncbi.nlm.nih.gov/8589427/)
53. Bradford MM. A Rapid and Sensitive Method for the Quantitation of Microgram Quantities of Protein Utilizing the Principle of Protein-Dye Binding. *Analyt. Biochem.* 1976; 72: 248–254. PMID: [942051](https://pubmed.ncbi.nlm.nih.gov/942051/)
54. Lavigne R, Becker E, Liu Y, Evrard B, Lardenois A, Primig M, et al. Direct iterative protein profiling (DIPP)-an innovative method for large-scale protein detection applied to budding yeast mitosis. *Mol. & Cel. Proteom.* 2012; 11: M111–O12682.
55. Vizcaíno JA, Deutsch EW, Wang R, Csordas A, Reisinger F, Ríos D, et al. ProteomeXchange provides globally co-ordinated proteomics data submission and dissemination. *Nature Biotechnol.* 2014; 30: 223–226 <https://doi.org/10.1038/nbt.2839> PMID: [24727771](https://pubmed.ncbi.nlm.nih.gov/24727771/).
56. Vizcaíno JA, Csordas A, Del-Toro N, Dianes JA, Griss J, Lavidas I, et al. 2016 update of the PRIDE database and related tools. *Nucleic Acids Res.* 2016; 44: D447–D456 <https://doi.org/10.1093/nar/gkv1145> PMID: [26527722](https://pubmed.ncbi.nlm.nih.gov/26527722/).
57. Huang DW, Sherman BT, Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID Bioinformatics Resources. *Nature Protoc.* 2009; 4: 44–57.
58. Huang DW, Sherman BT, Lempicki RA. Bioinformatics enrichment tools: paths toward the comprehensive functional analysis of large gene lists. *Nucleic Acids Res.* 2009; 37: 1–13. <https://doi.org/10.1093/nar/gkn923> PMID: [19033363](https://pubmed.ncbi.nlm.nih.gov/19033363/)
59. Mi H, Poudel S, Muruganujan A, Casagrande JT, Thomas PD. PANTHER version 10: expanded protein families and functions, and analysis tools. *Nucl. Acids Res.* 2016; 44: D336–D342. <https://doi.org/10.1093/nar/gkv1194> PMID: [26578592](https://pubmed.ncbi.nlm.nih.gov/26578592/)
60. Huaiyu Mi H, Thomas P. PANTHER Pathway: An Ontology-Based Pathway Database Coupled with Data Analysis Tools. In: Nikolsky Y, Bryant J, editors. *Methods in Molecular Biology*, Volume 563, Part 2. Humana Press, 2009. pp.123–140.
61. Szklarczyk D, Franceschini A, Wyder S, Forslund K, Heller D, Huerta-Cepas J, et al. STRING v10: protein-protein interaction networks, integrated over the tree of life. *Nucleic Acids Res.* 2015; 43: D447–52. <https://doi.org/10.1093/nar/gku1003> PMID: [25352553](https://pubmed.ncbi.nlm.nih.gov/25352553/)

**S1 Table. Proteins differentially regulated in the Pooled Samples Experiment.** List of the 892 proteins from the Pooled Samples Experiment that were considered to be differentially regulated between egg quality groups and whose distribution among various functional categories is illustrated in Fig 2a. These include proteins detected only in poor quality eggs (PQ UNIQUE, n=211), proteins in poor quality eggs with N-SC increased  $\geq 2$ -fold relative to values for good quality eggs (PQ INCREASED, n=186), proteins detected only in good quality eggs (GQ UNIQUE, n=136), and proteins in good quality eggs with N-SC increased  $\geq 2$ -fold relative to values for poor quality eggs (GQ INCREASED, n=359). For each protein, the Ensembl Protein ID and associated gene, transcript and protein name, functional category (Fig 2a), relative abundance (UNIQUE or INCREASED), and fold-difference in N-SC between egg quality groups (if available) is shown. Color shading corresponds to that used to designate functional categories in Fig 2.

Ensembl Protein ID	Associated Gene Name	Associated Transcript Name	Protein Full Name	Functional Category	Regulation	Fold Difference	
1	ENSDARP0000030257	si:ch211-226h8.8	si:ch211-226h8.8-201	Uncharacterized protein containing SUEL type lectin domain	Lectins	PQ UNIQUE	-
2	ENSDARP00000113274	si:ch211-226h8.8	si:ch211-226h8.8-001	Uncharacterized protein containing SUEL type lectin domain	Lectins	PQ UNIQUE	-
3	ENSDARP00000121868	zgc:172218	Novel (zgc:17218-001)	Uncharacterized protein containing 3SUEL type lectin domains	Lectins	PQ UNIQUE	-
4	ENSDARP00000117390	si:ch211-226h8.11	si:ch211-226h8.11-001	L-rhamnose-binding lectin CSL3-like isoform X1	Lectins	PQ UNIQUE	-
5	ENSDARP00000061148	ENSDARP00000122263	zgc:55461-001	TUBB - tubulin, beta 4A class IVa-like	Cell cycle, division, growth and fate	PQ UNIQUE	-
6	ENSDARP00000072581	zgc:172218	Novel (zgc:172218-201)	Uncharacterized protein--w 3 lectin domains	Lectins	PQ UNIQUE	-
7	ENSDARP00000104203	AL929192.3	AL929192.3-201	Novel protein containing galactose binding lectin domains	Lectins	PQ UNIQUE	-
8	ENSDARP00000095074	cnp	cnp-201	2',3'-cyclic nucleotide 3' phosphodiesterase	Cell cycle, division, growth and fate	PQ UNIQUE	-
9	ENSDARP00000053151	cbr1	cbr1-001	Carbonyl reductase 1	Lipid metabolism	PQ UNIQUE	-
10	ENSDARP00000024748	zgc:86598	zgc:86598-001	Uncharacterized protein--casein kinase family protein	Other	PQ UNIQUE	-
11	ENSDARP00000068088	hp	hp-201	Haptoglobin	Immune system related	PQ UNIQUE	-
12	ENSDARP00000108424	zgc:86598	zgc:86598-002	Protien kinase	Protein Synthesis	PQ UNIQUE	-
13	ENSDARP00000106833	ZP2 (4 of 4)	ZP2 (4 of 4)-201	Zona pellucida glycoprotein 2 (sperm receptor)	Zona Pellucida proteins	PQ UNIQUE	-
14	ENSDARP00000117065	zgc:152652	zgc:152652-001	Uncharacterized protein	Other	PQ UNIQUE	-
15	ENSDARP00000109829	zgc:171474	zgc:171474-001	Uncharacterized protein	Other	PQ UNIQUE	-
16	ENSDARP00000125025	hp	hp-001	Haptoglobin	Immune system related	PQ UNIQUE	-
17	ENSDARP00000118911	ck2a1	ck2a1-003	Casein kinase 2 alpha 1	Protein Synthesis	PQ UNIQUE	-
18	ENSDARP00000116024	ck2a1	ck2a1-004	Casein kinase 2 alpha 1	Protein Synthesis	PQ UNIQUE	-
19	ENSDARP00000129511	wdfy1	wdfy1-001	WD repeat and FYVE domain containing 1	Endosome-Lysosome related	PQ UNIQUE	-
20	ENSDARP00000103118	zgc:100918	Novel	uncharacterized Rab7-like, ras-related, protein	Endosome-Lysosome related	PQ UNIQUE	-
21	ENSDARP00000111138	zgc:100918	Novel	uncharacterized Rab7a-like, ras-related, protein	Endosome-Lysosome related	PQ UNIQUE	-
22	ENSDARP00000113694	ck2a1	ck2a1-002	Casein kinase 2 alpha 1	Protein Synthesis	PQ UNIQUE	-
23	ENSDARP00000014852	itln3	itln3-201	Intelectin 3	Immune system related	PQ UNIQUE	-
24	ENSDARP00000042593	hn1b	hn1b-001	Hematological and neurological expressed 1b	Cell cycle, division, growth and fate	PQ UNIQUE	-
25	ENSDARP00000110275	FARS2 (2 of 2)	FARS2 (2 of 2)-201	Phenylalanine-tRNA synthetase 2	Protein Synthesis	PQ UNIQUE	-
26	ENSDARP00000122499	CU467646.3	CU467646.3-201	Uncharacterized protein	Other	PQ UNIQUE	-
27	ENSDARP00000006001	ck2a1	ck2a1-001	Casein kinase 2 alpha 1	Protein Synthesis	PQ UNIQUE	-
28	ENSDARP00000056550	ck2a1	ck2a1-201	Casein kinase 2 alpha 1	Protein Synthesis	PQ UNIQUE	-
29	ENSDARP00000103535	BX548000.1	BX548000.1-201	Uncharacterized protein	Other	PQ UNIQUE	-
30	ENSDARP00000165440	rab11a1	rab11a1-001	RAB11a, member RAS oncogene family, like	Oncogenesis related	PQ UNIQUE	-
31	ENSDARP00000124572	hp	hp-002	Haptoglobin	Immune system related	PQ UNIQUE	-
32	ENSDARP00000053863	gcdh	gcdh-201	Glutaryl-Coenzyme A dehydrogenase	Lipid metabolism	PQ UNIQUE	-
33	ENSDARP00000112983	gcdh	gcdh-001	Glutaryl-Coenzyme A dehydrogenase	Lipid metabolism	PQ UNIQUE	-
34	ENSDARP00000120266	C9H21orf33	C9H21orf33-001	Chromosome 21 open reading frame 33	Energy metabolism	PQ UNIQUE	-
35	ENSDARP00000071656	cox7a3	cox7a3-001	Cytochrome c oxidase subunit VIIa polypeptide 3	Energy metabolism	PQ UNIQUE	-
36	ENSDARP00000125277	USMG5	USMG5-001	Up-regulated during skeletal muscle growth 5 homolog (mouse)	Cell cycle, division, growth and fate	PQ UNIQUE	-
37	ENSDARP00000125356	USMG5	USMG5-002	Up-regulated during skeletal muscle growth 5 homolog (mouse)	Cell cycle, division, growth and fate	PQ UNIQUE	-
38	ENSDARP00000112178	fgg	fgg-201	Fibrinogen, gamma polypeptide	Immune system related	PQ UNIQUE	-
39	ENSDARP00000124470	si:dkey-87o1.2	si:dkey-87o1.2-001	Uncharacterized protein	Other	PQ UNIQUE	-
40	ENSDARP00000121763	coro1cb	coro1cb-002	Coronin, actin binding protein, 1Cb	Endosome-Lysosome related	PQ UNIQUE	-
41	ENSDARP00000108470	SMIM20	SMIM20-201	Small integral membrane protein 20	Other	PQ UNIQUE	-
42	ENSDARP00000049002	atp6v1aa-001	atp6v1aa-001	ATPase, H+ transporting, lysosomal V1 subunit Aa	Endosome-Lysosome related	PQ UNIQUE	-
43	ENSDARP00000116576	fkbp3	fkbp3-001	FK506 binding protein 3	Protein Synthesis	PQ UNIQUE	-
44	ENSDARP00000122221	csb1	csb1-003	Cysteine conjugate-beta lyase, cytoplasmic (glutamine transaminase K, kynurenine aminotransferase)	Oncogenesis related	PQ UNIQUE	-
45	ENSDARP00000063415	mase12	mase12-001	Ribonuclease like 2	Immune system related	PQ UNIQUE	-
46	ENSDARP00000113451	si:dkeyp-20e4.8	si:dkeyp-20e4.8-001	Uncharacterized protein	Other	PQ UNIQUE	-
47	ENSDARP00000088889	ita1	ita1-001	Cytotoxic granule-associated RNA binding protein 1	Apoptosis related	PQ UNIQUE	-
48	ENSDARP00000003248	zgc:77118	zgc:77118-001	Palmitoyl-(protein) hydrolase activity	Other	PQ UNIQUE	-
49	ENSDARP00000126272	actr10	actr10-001	Actin-related protein 10 homolog (S. cerevisiae)	Cell cycle, division, growth and fate	PQ UNIQUE	-
50	ENSDARP00000123855	si:dkey-87o1.2	si:dkey-87o1.2-003	Uncharacterized protein	Other	PQ UNIQUE	-
51	ENSDARP00000124841	si:dkey-87o1.2	si:dkey-87o1.2-002	Uncharacterized protein	Other	PQ UNIQUE	-
52	ENSDARP00000128259	sh3glb2a	sh3glb2a-004	SH3-domain GRB2-like endophilin B2a	Endosome-Lysosome related	PQ UNIQUE	-
53	ENSDARP00000026575	rbm8a	rbm8a-001	RNA binding motif protein 8A	Protein Synthesis	PQ UNIQUE	-
54	ENSDARP00000114997	hmbg2a	hmbg2a-003	High-mobility group box 2a	Apoptosis related	PQ UNIQUE	-
55	ENSDARP00000124034	psmc1a	psmc1a-002	Proteasome (prosome, macropain) 26S subunit, ATPase, 1a	Protein degradation and synthesis inhibition	PQ UNIQUE	-
56	ENSDARP00000090477	si:ch73-95i15.3	si:ch73-95i15.3-201	Fatty acid elongation in mitochondria-lysosome	Lipid metabolism	PQ UNIQUE	-
57	ENSDARP00000128868	si:ch73-95i15.3	si:ch73-95i15.3-001	Fatty acid elongation in mitochondria-lysosome	Lipid metabolism	PQ UNIQUE	-
58	ENSDARP00000100627	purbb	purbb-201	Purine-rich element binding protein Bb	Protein Synthesis	PQ UNIQUE	-
59	ENSDARP00000120767	ufd1l	ufd1l-003	Ubiquitin fusion degradation 1-like	Protein degradation and synthesis inhibition	PQ UNIQUE	-

60	ENSDARP00000124354	mapk1	mapk1-004	Mitogen-activated protein kinase 1	Apoptosis related	PQ UNIQUE	-
61	ENSDARP00000117412	med20	med20-001	Mediator complex subunit 20	Protein Synthesis	PQ UNIQUE	-
62	ENSDARP00000126190	krt17	krt17-002	Keratin 15	Cell cycle, division, growth and fate	PQ UNIQUE	-
63	ENSDARP00000067637	med20	med20-201	Mediator complex subunit 20	Protein Synthesis	PQ UNIQUE	-
64	ENSDARP0000007602	ppp2r2ab	ppp2r2ab-201	Protein phosphatase 2, regulatory subunit B, alpha b	Protein Synthesis	PQ UNIQUE	-
65	ENSDARP00000117378	ppp2r2ab	ppp2r2ab-001	Protein phosphatase 2, regulatory subunit B, alpha b	Cell cycle, division, growth and fate	PQ UNIQUE	-
66	ENSDARP00000066854	fars2	fars2-001	phenylalanyl-tRNA synthetase 2, mitochondrial	Protein Synthesis	PQ UNIQUE	-
67	ENSDARP00000128723	sh3glb2a	sh3glb2a-001	SH3-domain GRB2-like endophilin B2a	Endosome-Lysosome related	PQ UNIQUE	-
68	ENSDARP00000118809	si:dkey-51e6.1	si:dkey-51e6.1-001	Uncharacterized protein	Other	PQ UNIQUE	-
69	ENSDARP00000061755	si:dkey-51e6.1	si:dkey-51e6.1-201	Uncharacterized protein	Other	PQ UNIQUE	-
70	ENSDARP00000110749	casp3	casp3-002	Nigella arvensis cysteine protease 30, Nlike catalytic subunit	Oncogenes related	PQ UNIQUE	-
71	ENSDARP00000116767	comtd1	comtd1-002	Catechol-O-methyltransferase domain containing 1	Other	PQ UNIQUE	-
72	ENSDARP00000115915	casp3a	casp3a-004	Caspase 3, apoptosis-related cysteine protease a	Apoptosis related	PQ UNIQUE	-
73	ENSDARP00000111328	BX470131.2	BX470131.2-201	Uncharacterized protein--LOC568697 (LOC568697), mRNA	Other	PQ UNIQUE	-
74	ENSDARP00000112094	polr1c	polr1c-001	Polymerase (RNA) I polypeptide C	Protein Synthesis	PQ UNIQUE	-
75	ENSDARP00000127587	sh3glb2a	sh3glb2a-002	SH3-domain GRB2-like endophilin B2a	Endosome-Lysosome related	PQ UNIQUE	-
76	ENSDARP00000053935	pfnd6	pfnd6-001	Prefoldin subunit 6	Protein Synthesis	PQ UNIQUE	-
77	ENSDARP00000087463	nhp21a	nhp21a-001	NHP2 non-histone chromosome protein 2-like 1a (S. cerevisiae)	Protein Synthesis	PQ UNIQUE	-
78	ENSDARP00000127398	fnb1	fnb1-003	Farnesyltransferase, CAAX box, beta	Other	PQ UNIQUE	-
79	ENSDARP00000006309	wdfy1	wdfy1-201	WD repeat and FYVE domain containing 1	Endosome-Lysosome related	PQ UNIQUE	-
80	ENSDARP00000100638	atp6v0d1	atp6v0d1-201	ATPase, H+ transporting, V0 subunit D isoform 1	Endosome-Lysosome related	PQ UNIQUE	-
81	ENSDARP00000113069	NAPB (2 of 2)	NAPB (2 of 2)-001	N-ethylmaleimide-sensitive factor attachment protein, beta	Protein Synthesis	PQ UNIQUE	-
82	ENSDARP00000127072	scrm2	scrm2-002	Secernin 2	Protein degradation and synthesis inhibition	PQ UNIQUE	-
83	ENSDARP00000129285	ECH1 (2 of 2)	ECH1 (2 of 2)-002	Enoyl CoA hydratase 1, peroxisomal	Lipid metabolism	PQ UNIQUE	-
84	ENSDARP00000059475	psmg1	psmg1-001	Proteasome (prosome, macropain) assembly chaperone 1	Protein degradation and synthesis inhibition	PQ UNIQUE	-
85	ENSDARP00000090911	actr10	actr10-201	Actin-related protein 10 homolog (S. cerevisiae)	Cell cycle, division, growth and fate	PQ UNIQUE	-
86	ENSDARP00000105905	CU928126.3	CU928126.3-201	Casein kinase II subunit alpha-like isoform X1	Protein Synthesis	PQ UNIQUE	-
87	ENSDARP00000115880	comtd1	comtd1-001	Catechol-O-methyltransferase domain containing 1	Other	PQ UNIQUE	-
88	ENSDARP00000094516	ppp4ca	ppp4ca-001	Protein phosphatase 4 (formerly X), catalytic subunit a	Apoptosis related	PQ UNIQUE	-
89	ENSDARP00000124293	cbx1b	cbx1b-003	Chromobox homolog 1b (HP1 beta homolog Drosophila)	Cell cycle, division, growth and fate	PQ UNIQUE	-
90	ENSDARP00000101062	purba	purba-001	Purine-rich element binding protein Ba	Protein Synthesis	PQ UNIQUE	-
91	ENSDARP00000125785	seh1l	seh1l-002	SEH1-like (S. cerevisiae)	Cell cycle, division, growth and fate	PQ UNIQUE	-
92	ENSDARP00000112994	zgc:171977	zgc:171977-001	Uncharacterized protein	Other	PQ UNIQUE	-
93	ENSDARP00000122910	snx12	snx12-005	Sorting nexin 12	Endosome-Lysosome related	PQ UNIQUE	-
94	ENSDARP00000008027	snx12	snx12-001	Sorting nexin 12	Endosome-Lysosome related	PQ UNIQUE	-
95	ENSDARP00000122028	pbdc1	pbdc1-001	Polysaccharide biosynthesis domain containing 1	Protein degradation and synthesis inhibition	PQ UNIQUE	-
96	ENSDARP00000123575	hmgb2a	hmgb2a-004	High-mobility group box 2a	Apoptosis related	PQ UNIQUE	-
97	ENSDARP00000088891	ddrgk1	ddrgk1-202	DDRKG domain containing 1	Protein degradation and synthesis inhibition	PQ UNIQUE	-
98	ENSDARP000000004839	dnajb11	dnajb11-201	DnaJ (Hsp40) homolog, subfamily B, member 11	Protein Synthesis	PQ UNIQUE	-
99	ENSDARP00000107433	dnajb11	dnajb11-001	DnaJ (Hsp40) homolog, subfamily B, member 11	Protein Synthesis	PQ UNIQUE	-
100	ENSDARP00000122189	nasp	nasp-003	Nuclear autoantigenic sperm protein (histone-binding)	Cell cycle, division, growth and fate	PQ UNIQUE	-
101	ENSDARP00000004932	myl1	myl1-001	Myosin, light chain 1, alkali; skeletal, fast	Cell cycle, division, growth and fate	PQ UNIQUE	-
102	ENSDARP00000051402	sh3glb2a	sh3glb2a-201	SH3-domain GRB2-like endophilin B2a	Endosome-Lysosome related	PQ UNIQUE	-
103	ENSDARP00000072059	cfb	cfb-001	Complement factor B	Immune system related	PQ UNIQUE	-
104	ENSDARP00000106788	ctsa	ctsa-201	Cathepsin A	Protein degradation and synthesis inhibition	PQ UNIQUE	-
105	ENSDARP00000017647	gins1	gins1-201	GINS complex subunit 1 (Psf1 homolog)	Cell cycle, division, growth and fate	PQ UNIQUE	-
106	ENSDARP00000119427	uba1	uba1-003	Ubiquitin-like modifier activating enzyme 1	Protein degradation and synthesis inhibition	PQ UNIQUE	-
107	ENSDARP00000128686	sh3glb2a	sh3glb2a-003	SH3-domain GRB2-like endophilin B2a	Endosome-Lysosome related	PQ UNIQUE	-
108	ENSDARP00000039666	cbx1b	cbx1b-201	Chromobox homolog 1b (HP1 beta homolog Drosophila)	Cell cycle, division, growth and fate	PQ UNIQUE	-
109	ENSDARP00000109344	novel-actn4_rat	Novel	Novel	Oncogenes related	PQ UNIQUE	-
110	ENSDARP00000113004	cbx1b	cbx1b-001	Chromobox homolog 1b (HP1 beta homolog Drosophila)	Cell cycle, division, growth and fate	PQ UNIQUE	-
111	ENSDARP00000127314	capgb	capgb-002	Capping protein (actin filament), gelsolin-like b	Cell cycle, division, growth and fate	PQ UNIQUE	-
112	ENSDARP00000123185	actn1	actn1-003	Actinin, alpha 1	Cell cycle, division, growth and fate	PQ UNIQUE	-
113	ENSDARP00000095774	krt17	krt17-001	Keratin 15	Cell cycle, division, growth and fate	PQ UNIQUE	-
114	ENSDARP00000118428	psmb7	psmb7-003	Proteasome (prosome, macropain) subunit, beta type, 7	Protein degradation and synthesis inhibition	PQ UNIQUE	-
115	ENSDARP00000118656	cbx1a	cbx1a-001	Chromobox homolog 1a (HP1 beta homolog Drosophila)	Protein degradation and synthesis inhibition	PQ UNIQUE	-
116	ENSDARP00000031553	eif4e1c	eif4e1c-001	Eukaryotic translation initiation factor 4E family member 1c	Protein Synthesis	PQ UNIQUE	-
117	ENSDARP00000047158	hmgb2a	hmgb2a-001	High-mobility group box 2a	Apoptosis related	PQ UNIQUE	-
118	ENSDARP0000016201	tm9sf2	tm9sf2-001	Transmembrane 9 superfamily member 2	Endosome-Lysosome related	PQ UNIQUE	-
119	ENSDARP00000061395	chmp5b	chmp5b-001	charged multivesicular body protein 5b	Endosome-Lysosome related	PQ UNIQUE	-
120	ENSDARP00000127370	eef1db	eef1db-005	Elongation factor-1, delta, b	Protein Synthesis	PQ UNIQUE	-
121	ENSDARP00000129156	napba	napba-001	N-ethylmaleimide-sensitive factor attachment protein, beta a	Protein degradation and synthesis inhibition	PQ UNIQUE	-
122	ENSDARP00000009369	krt15	krt15-201	Keratin 15	Cell cycle, division, growth and fate	PQ UNIQUE	-
123	ENSDARP00000095029	krt15	krt15-001	Keratin 15	Cell cycle, division, growth and fate	PQ UNIQUE	-
124	ENSDARP00000119224	eif4e1c	eif4e1c-003	Eukaryotic translation initiation factor 4E family member 1c	Protein Synthesis	PQ UNIQUE	-
125	ENSDARP00000128345	fars2	fars2-201	Phenylalanyl-tRNA synthetase 2	Protein Synthesis	PQ UNIQUE	-
126	ENSDARP00000024741	napba	napba-201	N-ethylmaleimide-sensitive factor attachment protein, beta a	Protein degradation and synthesis inhibition	PQ UNIQUE	-
127	ENSDARP00000028134	psma6b	psma6b-001	Proteasome (prosome, macropain) subunit, alpha type, 6b	Protein degradation and synthesis inhibition	PQ UNIQUE	-

128	ENSDARP0000006106	bcap31	bcap31-001	B-cell receptor-associated protein 31	Protein Synthesis	PQ UNIQUE	-
129	ENSDARP0000010825	bcap31	bcap31-201	B-cell receptor-associated protein 31	Protein Synthesis	PQ UNIQUE	-
130	ENSDARP00000098086	cfb	cfb-201	Complement factor B	Immune system related	PQ UNIQUE	-
131	ENSDARP00000060174	si:dkey-12e7.4	si:dkey-12e7.4-001	Oxidoreductase-NAD(p) binding domain	Lipid metabolism	PQ UNIQUE	-
132	ENSDARP00000112303	psmb7	psmb7-001	Proteasome (prosome, macropain) subunit, beta type, 7	Protein degradation and synthesis inhibition	PQ UNIQUE	-
133	ENSDARP00000035106	PURA (1 of 2)	PURA (1 of 2)-201	Purine-rich element binding protein A [	Cell cycle, division, growth and fate	PQ UNIQUE	-
134	ENSDARP00000059013	zgc:173443	zgc:173443-001	Uncharacterized protein	Other	PQ UNIQUE	-
135	ENSDARP00000055324	psmb7	psmb7-002	Proteasome (prosome, macropain) subunit, beta type, 7	Protein degradation and synthesis inhibition	PQ UNIQUE	-
136	ENSDARP00000101909	pura	pura-002	Purine-rich element binding protein A	Protein Synthesis	PQ UNIQUE	-
137	ENSDARP00000112873	snx12	snx12-002	Sorting nexin 12	Endosome-Lysosome related	PQ UNIQUE	-
138	ENSDARP00000122416	pura	pura-001	Purine-rich element binding protein A	Protein Synthesis	PQ UNIQUE	-
139	ENSDARP00000088108	NAPA (2 of 2)	NAPA (2 of 2)-001	N-ethylmaleimide-sensitive factor attachment protein, alpha	Endosome-Lysosome related	PQ UNIQUE	-
140	ENSDARP00000021426	zgc:66479	zgc:66479-001	Uncharacterized protein	Other	PQ UNIQUE	-
141	ENSDARP00000033064	wdr61	wdr61-201	WD repeat domain 61	Cell cycle, division, growth and fate	PQ UNIQUE	-
142	ENSDARP00000110861	wdr61	wdr61-202	WD repeat domain 61	Cell cycle, division, growth and fate	PQ UNIQUE	-
143	ENSDARP00000025772	syap1	syap1-001	Synapse associated protein 1	Other	PQ UNIQUE	-
144	ENSDARP00000026028	hmgcl	hmgcl-001	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	Lipid metabolism	PQ UNIQUE	-
145	ENSDARP00000104510	hmgcl	hmgcl-201	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	Lipid metabolism	PQ UNIQUE	-
146	ENSDARP00000129523	glg1a	glg1a-002	Golgi glycoprotein 1a	Cell cycle, division, growth and fate	PQ UNIQUE	-
147	ENSDARP00000045487	ck2a2b	ck2a2b-201	Casein kinase 2 alpha 2b	Apoptosis related	PQ UNIQUE	-
148	ENSDARP00000103569	act16b	act16b-201	Actin-like 6B	Protein Synthesis	PQ UNIQUE	-
149	ENSDARP00000024096	ACTR2 (1 of 3)	ACTR2 (1 of 3)-001	ARP2 actin-related protein 2 homolog (yeast)	Oncogenes related	PQ UNIQUE	-
150	ENSDARP00000057868	mat1a	mat1a-001	Methionine adenosyltransferase 1, alpha	Protein Synthesis	PQ UNIQUE	-
151	ENSDARP00000124307	act16b	act16b-001	Actin-like 6B	Protein Synthesis	PQ UNIQUE	-
152	ENSDARP00000071166	aars	aars-201	Alanyl-tRNA synthetase	Protein Synthesis	PQ UNIQUE	-
153	ENSDARP00000088880	viml	viml-201	Vimentin like	Cell cycle, division, growth and fate	PQ UNIQUE	-
154	ENSDARP0000016261	vim	vim-001	Vimentin	Cell cycle, division, growth and fate	PQ UNIQUE	-
155	ENSDARP00000023622	bfb	bfb-001	Complement component bfb	Endosome-Lysosome related	PQ UNIQUE	-
156	ENSDARP00000107935	bfb	bfb-201	Complement component bfb	Endosome-Lysosome related	PQ UNIQUE	-
157	ENSDARP00000113857	coro1cb	coro1cb-001	Coronin, actin binding protein, 1Cb	Endosome-Lysosome related	PQ UNIQUE	-
158	ENSDARP00000039795	coro1cb	coro1cb-201	Coronin, actin binding protein, 1Cb	Endosome-Lysosome related	PQ UNIQUE	-
159	ENSDARP00000091174	aars	aars-001	Alanyl-tRNA synthetase	Protein Synthesis	PQ UNIQUE	-
160	ENSDARP0000012553	aaas	aaas-201	Achalasia, adrenocortical insufficiency, alacrimia	Cell cycle, division, growth and fate	PQ UNIQUE	-
161	ENSDARP00000110386	aars	aars-202	Alanyl-tRNA synthetase	Protein Synthesis	PQ UNIQUE	-
162	ENSDARP00000120649	aars	aars-002	Alanyl-tRNA synthetase	Protein Synthesis	PQ UNIQUE	-
163	ENSDARP00000105615	CU695117.1	CU695117.1-201	Zinc finger MYM-type protein 1	Protein synthesis	PQ UNIQUE	-
164	ENSDARP00000109275	CU929506.1	CU929506.1-201	Zinc finger MYM-type protein 1	Protein synthesis	PQ UNIQUE	-
165	ENSDARP00000074082	C4B	C4B-201	Complement component 4B (Chido blood group)	Immune system related	PQ UNIQUE	-
166	ENSDARP00000115743	C4B	C4B-001	Complement component 4B (Chido blood group)	Immune system related	PQ UNIQUE	-
167	ENSDARP0000000803	actn3b	actn3b-001	Actinin alpha 3b	Cell cycle, division, growth and fate	PQ UNIQUE	-
168	ENSDARP00000005224	actn3a	actn3a-001	Actinin alpha 3b	Cell cycle, division, growth and fate	PQ UNIQUE	-
169	ENSDARP00000090990	actn1	actn1-201	Actinin, alpha 1	Cell cycle, division, growth and fate	PQ UNIQUE	-
170	ENSDARP00000110976	actn1	actn1-202	Actinin, alpha 1	Cell cycle, division, growth and fate	PQ UNIQUE	-
171	ENSDARP00000120755	actn1	actn1-002	Actinin, alpha 1	Cell cycle, division, growth and fate	PQ UNIQUE	-
172	ENSDARP00000123299	actn1	actn1-001	Actinin, alpha 1	Cell cycle, division, growth and fate	PQ UNIQUE	-
173	ENSDARP00000077418	clip2	clip2-201	CAP-GLY domain containing linker protein 2	Cell cycle, division, growth and fate	PQ UNIQUE	-
174	ENSDARP00000124509	clip2	clip2-001	CAP-GLY domain containing linker protein 2	Cell cycle, division, growth and fate	PQ UNIQUE	-
175	ENSDARP00000109853	hdlbpb	hdlbpb-201	High density lipoprotein-binding protein b	Lipid metabolism	PQ UNIQUE	-
176	ENSDARP00000127252	hdlbpb	hdlbpb-001	High density lipoprotein-binding protein b	Lipid metabolism	PQ UNIQUE	-
177	ENSDARP00000052837	acta1a	acta1a-001	Actin alpha 1a skeletal muscle	Cell cycle, division, growth and fate	PQ UNIQUE	-
178	ENSDARP00000055135	actc1b	actc1b-201	Actin, alpha, cardiac muscle 1b	Cell cycle, division, growth and fate	PQ UNIQUE	-
179	ENSDARP00000055379	tubb5	tubb5-201	Tubulin, beta 5	Cell cycle, division, growth and fate	PQ UNIQUE	-
180	ENSDARP00000058628	acta1b	acta1b-001	Actin, alpha 1b, skeletal muscle	Cell cycle, division, growth and fate	PQ UNIQUE	-
181	ENSDARP00000062369	actc1a	actc1a-001	Actin, alpha, cardiac muscle 1a	Cell cycle, division, growth and fate	PQ UNIQUE	-
182	ENSDARP00000063082	zgc:174637	zgc:174637-201	Arylesterase activity	Immune system related	PQ UNIQUE	-
183	ENSDARP00000066429	acta2	acta2-201	Actin, alpha 2, smooth muscle, aorta	Cell cycle, division, growth and fate	PQ UNIQUE	-
184	ENSDARP00000066858	tubb4b	tubb4b-001	Tubulin, beta 4B class IVb	Cell cycle, division, growth and fate	PQ UNIQUE	-
185	ENSDARP00000069926	PPP2CA	PPP2CA-201	Protein phosphatase 2, catalytic subunit, alpha isozyme	Protein Synthesis	PQ UNIQUE	-
186	ENSDARP00000074935	ywhag1	ywhag1-001	3-monoxygenase/tryptophan 5-monoxygenase activation protein, gamma polypeptide 1	Cell cycle, division, growth and fate	PQ UNIQUE	-
187	ENSDARP00000075110	CH211-260D9.2	CH211-260D9.2-001	Actin-novel	Cell cycle, division, growth and fate	PQ UNIQUE	-
188	ENSDARP00000095894	si:dkey-90i23.2	Novel	L-rhamnose-binding lectin CSL3-like isoform X2	Lectins	PQ UNIQUE	-
189	ENSDARP00000096898	ywhag2	ywhag2-001	3-monoxygenase/tryptophan 5-monoxygenase activation protein, gamma polypeptide 2	Cell cycle, division, growth and fate	PQ UNIQUE	-
190	ENSDARP00000100195	zgc:86725	zgc:86725	Actin alpha 1 (ACTA1)-like	Cell cycle, division, growth and fate	PQ UNIQUE	-
191	ENSDARP00000100434	actc1a	Novel	Actin, alpha, cardiac muscle 1a, novel	Cell cycle, division, growth and fate	PQ UNIQUE	-
192	ENSDARP00000102472	vtg4	vtg4-202	Vitellogenin 4	Vitellogenins	PQ UNIQUE	-
193	ENSDARP00000103251	qdrpb2	qdrpb2-201	Quinoid dihydropteridine reductase b2	REDOX/Detox related	PQ UNIQUE	-
194	ENSDARP00000104702	qdrpb2	qdrpb2-001	Quinoid dihydropteridine reductase b2	REDOX/Detox related	PQ UNIQUE	-
195	ENSDARP00000105815	zgc:173556	zgc:173556-001	Zona pellucida glycoprotein 3.1	Zona Pellucida proteins	PQ UNIQUE	-

196	ENSDARP00000106988	si:dkeyp-98a7.5	si:dkeyp-98a7.5-202	Novel rhamnose binding lectin-like precursor	Lectins	PQ UNIQUE	-
197	ENSDARP00000107122	tubb4b	tubb4b-201	Tubulin, beta 4B class IVb	Cell cycle, division, growth and fate	PQ UNIQUE	-
198	ENSDARP00000107578	si:dkeyp-98a7.4	si:dkeyp-98a7.4-201	SUEL type lectin domain	Lectins	PQ UNIQUE	-
199	ENSDARP00000109226	AL929192.2	AL929192.2-201	Gal lectin superfamily	Lectins	PQ UNIQUE	-
200	ENSDARP00000110519	AL929192.1	AL929192.1-201	Gal lectin superfamily	Lectins	PQ UNIQUE	-
201	ENSDARP00000111434	si:dkeyp-98a7.5	si:dkeyp-98a7.5-201	SUEL type lectin domain	Lectins	PQ UNIQUE	-
202	ENSDARP00000111784	si:dkeyp-98a7.3	si:dkeyp-98a7.3-201	SUEL type lectin domain	Lectins	PQ UNIQUE	-
203	ENSDARP00000120702	si:dkeyp-98a7.5	si:dkeyp-98a7.5-001	SUEL type lectin domain	Lectins	PQ UNIQUE	-
204	ENSDARP00000124371	acta2	acta2-001	Actin, alpha 2, smooth muscle, aorta	Cell cycle, division, growth and fate	PQ UNIQUE	-
205	ENSDARP00000125193	si:dkeyp-98a7.7	si:dkeyp-98a7.7-001	SUEL type lectin domain	Lectins	PQ UNIQUE	-
206	ENSDARP00000125214	si:dkeyp-98a7.8	si:dkeyp-98a7.8-001	SUEL type lectin domain	Lectins	PQ UNIQUE	-
207	ENSDARP00000125238	si:dkeyp-98a7.4	si:dkeyp-98a7.4-001	SUEL type lectin domain	Lectins	PQ UNIQUE	-
208	ENSDARP00000125244	si:dkeyp-98a7.3	si:dkeyp-98a7.3-001	SUEL type lectin domain	Lectins	PQ UNIQUE	-
209	ENSDARP00000125496	si:ch211-250e5.9	si:ch211-250e5.9-001	SUEL type lectin domain	Lectins	PQ UNIQUE	-
210	ENSDARP00000125818	PPP2CA	PPP2CA-001	Protein phosphatase 2, catalytic subunit, alpha isozyme	Protein Synthesis	PQ UNIQUE	-
211	ENSDARP00000126883	ACTC1 (2 of 2)	ACTC1 (2 of 2)-001	Actin, alpha, cardiac muscle 1a	Cell cycle, division, growth and fate	PQ UNIQUE	-
212	ENSDARP00000094165	wu:fl42e03	wu:fl42e03-201	PAX-interacting protein 1	Cell cycle, division, growth and fate	PQ INCREASED	27.99
213	ENSDARP00000091393	ZP2 (2 of 4)	ZP2 (2 of 4)-001	Zona pellucida glycoprotein 2 (sperm receptor)	Zona Pellucida proteins	PQ INCREASED	12.17
214	ENSDARP00000116912	zgc:173856	zgc:173856-001	Nuclear receptor coactivator 6-like	Protein Synthesis	PQ INCREASED	11.43
215	ENSDARP00000072211	zp21	zp21-001	Zona pellucida glycoprotein 2, like 1	Zona Pellucida proteins	PQ INCREASED	10.63
216	ENSDARP00000107576	sudc2	sudc2-201	Succinate-CoA ligase, GDP-forming, beta subunit	Energy metabolism	PQ INCREASED	9.58
217	ENSDARP00000068662	zp3.2	zp3.2-202	Zona pellucida glycoprotein 3, tandem duplicate 2	Zona Pellucida proteins	PQ INCREASED	9.13
218	ENSDARP00000122970	zp3b	zp3b-002	Zona pellucida glycoprotein 3b	Zona Pellucida proteins	PQ INCREASED	8.85
219	ENSDARP00000081954	sudc2	sudc2-001	Succinate-CoA ligase, GDP-forming, beta subunit	Energy metabolism	PQ INCREASED	8.74
220	ENSDARP00000071171	zp3b	zp3b-201	Zona pellucida glycoprotein 3b	Zona Pellucida proteins	PQ INCREASED	7.40
221	ENSDARP00000071703	alg1	alg1-001	Asparagine-linked glycosylation 1 homolog (yeast, beta-1,4-mannosyltransferase)	Protein Synthesis	PQ INCREASED	6.96
222	ENSDARP00000099884	ZP2 (3 of 4)	ZP2 (3 of 4)-201	Zona pellucida glycoprotein 2 (sperm receptor)	Zona Pellucida proteins	PQ INCREASED	6.54
223	ENSDARP00000058255	zp3b	zp3b-001	Zona pellucida glycoprotein 3b	Zona Pellucida proteins	PQ INCREASED	6.53
224	ENSDARP00000054229	fgg	fgg-001	Fibrinogen, gamma polypeptide	Immune system related	PQ INCREASED	6.11
225	ENSDARP00000088788	ERLIN2	ERLIN2-201	ER lipid raft associated 2 (erlin2), mRNA	Lipid metabolism	PQ INCREASED	6.10
226	ENSDARP00000121177	ERLIN2	ERLIN2-001	ER lipid raft associated 2 (erlin2), mRNA	Lipid metabolism	PQ INCREASED	6.10
227	ENSDARP00000124617	rpa2	rpa2-002	Replication protein A2	Cell cycle, division, growth and fate	PQ INCREASED	5.24
228	ENSDARP00000094808	sdf4	sdf4-001	Stromal cell derived factor 4	Immune system related	PQ INCREASED	5.22
229	ENSDARP00000122503	pus1	pus1-001	Pseudouridine synthase 1	Cell cycle, division, growth and fate	PQ INCREASED	5.22
230	ENSDARP00000121591	CRP	CRP-001	C-reactive protein, pentraxin-related	Immune system related	PQ INCREASED	5.22
231	ENSDARP00000054025	rcc1	rcc1-001	Regulator of chromosome condensation 1	Cell cycle, division, growth and fate	PQ INCREASED	5.20
232	ENSDARP00000127355	capgb	capgb-001	Capping protein (actin filament), gelsolin-like b	Cell cycle, division, growth and fate	PQ INCREASED	4.37
233	ENSDARP00000036766	zgc:165539	zgc:165539-201	Uncharacterized protein	Cell cycle, division, growth and fate	PQ INCREASED	4.36
234	ENSDARP00000029607	gfap	gfap-001	Glial fibrillary acidic protein	Cell cycle, division, growth and fate	PQ INCREASED	4.35
235	ENSDARP00000116942	zgc:165539	zgc:165539-001	Uncharacterized protein	Cell cycle, division, growth and fate	PQ INCREASED	4.35
236	ENSDARP00000107173	si:dkey-24117.5	si:dkey-24117.5-001	C type lectin	Lectins	PQ INCREASED	4.32
237	ENSDARP00000109765	zgc:171670	zgc:171670-001	C type lectin	Lectins	PQ INCREASED	4.32
238	ENSDARP00000127261	zgc:171670	zgc:171670-002	C type lectin	Lectins	PQ INCREASED	4.32
239	ENSDARP00000127453	si:dkey-24117.5	si:dkey-24117.5-002	C type lectin	Lectins	PQ INCREASED	4.32
240	ENSDARP00000018923	eif4a1b	eif4a1b-001	Eukaryotic translation initiation factor 4A, isoform 1B	Protein Synthesis	PQ INCREASED	4.04
241	ENSDARP00000128336	eif4a3	eif4a3-002	Eukaryotic translation initiation factor 4A, isoform 1B	Protein Synthesis	PQ INCREASED	4.01
242	ENSDARP00000061750	zp3a.2	zp3a.2-001	Zona pellucida glycoprotein 3a, tandem duplicate 2	Zona Pellucida proteins	PQ INCREASED	3.98
243	ENSDARP00000004016	fen1	fen1-201	Flap structure-specific endonuclease 1	Cell cycle, division, growth and fate	PQ INCREASED	3.91
244	ENSDARP00000043687	si:dkey-24117.2	si:dkey-24117.2-001	C type lectin	Lectins	PQ INCREASED	3.84
245	ENSDARP00000127204	si:dkey-24117.2	si:dkey-24117.2-002	C type lectin	Lectins	PQ INCREASED	3.84
246	ENSDARP00000127328	si:dkey-24117.2	si:dkey-24117.2-003	C type lectin	Lectins	PQ INCREASED	3.84
247	ENSDARP00000104065	zgc:173837	zgc:173837-201	Uncharacterized dopey family member 2-like protein	Endosome-Lysosome related	PQ INCREASED	3.80
248	ENSDARP00000070941	ap2a1	ap2a1-201	Adaptor-related protein complex 2, alpha 1 subunit	Protein degradation and synthesis inhibition	PQ INCREASED	3.53
249	ENSDARP00000105782	mat2aa	mat2aa-001	S-adenosylmethionine synthase-Methionine adenosyltransferase II, alpha a	Protein Synthesis	PQ INCREASED	3.50
250	ENSDARP00000028571	ndufs1	ndufs1-001	NADH dehydrogenase (ubiquinone) Fe-S protein 1	Energy metabolism	PQ INCREASED	3.49
251	ENSDARP00000118532	erlin2	erlin2-001	ER lipid raft associated 2 (erlin2), mRNA	Lipid metabolism	PQ INCREASED	3.49
252	ENSDARP00000110335	isoc1	isoc1-201	Isochorismatase domain containing 1	REDOX/Detox related	PQ INCREASED	3.49
253	ENSDARP00000063856	scrm2	scrm2-001	Secernin 2	Protein degradation and synthesis inhibition	PQ INCREASED	3.49
254	ENSDARP00000114795	casp3a	casp3a-003	Caspase 3, apoptosis-related cysteine protease a	Apoptosis related	PQ INCREASED	3.49
255	ENSDARP00000110330	HOMER2	HOMER2-201	Homer homolog 2 (Drosophila)	Other	PQ INCREASED	3.48
256	ENSDARP00000116562	sepp1a	sepp1a-001	Selenoprotein P, plasma, 1a	REDOX/Detox related	PQ INCREASED	3.48
257	ENSDARP00000090521	nap14b	nap14b-201	Nucleosome assembly protein 1-like 4b	Cell cycle, division, growth and fate	PQ INCREASED	3.48
258	ENSDARP00000115833	nap14b	nap14b-001	Nucleosome assembly protein 1-like 4b	Cell cycle, division, growth and fate	PQ INCREASED	3.48
259	ENSDARP00000076885	HOMER2	HOMER2-202	Homer homolog 2 (Drosophila)	Other	PQ INCREASED	3.48
260	ENSDARP00000057824	cfd	cfd-001	Complement factor D (adipsin)	Protein degradation and synthesis inhibition	PQ INCREASED	3.48
261	ENSDARP00000034563	fnb	fnb-001	Farnesyltransferase, CAAX box, beta	Cell cycle, division, growth and fate	PQ INCREASED	3.48
262	ENSDARP00000025160	psmd8	psmd8-001	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	Protein Synthesis	PQ INCREASED	3.48
263	ENSDARP00000078713	isoc1	isoc1-001	Isochorismatase domain containing 1	REDOX/Detox related	PQ INCREASED	3.47

264	ENSDARP0000060245	dnajc3	dnajc3-001	DnaJ (Hsp40) homolog, subfamily C, member 3	Protein Synthesis	PQ INCREASED	3.47
265	ENSDARP00000128168	ap2a1	ap2a1-001	Adaptor-related protein complex 2, alpha 1 subunit	Protein degradation and synthesis inhibition	PQ INCREASED	3.44
266	ENSDARP00000073542	CR559930.2	CR559930.2-201	Serpin superfamily	Other	PQ INCREASED	3.40
267	ENSDARP00000095519	zgc.171927	zgc.171927-001	Uncharacterized protein	Apoptosis related	PQ INCREASED	3.35
268	ENSDARP00000100922	CABZ01059627.2	CABZ01059627.2-202	Mucin-5AC	Cell cycle, division, growth and fate	PQ INCREASED	3.35
269	ENSDARP00000107790	zp3a.1	zp3a.1-201	Zona pellucida glycoprotein 3a, tandem duplicate 1	Zona Pellucida proteins	PQ INCREASED	3.34
270	ENSDARP00000103071	zgc.173770	zgc.173770-201	Mucin-5AC-like	Cell cycle, division, growth and fate	PQ INCREASED	3.31
271	ENSDARP00000118880	rplp1	rplp1-002	Ribosomal protein, large, P1	Protein Synthesis	PQ INCREASED	3.14
272	ENSDARP00000027643	zgc.63587	zgc.63587-201	Uncharacterized protein	Cell cycle, division, growth and fate	PQ INCREASED	3.10
273	ENSDARP00000058955	ywhabl	ywhabl-001	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide like	Cell cycle, division, growth and fate	PQ INCREASED	3.08
274	ENSDARP00000103720	ywhabl	ywhabl-201	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide like	Cell cycle, division, growth and fate	PQ INCREASED	3.08
275	ENSDARP00000060688	eif2b2	eif2b2-001	Eukaryotic translation initiation factor 2B, subunit 2 beta	Protein Synthesis	PQ INCREASED	3.05
276	ENSDARP00000096076	si:ch211-226h8.6	si:ch211-226h8.6-001	Uncharacterized protein	Other	PQ INCREASED	3.05
277	ENSDARP00000122128	si:ch211-11k18.4	si:ch211-11k18.4-002	Uncharacterized protein	Other	PQ INCREASED	3.05
278	ENSDARP00000011707	uqcrf1	uqcrf1-001	Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Energy metabolism	PQ INCREASED	3.05
279	ENSDARP00000099928	uqcrf1	uqcrf1-201	Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Energy metabolism	PQ INCREASED	3.05
280	ENSDARP00000103915	c9	c9-202	Complement component 9	Immune system related	PQ INCREASED	2.95
281	ENSDARP00000121323	c9	c9-001	Complement component 9	Immune system related	PQ INCREASED	2.95
282	ENSDARP00000128894	thop1	thop1-002	Thimet oligopeptidase 1	Protein degradation and synthesis inhibition	PQ INCREASED	2.91
283	ENSDARP00000051373	c9	c9-201	Complement component 9	Immune system related	PQ INCREASED	2.90
284	ENSDARP00000109027	cdk1	cdk1-001	Cyclin-dependent kinase 1	Cell cycle, division, growth and fate	PQ INCREASED	2.90
285	ENSDARP00000054077	rpa2	rpa2-001	Replication protein A2	Cell cycle, division, growth and fate	PQ INCREASED	2.90
286	ENSDARP00000058424	CABZ01059627.1	CABZ01059627.1-201	Mucin 5Ac	Cell cycle, division, growth and fate	PQ INCREASED	2.87
287	ENSDARP00000069494	eif2s2	eif2s2-001	Translation initiation factor 2 subunit 2	Protein Synthesis	PQ INCREASED	2.74
288	ENSDARP00000065372	eef1b2	eef1b2-001	Elongation factor 1-beta	Protein Synthesis	PQ INCREASED	2.72
289	ENSDARP00000009441	pcid2	pcid2.001	PCI domain containing 2	Immune system related	PQ INCREASED	2.62
290	ENSDARP00000116670	nap114b	nap114b-002	Nucleosome assembly protein 1-like 4b	Cell cycle, division, growth and fate	PQ INCREASED	2.62
291	ENSDARP00000096322	arl3	arl3-001	ADP-ribosylation factor-like 3	Cell cycle, division, growth and fate	PQ INCREASED	2.62
292	ENSDARP00000095451	tpd52i2b	tpd52i2b-002	Tumor protein D52-like 2b	Oncogenes related	PQ INCREASED	2.62
293	ENSDARP00000022360	anp32a	anp32a-001	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Cell cycle, division, growth and fate	PQ INCREASED	2.62
294	ENSDARP00000123639	lcn2l	lcn2l-003	Transcobalamin II	Other	PQ INCREASED	2.62
295	ENSDARP00000112902	srsf1b	srsf1b-002	Serine/arginine-rich splicing factor 1b	Protein Synthesis	PQ INCREASED	2.62
296	ENSDARP00000120687	actr2b	actr2b-002	Actin-related protein 2b homolog	Cell cycle, division, growth and fate	PQ INCREASED	2.62
297	ENSDARP00000107467	snrpa1	snrpa1-002	Small nuclear ribonucleoprotein polypeptide A	Protein Synthesis	PQ INCREASED	2.62
298	ENSDARP00000116615	anp32a	anp32a-002	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Cell cycle, division, growth and fate	PQ INCREASED	2.62
299	ENSDARP00000015887	skp1	skp1-001	S-phase kinase-associated protein 1	Protein degradation and synthesis inhibition	PQ INCREASED	2.62
300	ENSDARP00000115511	tpd52i2b	tpd52i2b-004	Tumor protein D52-like 2b	Oncogenes related	PQ INCREASED	2.62
301	ENSDARP00000060303	dhrs13a.3	dhrs13a.3-001	Dehydrogenase/reductase (SDR family) member 13a, duplicate 3	REDOX/Detox related	PQ INCREASED	2.62
302	ENSDARP00000127050	nup43	nup43-003	Nucleoporin 43	Protein Synthesis	PQ INCREASED	2.62
303	ENSDARP00000117901	tpd52i2b	tpd52i2b-006	Tumor protein D52-like 2b	Oncogenes related	PQ INCREASED	2.62
304	ENSDARP00000105248	ist1	ist1-201	Increased sodium tolerance 1 homolog (yeast)	Protein degradation and synthesis inhibition	PQ INCREASED	2.62
305	ENSDARP00000116690	pus1	pus1-002	Pseudouridylylase 1	Protein Synthesis	PQ INCREASED	2.61
306	ENSDARP00000116432	slc25a5	slc25a5-003	Solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	Other	PQ INCREASED	2.61
307	ENSDARP00000059040	h1m	h1m-201	Linker histone 1M	Cell cycle, division, growth and fate	PQ INCREASED	2.61
308	ENSDARP00000104211	myl9b	myl9b-201	Myosin, light chain 9b, regulatory	Cell cycle, division, growth and fate	PQ INCREASED	2.61
309	ENSDARP00000121790	tpd52i2b	tpd52i2b-008	Tumor protein D52-like 2b	Oncogenes related	PQ INCREASED	2.61
310	ENSDARP00000094070	ndufa5	ndufa5-001	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 5	Energy metabolism	PQ INCREASED	2.61
311	ENSDARP00000023772	marcksb	marcksb-001	Myristoylated alanine-rich C-kinase substrate	Apoptosis related	PQ INCREASED	2.61
312	ENSDARP00000066545	nif31	nif31-001	NIF3 NGG1 interacting factor 3-like 1	Other	PQ INCREASED	2.61
313	ENSDARP00000117802	tpd52i2b	tpd52i2b-009	Tumor protein D52-like 2b	Oncogenes related	PQ INCREASED	2.61
314	ENSDARP00000116734	ist1	ist1-002	Increased sodium tolerance 1 homolog (yeast)	Protein degradation and synthesis inhibition	PQ INCREASED	2.61
315	ENSDARP00000117716	casp3a	casp3a-002	Aspase 3, apoptosis-related cysteine peptidase a	Apoptosis related	PQ INCREASED	2.61
316	ENSDARP00000068086	ist1	ist1-001	Increased sodium tolerance 1 homolog (yeast)	Protein degradation and synthesis inhibition	PQ INCREASED	2.61
317	ENSDARP00000067511	psma4	psma4-001	Proteasome (prosome, macropain) subunit, alpha type, 4	Protein degradation and synthesis inhibition	PQ INCREASED	2.61
318	ENSDARP00000025342	cox5aa	cox5aa-201	Cytochrome c oxidase subunit 5a	Energy metabolism	PQ INCREASED	2.61
319	ENSDARP00000105687	cox5aa	cox5aa-203	Cytochrome c oxidase subunit 5a	Energy metabolism	PQ INCREASED	2.61
320	ENSDARP00000106612	cox5aa	cox5aa-202	Cytochrome c oxidase subunit 5a	Energy metabolism	PQ INCREASED	2.61
321	ENSDARP00000123538	cox5aa	cox5aa-001	Cytochrome c oxidase subunit 5a	Energy metabolism	PQ INCREASED	2.61
322	ENSDARP00000051185	ncgrp1	ncgrp1-001	Non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	Immune system related	PQ INCREASED	2.61
323	ENSDARP00000073363	fdx1	fdx1-005	Ferredoxin 1	REDOX/Detox related	PQ INCREASED	2.61
324	ENSDARP00000113657	fdx1	fdx1-002	Ferredoxin 1	REDOX/Detox related	PQ INCREASED	2.61
325	ENSDARP00000124949	fdx1	fdx1-004	Ferredoxin 1	REDOX/Detox related	PQ INCREASED	2.61
326	ENSDARP00000064438	nup43	nup43-001	Nucleoporin 43	Protein Synthesis	PQ INCREASED	2.61
327	ENSDARP00000069298	si:ch73-207h17.1	si:ch73-207h17.1-201	Uncharacterized protein	Other	PQ INCREASED	2.61
328	ENSDARP00000121841	tpd52i2b	tpd52i2b-007	Tumor protein D52-like 2b	Oncogenes related	PQ INCREASED	2.61
329	ENSDARP00000003222	cyp20a1	cyp20a1-001	Cytochrome P450, family 20, subfamily A, polypeptide 1	REDOX/Detox related	PQ INCREASED	2.61
330	ENSDARP00000097644	anp32a	anp32a-201	Anp32a-001	Cell cycle, division, growth and fate	PQ INCREASED	2.61
331	ENSDARP00000129796	ap2a1	ap2a1-003	Adaptor-related protein complex 2, alpha 1 subunit	Protein degradation and synthesis inhibition	PQ INCREASED	2.61

332	ENSDARP00000051197	mis18a	mis18a-001	MIS18 kinetochore protein A	Cell cycle, division, growth and fate	PQ INCREASED	2.61
333	ENSDARP00000003173	seh1l	seh1l-001	Nucleoporin SEH1	Cell cycle, division, growth and fate	PQ INCREASED	2.61
334	ENSDARP00000040239	tipr1	tipr1-201	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	Cell cycle, division, growth and fate	PQ INCREASED	2.61
335	ENSDARP000000023199	tpo522b	tpo522b-001	Tumor protein D52-like 2b	Oncogenes related	PQ INCREASED	2.61
336	ENSDARP00000104624	tpo522b	tpo522b-201	Tumor protein D52-like 2b	Oncogenes related	PQ INCREASED	2.61
337	ENSDARP00000044554	zgc.63637	zgc.63637-001	RAB41, member RAS oncogene family [	Oncogenes related	PQ INCREASED	2.60
338	ENSDARP00000110405	zgc.63637	zgc.63637-201	RAB41, member RAS oncogene family [	Oncogenes related	PQ INCREASED	2.60
339	ENSDARP00000095078	actl6a	actl6a-001	Actin-like 6A	Cell cycle, division, growth and fate	PQ INCREASED	2.60
340	ENSDARP00000015934	rragd	rragd-001	Ras-related GTP binding D	Apoptosis related	PQ INCREASED	2.60
341	ENSDARP00000044837	ndrg1a	ndrg1a-001	N-myc downstream regulated 1a	Cell cycle, division, growth and fate	PQ INCREASED	2.49
342	ENSDARP00000027276	eif4a3	eif4a3-001	Eukaryotic translation initiation factor 4A3	Protein Synthesis	PQ INCREASED	2.43
343	ENSDARP00000039951	ldh3a	ldh3a-201	Isocitrate dehydrogenase 3 (NAD+) alpha	Energy metabolism	PQ INCREASED	2.40
344	ENSDARP00000105892	ddost	ddost-001	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit (non-catalytic	Protein Synthesis	PQ INCREASED	2.39
345	ENSDARP00000121212	myl6	myl6-004	Myosin light chain 6	Cell cycle, division, growth and fate	PQ INCREASED	2.37
346	ENSDARP00000033600	rplp1	rplp1-001	Ribosomal protein, large, P1	Protein Synthesis	PQ INCREASED	2.36
347	ENSDARP00000075666	krt5	krt5-201	Keratin 5	Cell cycle, division, growth and fate	PQ INCREASED	2.33
348	ENSDARP00000079733	l2hgdh	l2hgdh-001	L-2-hydroxyglutarate dehydrogenase [	REDOX/DeTox related	PQ INCREASED	2.33
349	ENSDARP000000092718	rragca	rragca-001	Ras-related GTP binding Ca	Cell cycle, division, growth and fate	PQ INCREASED	2.32
350	ENSDARP00000107677	ppid	ppid-201	Peptidylprolyl isomerase D	Protein Synthesis	PQ INCREASED	2.32
351	ENSDARP00000108711	krt5	krt5-001	Keratin 5	Cell cycle, division, growth and fate	PQ INCREASED	2.32
352	ENSDARP00000016453	krt4	krt4-001	Keratin 4	Cell cycle, division, growth and fate	PQ INCREASED	2.32
353	ENSDARP00000006530	krt4	krt4-201	Keratin 4	Cell cycle, division, growth and fate	PQ INCREASED	2.32
354	ENSDARP00000126991	nif3l1	nif3l1-002	NIF3 NGG1 interacting factor 3-like 1	Other	PQ INCREASED	2.32
355	ENSDARP00000061743	zp3a.1	zp3a.1-001	zona pellucida glycoprotein 3a, tandem duplicate 1	Zona Pellucida proteins	PQ INCREASED	2.27
356	ENSDARP00000103385	ppp4cb	ppp4cb-001	Protein phosphatase 4, catalytic subunit b	Protein degradation and synthesis inhibition	PQ INCREASED	2.23
357	ENSDARP00000093277	anp32b	anp32b-001	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	Cell cycle, division, growth and fate	PQ INCREASED	2.18
358	ENSDARP00000055503	cyc1	cyc1-001	Ubiquinol-cytochrome c reductase cytochrome c1 subunit	Energy metabolism	PQ INCREASED	2.18
359	ENSDARP00000075074	arpc3	arpc3-001	Actin related protein 2/3 complex, subunit 3	Apoptosis related	PQ INCREASED	2.18
360	ENSDARP000000094142	ociad1	ociad1-001	OCIA domain containing 2	Endosome-Lysosome related	PQ INCREASED	2.18
361	ENSDARP00000111978	ociad1	ociad1-201	OCIA domain containing 2	Endosome-Lysosome related	PQ INCREASED	2.18
362	ENSDARP00000112683	ociad1	ociad1-002	OCIA domain containing 2	Endosome-Lysosome related	PQ INCREASED	2.18
363	ENSDARP000000039222	gnpda2	gnpda2-201	Glucosamine-6-phosphate deaminase 2	Energy metabolism	PQ INCREASED	2.18
364	ENSDARP00000114418	gnpda2	gnpda2-001	Glucosamine-6-phosphate deaminase 2	Energy metabolism	PQ INCREASED	2.18
365	ENSDARP00000086977	rpl23	rpl23-001	Ribosomal protein L23	Protein Synthesis	PQ INCREASED	2.18
366	ENSDARP00000109902	zgc.162816	zgc.162816-201	D-serine dehydratase-like	Other	PQ INCREASED	2.18
367	ENSDARP00000117083	tomm70a	tomm70a-001	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	Other	PQ INCREASED	2.18
368	ENSDARP00000011426	ambp	ambp-001	Arginyl aminopeptidase (aminopeptidase B)	Protein degradation and synthesis inhibition	PQ INCREASED	2.18
369	ENSDARP00000098620	mvda	mvda-001	Mevalonate (diphospho) decarboxylase a	Lipid metabolism	PQ INCREASED	2.18
370	ENSDARP00000127428	rrm2	rrm2-004	Ribonucleotide reductase M2 polypeptide	Cell cycle, division, growth and fate	PQ INCREASED	2.18
371	ENSDARP00000107514	fkbp3	fkbp3-202	FK506 binding protein 3	Protein Synthesis	PQ INCREASED	2.17
372	ENSDARP00000008918	map2k1	map2k1-001	Mitogen-activated protein kinase kinase 1	Apoptosis related	PQ INCREASED	2.17
373	ENSDARP00000027385	hnrmp1l	hnrmp1l-001	Heterogeneous nuclear ribonucleoprotein H1, like	Protein Synthesis	PQ INCREASED	2.17
374	ENSDARP00000128433	serpinb1l3	serpinb1l3-002	Serpin peptidase inhibitor, clade B (ovalbumin), member 1, like 3	Other	PQ INCREASED	2.12
375	ENSDARP00000014914	map2k2a	map2k2a-001	Mitogen-activated protein kinase kinase 2a	Apoptosis related	PQ INCREASED	2.12
376	ENSDARP00000059346	bckdha	bckdha-001	Branched chain keto acid dehydrogenase E1, alpha polypeptide	Protein degradation and synthesis inhibition	PQ INCREASED	2.12
377	ENSDARP00000106474	bckdha	bckdha-201	Branched chain keto acid dehydrogenase E1, alpha polypeptide	Protein degradation and synthesis inhibition	PQ INCREASED	2.12
378	ENSDARP00000093670	ndrg1a	ndrg1a-002	N-myc downstream regulated gene 1a	Cell cycle, division, growth and fate	PQ INCREASED	2.12
379	ENSDARP00000047263	eef1db	eef1db-202	Elongation factor-1, delta, b	Protein Synthesis	PQ INCREASED	2.09
380	ENSDARP00000129723	thop1	thop1-003	Thimet oligopeptidase 1	Protein degradation and synthesis inhibition	PQ INCREASED	2.09
381	ENSDARP00000109129	si:ch211-11k18.4	si:ch211-11k18.4-201	Uncharacterized protein	Other	PQ INCREASED	2.09
382	ENSDARP00000123562	si:ch211-11k18.4	si:ch211-11k18.4-001	Uncharacterized protein	Other	PQ INCREASED	2.09
383	ENSDARP00000100592	eef1db	eef1db-001	Elongation factor-1, delta, b	Protein Synthesis	PQ INCREASED	2.08
384	ENSDARP00000029821	eef1db	eef1db-201	Elongation factor-1, delta, b	Protein Synthesis	PQ INCREASED	2.08
385	ENSDARP00000104512	hsp90ab1	hsp90ab1-201	Heat shock protein 90kDa alpha (cytosolic), class B member 1	Protein Synthesis	PQ INCREASED	2.08
386	ENSDARP000000014978	hsp90ab1	hsp90ab1-001	Heat shock protein 90kDa alpha (cytosolic), class B member 1	Protein Synthesis	PQ INCREASED	2.08
387	ENSDARP00000042703	eef1db	eef1db-002	Elongation factor-1, delta, b	Protein Synthesis	PQ INCREASED	2.08
388	ENSDARP00000070780	pca	pca-001	Proliferating cell nuclear antigen	Cell cycle, division, growth and fate	PQ INCREASED	2.07
389	ENSDARP00000022789	bzw1a	bzw1a-001	Basic leucine zipper and W2 domains 1a	Cell cycle, division, growth and fate	PQ INCREASED	2.07
390	ENSDARP00000038550	mapk1	mapk1-001	Mitogen-activated protein kinase kinase 2a	Apoptosis related	PQ INCREASED	2.03
391	ENSDARP00000123916	mapk1	mapk1-002	Mitogen-activated protein kinase kinase 2a	Apoptosis related	PQ INCREASED	2.03
392	ENSDARP00000076624	rragcb	rragcb-001	Ras-related GTP binding Ca	Cell cycle, division, growth and fate	PQ INCREASED	2.03
393	ENSDARP000000064746	stoml2	stoml2-201	Stomatin (EPB72)-like 2	Other	PQ INCREASED	2.03
394	ENSDARP00000124593	ldh3b	ldh3b-001	Isocitrate dehydrogenase 3 (NAD+) beta	Energy metabolism	PQ INCREASED	2.03
395	ENSDARP00000048382	creld2	creld2-001	Cysteine-rich with EGF-like domains 2	Other	PQ INCREASED	2.03
396	ENSDARP00000109480	vtg5	vtg5-201	Vitellogenin 5	Vitellogenins	PQ INCREASED	2.03
397	ENSDARP00000123659	tpi1b	tpi1b-002	Triosephosphate isomerase 1b	Energy metabolism	PQ INCREASED	2.00
398	ENSDARP00000113319	eif3ea	eif3ea-003	Translation initiation factor 3 subunit E	Protein Synthesis	GQ INCREASED	0.50
399	ENSDARP00000037758	cot1l	cot1l-001	Coactosin-like 1 (Dictyostelium)	Cell cycle, division, growth and fate	GQ INCREASED	0.50

400	ENSDARP0000022310	adsl	adsl-001	Adenylosuccinate lyase	Cell cycle, division, growth and fate	GG INCREASED	0.50
401	ENSDARP0000007588	pgd	pgd-001	Phosphoglucuronate hydrogenase	Energy metabolism	GG INCREASED	0.50
402	ENSDARP0000014732	cyb5b3	cyb5b3-001	Cytochrome b5 reductase 3	Energy metabolism	GG INCREASED	0.50
403	ENSDARP00000097681	prps1a	prps1a-002	Phosphoribosyl pyrophosphate synthetase 1A	Protein Synthesis	GG INCREASED	0.50
404	ENSDARP0000009909	gpia	gpia-001	Glucose phosphate isomerase a	Energy metabolism	GG INCREASED	0.50
405	ENSDARP0000003107	cct7	cct7-001	Chaperonin containing TCP1, subunit 7	Protein Synthesis	GG INCREASED	0.50
406	ENSDARP00000123779	fasn	fasn-001	Fatty acid synthase	Lipid metabolism	GG INCREASED	0.50
407	ENSDARP0000017693	ppp2r1b	ppp2r1b-001	Protein phosphatase 2	Protein Synthesis	GG INCREASED	0.50
408	ENSDARP00000127789	si:ch211-157j23.3	si:ch211-157j23.3-202	NXPE family member 3-like	Other	GG INCREASED	0.50
409	ENSDARP00000114435	si:dkey-105h11.2	si:dkey-105h11.2-001	NXPE family member 3-like	Other	GG INCREASED	0.50
410	ENSDARP00000058383	gapdhs	gapdhs-001	Glyceraldhyde-3-phosphate dehydrogenase, spermatogenic	Energy metabolism	GG INCREASED	0.50
411	ENSDARP00000093927	FBXO2	FBXO2-201	F-box protein 2	Protein degradation and synthesis inhibition	GG INCREASED	0.50
412	ENSDARP0000018064	acat2	acat2-001	Acetyl-CoA acetyltransferase 2	Energy metabolism	GG INCREASED	0.50
413	ENSDARP00000108188	ssr1	ssr1-201	Translocan-associated protein subunit alpha	Protein Synthesis	GG INCREASED	0.50
414	ENSDARP0000012454	phc2b	phc2b-201	Polyhomeotic-like protein 2-Histone H2A	Cell cycle, division, growth and fate	GG INCREASED	0.50
415	ENSDARP00000029067	rpa1	rpa1-001	Replication protein A1	Cell cycle, division, growth and fate	GG INCREASED	0.50
416	ENSDARP00000093898	p4hb	p4hb-001	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	Protein Synthesis	GG INCREASED	0.50
417	ENSDARP00000104575	tcp1	tcp1-201	T-complex polypeptide 1	Protein Synthesis	GG INCREASED	0.50
418	ENSDARP00000034904	psmc4	psmc4-001	Proteasome (prosome, macropain) 26S subunit, ATPase, 4	Protein Synthesis	GG INCREASED	0.50
419	ENSDARP00000113985	si:ch211-251f6.7	si:ch211-251f6.7-001	Fish egg lectin like	Lectins	GG INCREASED	0.50
420	ENSDARP0000009285	napa	napa-001	N-ethylmaleimide-sensitive factor attachment protein, alpha	Other	GG INCREASED	0.50
421	ENSDARP00000048990	si:ch211-157j23.2	si:ch211-157j23.2-001	NXPE family member 3-like	Other	GG INCREASED	0.50
422	ENSDARP00000129506	eprs	eprs-001	Glutamyl-prolyl-tRNA synthetase	Protein Synthesis	GG INCREASED	0.49
423	ENSDARP00000125075	sept7b	Novel	Cytoskeleton proteins	Cell cycle, division, growth and fate	GG INCREASED	0.49
424	ENSDARP00000112912	impa1	impa1-002	Inositol(myo)-1(or 4)-monophosphatase 1	Cell cycle, division, growth and fate	GG INCREASED	0.49
425	ENSDARP00000076390	rtn4a	rtn4a-003	Reticulon 4a	Protein Synthesis	GG INCREASED	0.49
426	ENSDARP00000079227	prosc	prosc-201	Proline synthetase co-transcribed homolog (bacterial)	Protein Synthesis	GG INCREASED	0.49
427	ENSDARP00000116169	prosc	prosc-001	Proline synthetase co-transcribed homolog (bacterial)	Protein Synthesis	GG INCREASED	0.49
428	ENSDARP00000018737	rpl27	rpl27-001	Arge subunit ribosomal protein L27e	Protein Synthesis	GG INCREASED	0.49
429	ENSDARP00000117864	rpl27	rpl27-002	Arge subunit ribosomal protein L27e	Protein Synthesis	GG INCREASED	0.49
430	ENSDARP00000072525	C20H6orf211	C20H6orf211-001	Protein-glutamate O-methyltransferase	Cell cycle, division, growth and fate	GG INCREASED	0.49
431	ENSDARP00000066897	rps16	rps16-001	Ribosomal protein S16	Protein Synthesis	GG INCREASED	0.49
432	ENSDARP00000089806	si:ch211-251f6.7	si:ch211-251f6.7-201	Fish egg lectin like	Lectins	GG INCREASED	0.49
433	ENSDARP00000075671	abhd14a	abhd14a-001	Abhydrolase domain containing 14A	Protein degradation and synthesis inhibition	GG INCREASED	0.49
434	ENSDARP00000109466	abhd14a	abhd14a-201	Abhydrolase domain containing 14A	Protein degradation and synthesis inhibition	GG INCREASED	0.49
435	ENSDARP00000028641	dnaj2a	dnaj2a-201	DnaJ homolog subfamily A member 2	Protein Synthesis	GG INCREASED	0.49
436	ENSDARP00000045893	rnaseh2a	rnaseh2a-001	Ribonuclease H2 subunit A	Cell cycle, division, growth and fate	GG INCREASED	0.49
437	ENSDARP00000108257	sept2	sept2-001	Septin 2	Cell cycle, division, growth and fate	GG INCREASED	0.49
438	ENSDARP00000105058	sept2	sept2-203	Septin 2	Cell cycle, division, growth and fate	GG INCREASED	0.49
439	ENSDARP00000056965	sept2	sept2-201	Septin 2	Cell cycle, division, growth and fate	GG INCREASED	0.49
440	ENSDARP00000105338	sept2	sept2-202	Septin 2	Cell cycle, division, growth and fate	GG INCREASED	0.49
441	ENSDARP00000046972	capza1a	capza1a-201	Capping protein (actin filament) muscle Z-line, alpha 1a	Cell cycle, division, growth and fate	GG INCREASED	0.49
442	ENSDARP00000062644	scarb1	scarb1-201	Scavenger receptor class B, member 1	Endosome-Lysosome related	GG INCREASED	0.49
443	ENSDARP00000104653	eif4a2	eif4a2-001	Eukaryotic translation initiation factor 4A, isoform 1B	Protein Synthesis	GG INCREASED	0.49
444	ENSDARP00000070224	eprs	eprs-201	Glutamyl-prolyl-tRNA synthetase	Protein Synthesis	GG INCREASED	0.49
445	ENSDARP00000121669	dctn2	dctn2-001	Dynactin 2	Cell cycle, division, growth and fate	GG INCREASED	0.49
446	ENSDARP00000093918	dctn2	dctn2-202	Dynactin 2	Cell cycle, division, growth and fate	GG INCREASED	0.49
447	ENSDARP00000127771	zgc:152830	zgc:152830-001	Peplidase M17 superfamily-	Protein degradation and synthesis inhibition	GG INCREASED	0.49
448	ENSDARP00000097937	zgc:152830	zgc:152830-001	Cytosol aminopeptidase family	Protein degradation and synthesis inhibition	GG INCREASED	0.49
449	ENSDARP00000119229	si:ch211-157j23.5	si:ch211-157j23.5-201	NXPE family member 3-like	Other	GG INCREASED	0.49
450	ENSDARP00000129574	si:ch211-157j23.5	si:ch211-157j23.5-001	NXPE family member 3-like	Other	GG INCREASED	0.49
451	ENSDARP00000057943	rpl26	rpl26-001	Ribosomal protein L26	Protein Synthesis	GG INCREASED	0.49
452	ENSDARP00000126732	rpl24	rpl24-001	Ribosomal protein L24	Protein Synthesis	GG INCREASED	0.49
453	ENSDARP00000105266	zgc:152830	zgc:152830-201	Peplidase M17 superfamily-	Protein degradation and synthesis inhibition	GG INCREASED	0.48
454	ENSDARP00000103413	vars	vars-202	Valyl-tRNA synthetase	Protein Synthesis	GG INCREASED	0.48
455	ENSDARP00000094372	npc1	npc1-001	Niemann-Pick disease, type C1	Endosome-Lysosome related	GG INCREASED	0.48
456	ENSDARP00000059310	siae	siae-001	Sialic acid acetyltransferase	Immune system related	GG INCREASED	0.48
457	ENSDARP00000042594	dctn2	dctn2-201	Dynactin 2	Cell cycle, division, growth and fate	GG INCREASED	0.48
458	ENSDARP00000124582	cnp	cnp-001	2',3'-cyclic nucleotide 3' phosphodiesterase	Cell cycle, division, growth and fate	GG INCREASED	0.48
459	ENSDARP00000061100	igt2r	igt2r-001	Insulin-like growth factor 2 receptor	Endosome-Lysosome related	GG INCREASED	0.48
460	ENSDARP00000129036	si:dkey-2417.6	si:dkey-2417.6-201	C-type lectin	Lectins	GG INCREASED	0.48
461	ENSDARP00000060465	si:dkey-2417.6	si:dkey-2417.6-001	C-type lectin	Lectins	GG INCREASED	0.48
462	ENSDARP00000127254	si:dkey-2417.6	si:dkey-2417.6-003	C-type lectin	Lectins	GG INCREASED	0.48
463	ENSDARP00000066510	pgm1	pgm1-001	Phosphoglucutamate 1	Energy metabolism	GG INCREASED	0.48
464	ENSDARP00000092429	calr2	calr2-001	Calreticulin, like 2	Protein Synthesis	GG INCREASED	0.48
465	ENSDARP00000096883	ids	ids-001	Iduronate 2-sulfatase	Endosome-Lysosome related	GG INCREASED	0.48
466	ENSDARP00000090432	zgc:55413	zgc:55413-202	Palmitoyl-(prolein) hydrolase activity	Other	GG INCREASED	0.48
467	ENSDARP00000125995	pkma	pkma-002	Pyruvate kinase, muscle, a		GG INCREASED	0.48



468	ENSDARP00000125765	pkma	pkma-001	Pyruvate kinase, muscle, a	Energy metabolism	GQ INCREASED	0.48
469	ENSDARP00000099755	psmb5	psmb5-001	Proteasome (prosome, macropain) subunit, beta type, 5	Protein degradation and synthesis inhibition	GQ INCREASED	0.48
470	ENSDARP00000020154	ehd3	ehd3-001	EH-domain containing 3	Protein degradation and synthesis inhibition	GQ INCREASED	0.48
471	ENSDARP00000074719	pgam2	pgam2-001	Phosphoglycerate mutase 2 (muscle)	Energy metabolism	GQ INCREASED	0.48
472	ENSDARP0000004738	cct3	cct3-001	Chaperonin containing Top1, subunit 3	Protein Synthesis	GQ INCREASED	0.48
473	ENSDARP00000052929	ndufv1	ndufv1-001	NADH dehydrogenase (ubiquinone) flavoprotein 1	Energy metabolism	GQ INCREASED	0.47
474	ENSDARP00000087338	ppp1cab	ppp1cab-001	Protein phosphatase 1, catalytic subunit, alpha isoform b	Cell cycle, division, growth and fate	GQ INCREASED	0.47
475	ENSDARP00000019120	anxa11b	anxa11b-201	Annexin A11b	Immune system related	GQ INCREASED	0.47
476	ENSDARP000000124670	anxa11b	anxa11b-001	Annexin A11b	Immune system related	GQ INCREASED	0.47
477	ENSDARP00000112654	eif5a	eif5a-003	Eukaryotic translation initiation factor 5A	Protein Synthesis	GQ INCREASED	0.47
478	ENSDARP00000124216	cnp	cnp-007	2',3'-cyclic nucleotide 3' phosphodiesterase	Cell cycle, division, growth and fate	GQ INCREASED	0.47
479	ENSDARP00000112576	zgc:66313	zgc:66313-001	Alpha-amylase	Energy metabolism	GQ INCREASED	0.47
480	ENSDARP00000119679	cnp	cnp-010	2',3'-cyclic nucleotide 3' phosphodiesterase	Cell cycle, division, growth and fate	GQ INCREASED	0.47
481	ENSDARP00000127543	si:ch211-157 23.2	si:ch211-157 23.2-201	NXPE family member 3-like	Other	GQ INCREASED	0.47
482	ENSDARP00000062650	pkma	pkma-201	Pyruvate kinase, muscle, a	Energy metabolism	GQ INCREASED	0.47
483	ENSDARP00000069223	shmt1	shmt1-001	Serine hydroxymethyltransferase 1 (soluble)	Protein Synthesis	GQ INCREASED	0.46
484	ENSDARP00000120541	cnp	cnp-003	2',3'-cyclic nucleotide 3' phosphodiesterase	Cell cycle, division, growth and fate	GQ INCREASED	0.46
485	ENSDARP00000110339	pkma	pkma-203	Pyruvate kinase, muscle, a	Energy metabolism	GQ INCREASED	0.46
486	ENSDARP00000091365	pdia5	pdia5-001	Protein disulfide isomerase family A, member 5	Protein Synthesis	GQ INCREASED	0.46
487	ENSDARP00000108306	cdc42	cdc42-202	Cell division cycle 42	Cell cycle, division, growth and fate	GQ INCREASED	0.46
488	ENSDARP00000118065	zgc:66313	zgc:66313-007	Alpha-amylase	Energy metabolism	GQ INCREASED	0.46
489	ENSDARP00000015775	sars	sars-001	Seryl- aminoacyl-tRNA synthetase	Protein Synthesis	GQ INCREASED	0.46
490	ENSDARP00000114417	cnp	cnp-004	2',3'-cyclic nucleotide 3' phosphodiesterase	Cell cycle, division, growth and fate	GQ INCREASED	0.46
491	ENSDARP00000117465	cnp	cnp-009	2',3'-cyclic nucleotide 3' phosphodiesterase	Cell cycle, division, growth and fate	GQ INCREASED	0.46
492	ENSDARP00000118406	cnp	cnp-005	2',3'-cyclic nucleotide 3' phosphodiesterase	Cell cycle, division, growth and fate	GQ INCREASED	0.46
493	ENSDARP00000118615	zgc:66313	zgc:66313-003	Alpha-amylase	Energy metabolism	GQ INCREASED	0.45
494	ENSDARP00000112608	cct6a	cct6a-002	Chaperonin containing TCP1, subunit 6A	Protein Synthesis	GQ INCREASED	0.45
495	ENSDARP00000027102	nap111	nap111-201	Nucleosome assembly protein 1-like 1	Cell cycle, division, growth and fate	GQ INCREASED	0.45
496	ENSDARP0000003468	cct8	cct8-001	T-complex protein 1 subunit theta	Protein Synthesis	GQ INCREASED	0.45
497	ENSDARP00000107134	ktn1	ktn1-001	Kinectin 1	Other	GQ INCREASED	0.44
498	ENSDARP00000120480	zgc:66313	zgc:66313-002	Alpha-amylase	Energy metabolism	GQ INCREASED	0.44
499	ENSDARP00000122652	zgc:66313	zgc:66313-005	Alpha-amylase	Energy metabolism	GQ INCREASED	0.44
500	ENSDARP00000082159	igl2bp1	igl2bp1-001	Insulin-like growth factor 2 mRNA binding protein 1	Protein Synthesis	GQ INCREASED	0.44
501	ENSDARP00000005691	ktn1	ktn1-201	Kinectin 1	Other	GQ INCREASED	0.44
502	ENSDARP00000020770	mithfd1b	mithfd1b-001	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1	Cell cycle, division, growth and fate	GQ INCREASED	0.44
503	ENSDARP00000102463	sept8a	sept8a-001	Septin 8a	Cell cycle, division, growth and fate	GQ INCREASED	0.44
504	ENSDARP00000056720	ldhd	ldhd-001	D-lactate dehydrogenase (cytochrome)	Energy metabolism	GQ INCREASED	0.44
505	ENSDARP00000125746	neu3.4	neu3.4-001	Sialidase 3, tandem duplicate 4	Lipid metabolism	GQ INCREASED	0.44
506	ENSDARP00000037906	usp14	usp14-201	Ubiquitin specific peptidase 14	Protein degradation and synthesis inhibition	GQ INCREASED	0.44
507	ENSDARP00000127023	si:ch1073-13h15.3	si:ch1073-13h15.3-001	Putative all-trans-retinol 13,14-reductase	REDOX/DeTox related	GQ INCREASED	0.44
508	ENSDARP00000011673	ddi2	ddi2-001	DNA-damage inducible protein 2	Protein degradation and synthesis inhibition	GQ INCREASED	0.44
509	ENSDARP00000013512	zgc:112334	zgc:112334-201	Rab GDP dissociation inhibitor alpha	Other	GQ INCREASED	0.44
510	ENSDARP00000049225	acox1	acox1-001	Acyl-CoA oxidase 1, palmitoyl	Lipid metabolism	GQ INCREASED	0.44
511	ENSDARP00000067559	acox1	acox1-002	Acyl-CoA oxidase 1, palmitoyl	Lipid metabolism	GQ INCREASED	0.44
512	ENSDARP00000017123	glud1b	glud1b-201	Glutamate dehydrogenase 1b	Energy metabolism	GQ INCREASED	0.44
513	ENSDARP00000091816	glud1b	glud1b-001	Glutamate dehydrogenase 1b	Energy metabolism	GQ INCREASED	0.44
514	ENSDARP00000024643	adh8a	adh8a-001	Alcohol dehydrogenase 8a	REDOX/DeTox related	GQ INCREASED	0.44
515	ENSDARP00000090576	arpc2	arpc2-001	Actin related protein 2/3 complex, subunit 2	Apoptosis related	GQ INCREASED	0.44
516	ENSDARP00000111384	zgc:112334	zgc:112334-202	Rab GDP dissociation inhibitor alpha	Other	GQ INCREASED	0.44
517	ENSDARP00000069585	carhsp1	carhsp1-201	Calcium regulated heat stable protein 1	Protein Synthesis	GQ INCREASED	0.44
518	ENSDARP00000125927	carhsp1	carhsp1-001	Calcium regulated heat stable protein 1	Protein Synthesis	GQ INCREASED	0.44
519	ENSDARP00000064111	glrx5	glrx5-001	Monothiol glutaredoxin	Protein Synthesis	GQ INCREASED	0.44
520	ENSDARP00000041446	ktn1	ktn1-002	Kinectin 1	Other	GQ INCREASED	0.44
521	ENSDARP00000080584	ktn1	ktn1-202	Kinectin 1	Other	GQ INCREASED	0.44
522	ENSDARP00000005670	rap1aa	rap1aa-002	Rap-1A member of RAS oncogene family a	Oncogenes related	GQ INCREASED	0.44
523	ENSDARP00000116523	rap1aa	rap1aa-001	Rap-1A member of RAS oncogene family a	Oncogenes related	GQ INCREASED	0.44
524	ENSDARP00000112718	crz	crz-002	Crystallin, zeta (quinone reductase)	Energy metabolism	GQ INCREASED	0.44
525	ENSDARP00000008973	dlst	dlst-001	Dihydropyrimidine S-succinyltransferase	Energy metabolism	GQ INCREASED	0.44
526	ENSDARP00000067865	RPS17	RPS17-201	Ribosomal protein S17	Protein Synthesis	GQ INCREASED	0.44
527	ENSDARP00000129150	RPS17	RPS17-001	Ribosomal protein S17	Protein Synthesis	GQ INCREASED	0.44
528	ENSDARP00000095998	CABZ01034848.1	CABZ01034848.1-201	Myosin 9-like	Energy metabolism	GQ INCREASED	0.44
529	ENSDARP00000003030	hibadhb	hibadhb-001	3-hydroxyisobutyrate dehydrogenase b	Protein degradation and synthesis inhibition	GQ INCREASED	0.44
530	ENSDARP00000011148	rps6	rps6-201	Small subunit ribosomal protein S6e	Protein Synthesis	GQ INCREASED	0.44
531	ENSDARP00000093469	ppp2r5d	ppp2r5d-201	Protein phosphatase 2, regulatory subunit B', delta	Protein Synthesis	GQ INCREASED	0.44
532	ENSDARP00000024354	impdh2	impdh2-001	Inosine 5'-monophosphate dehydrogenase 2	Cell cycle, division, growth and fate	GQ INCREASED	0.44
533	ENSDARP00000125879	neu3.5	neu3.5-001	Sialidase 3, tandem duplicate 4	Lipid metabolism	GQ INCREASED	0.44
534	ENSDARP00000126188	rps18	rps18-006	Small subunit ribosomal protein S18e	Protein Synthesis	GQ INCREASED	0.44
535	ENSDARP00000095645	trap1	trap1-201	TNF receptor-associated protein 1	Protein Synthesis	GQ INCREASED	0.44

536	ENSDARP00000095167	smx5	smx5-201	U6 snRNA-associated Sm-like protein LSM2	Protein Synthesis	GQ INCREASED	0.44
537	ENSDARP00000127825	rps28	rps28-004	Small subunit ribosomal protein S28e	Protein Synthesis	GQ INCREASED	0.44
538	ENSDARP0000001585	echs1	echs1-001	Noyl CoA hydratase, short chain, 1, mitochondrial	Lipid metabolism	GQ INCREASED	0.44
539	ENSDARP00000121906	pcca	pcca-002	Propionyl CoA carboxylase, alpha polypeptide	Energy metabolism	GQ INCREASED	0.44
540	ENSDARP00000107200	si:dkey-179j5.5	si:dkey-179j5.5-202	Gal lectin superfamily	Lectins	GQ INCREASED	0.44
541	ENSDARP00000107323	trap1	trap1-202	TNF receptor-associated protein 1	Protein Synthesis	GQ INCREASED	0.44
542	ENSDARP00000052062	rps28	rps28-003	Small subunit ribosomal protein S28e	Protein Synthesis	GQ INCREASED	0.44
543	ENSDARP00000115796	rps28	rps28-001	Small subunit ribosomal protein S28e	Protein Synthesis	GQ INCREASED	0.44
544	ENSDARP00000072253	serpinb12	serpinb12-001	Serpin peptidase inhibitor, clade B (ovalbumin), member 1, like 2	Other	GQ INCREASED	0.44
545	ENSDARP00000093527	si:dkey-179j5.5	si:dkey-179j5.5-201	Gal lectin superfamily	Lectins	GQ INCREASED	0.44
546	ENSDARP00000114428	cpt2	cpt2-002	Camitine palmitoyltransferase II	Lipid metabolism	GQ INCREASED	0.44
547	ENSDARP00000121781	myh11a	myh11a-002	Myosin, heavy chain 11a, smooth muscle	Cell cycle, division, growth and fate	GQ INCREASED	0.44
548	ENSDARP00000047012	srprb	srprb-001	Signal recognition particle receptor, B subunit	Protein Synthesis	GQ INCREASED	0.44
549	ENSDARP00000112598	si:ch211-157j23.3	si:ch211-157j23.3-001	NXPE family member 3-like	Other	GQ INCREASED	0.44
550	ENSDARP00000103437	cpdb	cpdb-201	Carboxypeptidase D, b	Protein degradation and synthesis inhibition	GQ INCREASED	0.44
551	ENSDARP00000107538	CABZ01073085.1	CABZ01073085.1-201	Chaperonin containing TCP1, subunit 2 (beta)	Protein Synthesis	GQ INCREASED	0.44
552	ENSDARP00000115288	ufd1l	ufd1l-004	Ubiquitin fusion degradation 1-like	Protein degradation and synthesis inhibition	GQ INCREASED	0.44
553	ENSDARP000000007716	atp5f1	atp5f1-001	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	Energy metabolism	GQ INCREASED	0.44
554	ENSDARP00000126736	ca15b	ca15b-005	Carbonic anhydrase XV b	Energy metabolism	GQ INCREASED	0.44
555	ENSDARP00000025042	sub1b	sub1b-001	UB1 homolog b (S. cerevisiae)	Protein Synthesis	GQ INCREASED	0.44
556	ENSDARP00000117668	man2b1	man2b1-002	Mannosidase, alpha, class 2B, member 1	Energy metabolism	GQ INCREASED	0.44
557	ENSDARP00000118860	si:ch1073-75o15.4	si:ch1073-75o15.4-001	SUEL type lectin	Lectins	GQ INCREASED	0.44
558	ENSDARP00000113030	trap1	trap1-001	TNF receptor-associated protein 1	Protein Synthesis	GQ INCREASED	0.44
559	ENSDARP00000121416	si:ch1073-75o15.4	si:ch1073-75o15.4-002	SUEL type lectin	Lectins	GQ INCREASED	0.44
560	ENSDARP00000075627	neu3.3	neu3.3-001	Sialidase 3, tandem duplicate 4	Lipid metabolism	GQ INCREASED	0.44
561	ENSDARP00000079035	neu3.3	neu3.3-201	Sialidase 3, tandem duplicate 4	Lipid metabolism	GQ INCREASED	0.44
562	ENSDARP00000032037	pdcd5	pdcd5-001	Programmed cell death 5	Apoptosis related	GQ INCREASED	0.44
563	ENSDARP00000116530	snx3	snx3-003	Sorting nexin-3/12	Protein degradation and synthesis inhibition	GQ INCREASED	0.44
564	ENSDARP00000075204	SEPT7-	SEPT7-201	Cytoskeleton proteins	Cell cycle, division, growth and fate	GQ INCREASED	0.44
565	ENSDARP00000069063	hm:zeh0351	hm:zeh0351	Cytoskeleton proteins	Cell cycle, division, growth and fate	GQ INCREASED	0.44
566	ENSDARP00000117207	CU469531.2	CU469531.2-201	Ras-related protein Rab-11B	Other	GQ INCREASED	0.44
567	ENSDARP00000124654	glytck	glytck-001	Glycerate kinase	Energy metabolism	GQ INCREASED	0.43
568	ENSDARP00000113159	ppp2r5d	ppp2r5d-001	Protein phosphatase 2, regulatory subunit B', delta	Protein Synthesis	GQ INCREASED	0.43
569	ENSDARP0000012850	asns	asns-201	Asparagine synthetase (glutamine-hydrolyzing)	Protein Synthesis	GQ INCREASED	0.43
570	ENSDARP00000107713	asns	asns-001	Asparagine synthetase (glutamine-hydrolyzing)	Protein Synthesis	GQ INCREASED	0.43
571	ENSDARP00000110193	asns	asns-202	Asparagine synthetase (glutamine-hydrolyzing)	Protein Synthesis	GQ INCREASED	0.43
572	ENSDARP00000042511	pltlnbl	pltlnbl-201	Phosphatidylinositol transfer protein, beta, like	Lipid metabolism	GQ INCREASED	0.43
573	ENSDARP00000095113	pltlnbl	pltlnbl-202	Phosphatidylinositol transfer protein, beta, like	Lipid metabolism	GQ INCREASED	0.43
574	ENSDARP00000113091	adsl	adsl-002	Adenylosuccinate lyase	Cell cycle, division, growth and fate	GQ INCREASED	0.43
575	ENSDARP00000074214	ndufs2	ndufs2-201	NADH dehydrogenase (ubiquinone) Fe-S protein 2	Energy metabolism	GQ INCREASED	0.43
576	ENSDARP00000028858	sept8b	sept8b-001	Septin 8a	Cell cycle, division, growth and fate	GQ INCREASED	0.43
577	ENSDARP00000012094	snx3	snx3-001	Sorting nexin-3/12	Protein Synthesis	GQ INCREASED	0.43
578	ENSDARP00000124720	eil3eb	eil3eb-003	Eukaryotic translation initiation factor	Protein Synthesis	GQ INCREASED	0.43
579	ENSDARP00000114890	acat2	acat2-002	Acetyl-CoA acetyltransferase 2	Energy metabolism	GQ INCREASED	0.43
580	ENSDARP00000121223	sept8a	sept8a-002	Septin 8a	Cell cycle, division, growth and fate	GQ INCREASED	0.43
581	ENSDARP00000058796	hebp2	hebp2-201	Heme binding protein 2	Other	GQ INCREASED	0.43
582	ENSDARP00000062535	hebp2	hebp2-001	Heme binding protein 2	Other	GQ INCREASED	0.43
583	ENSDARP00000114030	scarb1	scarb1-002	Scavenger receptor class B, member 1	Endosome-Lysosome related	GQ INCREASED	0.43
584	ENSDARP00000123981	mcm7	mcm7-001	Inchrosome maintenance complex component 7	Cell cycle, division, growth and fate	GQ INCREASED	0.43
585	ENSDARP00000122752	pcca	pcca-003	Propionyl CoA carboxylase, alpha polypeptide	Energy metabolism	GQ INCREASED	0.43
586	ENSDARP00000070414	vtnb	vtnb-001	Vitronectin b	Immune system related	GQ INCREASED	0.43
587	ENSDARP00000106695	NHLRC3	NHLRC3-201	NHL repeat containing 3	Other	GQ INCREASED	0.43
588	ENSDARP00000042249	rap1b	rap1b-201	RAP1B, member of RAS oncogene family	Oncogenes related	GQ INCREASED	0.43
589	ENSDARP00000114387	rap1b	rap1b-001	RAP1B, member of RAS oncogene family	Oncogenes related	GQ INCREASED	0.43
590	ENSDARP00000035945	sccpdhb	sccpdhb-001	Saccharopine dehydrogenase b	Other	GQ INCREASED	0.43
591	ENSDARP00000052702	nucb2b	nucb2b-001	Nucleobindin 2	Other	GQ INCREASED	0.43
592	ENSDARP00000129420	ddi2	ddi2-002	DNA-damage inducible protein 2	Other	GQ INCREASED	0.43
593	ENSDARP00000068144	pcxb	pcxb-201	Pyruvate carboxylase b	Energy metabolism	GQ INCREASED	0.43
594	ENSDARP0000017335	gorasp2	gorasp2-001	Golgi reassembly stacking protein 2, 55kDa	Protein Synthesis	GQ INCREASED	0.43
595	ENSDARP00000069178	si:ch1073-13h15.3	si:ch1073-13h15.3-201	Putative all-trans-retinol 13, 14-reductase	REDOX/Detox related	GQ INCREASED	0.43
596	ENSDARP00000123687	shmt1	shmt1-003	Serine hydroxymethyltransferase 1 (soluble)	Protein Synthesis	GQ INCREASED	0.42
597	ENSDARP00000121832	shmt1	shmt1-002	Serine hydroxymethyltransferase 1 (soluble)	Protein Synthesis	GQ INCREASED	0.42
598	ENSDARP00000025374	uap1f1	uap1f1-001	UDP-N-acteylglucosamine pyrophosphorylase 1, like 1	Cell cycle, division, growth and fate	GQ INCREASED	0.42
599	ENSDARP00000054618	prps1b	prps1b-001	Phosphoribosyl pyrophosphate synthetase 1A	Protein Synthesis	GQ INCREASED	0.41
600	ENSDARP00000090402	eil3s6ip	eil3s6ip-201	Eukaryotic translation initiation factor 3, subunit 6 interacting protein	Protein Synthesis	GQ INCREASED	0.40
601	ENSDARP00000112498	eil3s6ip	eil3s6ip-202	Eukaryotic translation initiation factor 3, subunit 6 interacting protein	Protein Synthesis	GQ INCREASED	0.40
602	ENSDARP00000096295	ACTR3 (1 of 2)	ACTR3 (1 of 2)-201	ARP3 actin-related protein 3 homolog (yeast)	Cell cycle, division, growth and fate	GQ INCREASED	0.40
603	ENSDARP00000124779	cat	cat-001	Catalase	REDOX/Detox related	GQ INCREASED	0.40

604	ENSDARP0000026554	psmc3	psmc3-201	Proteasome (prosome, macropain) 26S subunit, ATPase, 3	Protein degradation and synthesis inhibition	GQ INCREASED	0.40
605	ENSDARP00000081816	ddx6	ddx6-201	DEAD (Asp-Glu-Ala-Asp) box helicase 6	Cell cycle, division, growth and fate	GQ INCREASED	0.40
606	ENSDARP00000120609	rps18	rps18-005	Small subunit ribosomal protein S18e	Protein Synthesis	GQ INCREASED	0.39
607	ENSDARP00000016831	cct6a	cct6a-201	Chaperonin containing TCP1, subunit 6A	Protein Synthesis	GQ INCREASED	0.39
608	ENSDARP00000118006	cct6a	cct6a-001	Chaperonin containing TCP1, subunit 6A	Protein Synthesis	GQ INCREASED	0.39
609	ENSDARP00000063876	prdx6	prdx6-001	Peroxioredoxin 6	REDOX/Detox related	GQ INCREASED	0.39
610	ENSDARP00000013402	cat	cat-201	Catalase	REDOX/Detox related	GQ INCREASED	0.38
611	ENSDARP00000107673	cat	cat-202	Catalase	REDOX/Detox related	GQ INCREASED	0.38
612	ENSDARP00000098561	cnp	cnp-202	2',3'-cyclic nucleotide 3' phosphodiesterase	Cell cycle, division, growth and fate	GQ INCREASED	0.38
613	ENSDARP00000117370	cnp	cnp-001	2',3'-cyclic nucleotide 3' phosphodiesterase	Cell cycle, division, growth and fate	GQ INCREASED	0.38
614	ENSDARP00000093249	dars	dars-201	Aspartyl-tRNA synthetase	Protein Synthesis	GQ INCREASED	0.38
615	ENSDARP00000090277	shmt2	shmt2-201	Serine hydroxymethyltransferase 2 (mitochondrial)	Protein Synthesis	GQ INCREASED	0.37
616	ENSDARP00000051290	hexa	hexa-001	Hexosaminidase A (alpha polypeptide)	Energy metabolism	GQ INCREASED	0.37
617	ENSDARP00000042258	clybl	clybl-001	Citrate lyase subunit beta / citryl-CoA lyase	Energy metabolism	GQ INCREASED	0.37
618	ENSDARP00000025466	cct4	cct4-201	Chaperonin containing Tcp1, subunit 4	Protein Synthesis	GQ INCREASED	0.37
619	ENSDARP00000102802	shmt2	shmt2-202	Serine hydroxymethyltransferase 2 (mitochondrial)	Protein Synthesis	GQ INCREASED	0.37
620	ENSDARP00000074247	vdac3	vdac3-201	Voltage-dependent anion channel 3	Other	GQ INCREASED	0.37
621	ENSDARP00000121437	vdac3	vdac3-001	Voltage-dependent anion channel 3	Other	GQ INCREASED	0.37
622	ENSDARP00000101564	CU914772.1	CU914772.1-201	Glycosidase	Energy metabolism	GQ INCREASED	0.37
623	ENSDARP00000102398	eif3s10	eif3s10-001	Eukaryotic translation initiation factor	Protein Synthesis	GQ INCREASED	0.37
624	ENSDARP00000052502	nudcd1	nudcd1-001	NudC domain containing 1	Other	GQ INCREASED	0.36
625	ENSDARP00000114483	kpna2	kpna2-202	Karyopherin alpha 2	Protein Synthesis	GQ INCREASED	0.36
626	ENSDARP00000055489	kpna2	kpna2-001	Karyopherin alpha 2	Protein Synthesis	GQ INCREASED	0.36
627	ENSDARP00000117923	eno3	eno3-002	Enolase 3	Energy metabolism	GQ INCREASED	0.36
628	ENSDARP00000014955	man2b1	man2b1-001	Mannosidase, alpha, class 2B, member 1	Energy metabolism	GQ INCREASED	0.35
629	ENSDARP00000006424	agla	agla-201	Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase a	Energy metabolism	GQ INCREASED	0.35
630	ENSDARP00000129094	agla	agla-001	Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase a	Energy metabolism	GQ INCREASED	0.35
631	ENSDARP00000008882	me3	me3-001	Maic enzyme	Energy metabolism	GQ INCREASED	0.35
632	ENSDARP00000075198	uba3	uba3-001	Ubiquitin-like modifier activating enzyme 3	Protein degradation and synthesis inhibition	GQ INCREASED	0.35
633	ENSDARP00000123254	pcxb	pcxb-001	Pyruvate carboxylase b	Energy metabolism	GQ INCREASED	0.35
634	ENSDARP00000041577	stx12	stx12-201	Syntaxin 12/13	Other	GQ INCREASED	0.35
635	ENSDARP00000107227	stx12	stx12-001	Syntaxin 12/13	Other	GQ INCREASED	0.35
636	ENSDARP00000072874	rps8a	rps8a-001	Ribosomal protein S8a	Protein Synthesis	GQ INCREASED	0.35
637	ENSDARP00000123532	vdac3	vdac3-002	Voltage-dependent anion channel 3	Cell cycle, division, growth and fate	GQ INCREASED	0.35
638	ENSDARP00000003850	akr7a3	akr7a3-201	Aldo-keto reductase family 7, member A3 -afatoxin B1 aldehyde reductase	REDOX/Detox related	GQ INCREASED	0.35
639	ENSDARP00000005719	rps18	rps18-001	Small subunit ribosomal protein S18e	Protein Synthesis	GQ INCREASED	0.35
640	ENSDARP00000008399	drp2	drp2-001	Developmentally regulated GTP binding protein 2	Cell cycle, division, growth and fate	GQ INCREASED	0.35
641	ENSDARP00000105639	drp2	drp2-002	Developmentally regulated GTP binding protein 2	Cell cycle, division, growth and fate	GQ INCREASED	0.35
642	ENSDARP00000112087	zgc:158614	zgc:158614-202	Aifm4-apoptosis-inducing factor, mitochondrion-associated, 4	Apoptosis related	GQ INCREASED	0.34
643	ENSDARP00000129014	zgc:158614	zgc:158614-001	Aifm4-apoptosis-inducing factor, mitochondrion-associated, 4	Apoptosis related	GQ INCREASED	0.34
644	ENSDARP00000110981	dars	dars-202	Aspartyl-tRNA synthetase	Protein Synthesis	GQ INCREASED	0.33
645	ENSDARP00000116150	uap1	uap1-002	UDP-N-acteylglucosamine pyrophosphorylase 1	Cell cycle, division, growth and fate	GQ INCREASED	0.33
646	ENSDARP00000005651	rpl8	rpl8-201	Ribosomal protein L8	Protein Synthesis	GQ INCREASED	0.33
647	ENSDARP00000115147	rpl8	rpl8-001	Ribosomal protein L8	Protein Synthesis	GQ INCREASED	0.33
648	ENSDARP00000006244	dnpep	dnpep-001	Aspartyl aminopeptidase	Protein degradation and synthesis inhibition	GQ INCREASED	0.33
649	ENSDARP00000110484	dnpep	dnpep-201	Aspartyl aminopeptidase	Protein degradation and synthesis inhibition	GQ INCREASED	0.33
650	ENSDARP00000027655	mpep	mpep-001	Cytochrome-c peroxidase	Energy metabolism	GQ INCREASED	0.33
651	ENSDARP00000008660	snmp200	snmp200-001	Small nuclear ribonucleoprotein 200kDa	Protein Synthesis	GQ INCREASED	0.32
652	ENSDARP00000070479	cpdb	cpdb-001	Carboxypeptidase D, b	Protein degradation and synthesis inhibition	GQ INCREASED	0.30
653	ENSDARP00000040031	rtn4ip1	rtn4ip1-001	Reticulon 4 interacting protein 1	Protein Synthesis	GQ INCREASED	0.29
654	ENSDARP00000124612	glyctk	glyctk-004	Glycerate kinase	Energy metabolism	GQ INCREASED	0.29
655	ENSDARP00000121663	clybl	clybl-002	Citrate lyase subunit beta / citryl-CoA lyase	Energy metabolism	GQ INCREASED	0.29
656	ENSDARP00000114273	tceb2	tceb2-001	Transcription elongation factor B, polypeptide 2	Protein degradation and synthesis inhibition	GQ INCREASED	0.29
657	ENSDARP00000128442	zgc:158614	zgc:158614-003	Aifm4-apoptosis-inducing factor, mitochondrion-associated, 4	Apoptosis related	GQ INCREASED	0.29
658	ENSDARP00000055359	tceb2	tceb2-002	Transcription elongation factor B, polypeptide 2	Protein degradation and synthesis inhibition	GQ INCREASED	0.29
659	ENSDARP00000084961	rhoae	rhoae-001	Ras homolog gene family, member A	Cell cycle, division, growth and fate	GQ INCREASED	0.29
660	ENSDARP00000123757	glyctk	glyctk-003	Glycerate kinase	Energy metabolism	GQ INCREASED	0.29
661	ENSDARP00000118814	rpl23a	rpl23a-004	Large subunit ribosomal protein L32e	Protein Synthesis	GQ INCREASED	0.29
662	ENSDARP00000104485	zgc:158614	zgc:158614-201	Aifm4-apoptosis-inducing factor, mitochondrion-associated, 4	Apoptosis related	GQ INCREASED	0.29
663	ENSDARP00000002234	oxct1a	oxct1a-001	3-oxoacid CoA transferase 1a	Energy metabolism	GQ INCREASED	0.29
664	ENSDARP000000089234	APOD (3 of 3)	APOD (3 of 3)-201	Apolipoprotein D	Lipid metabolism	GQ INCREASED	0.29
665	ENSDARP00000113343	APOD (3 of 3)	APOD (3 of 3)-001	Apolipoprotein D	Lipid metabolism	GQ INCREASED	0.29
666	ENSDARP00000117077	APOD (3 of 3)	APOD (3 of 3)-004	Apolipoprotein D	Lipid metabolism	GQ INCREASED	0.29
667	ENSDARP00000123122	APOD (3 of 3)	APOD (3 of 3)-003	Apolipoprotein D	Lipid metabolism	GQ INCREASED	0.29
668	ENSDARP00000123418	APOD (3 of 3)	APOD (3 of 3)-002	Apolipoprotein D	Lipid metabolism	GQ INCREASED	0.29
669	ENSDARP00000035324	selenbp1	selenbp1-201	Selenium binding protein 1	Protein Synthesis	GQ INCREASED	0.29
670	ENSDARP00000062897	ephx1	ephx1-001	Epoxide hydrolase 1, microsomal (xenobiotic)	REDOX/Detox related	GQ INCREASED	0.29
671	ENSDARP00000121216	rhoad	rhoad-002	Ras homolog gene family, member A	Cell cycle, division, growth and fate	GQ INCREASED	0.29

672	ENSDARP0000006624	rpl23a	rpl23a-001	Large subunit ribosomal protein L32e	Protein Synthesis	GQ INCREASED	0.29
673	ENSDARP0000022829	dph5	dph5-201	Diphthine synthas	Protein Synthesis	GQ INCREASED	0.29
674	ENSDARP00000108734	dph5	dph5-202	Diphthine synthas	Protein Synthesis	GQ INCREASED	0.29
675	ENSDARP00000111794	dph5	dph5-203	Diphthine synthas	Protein Synthesis	GQ INCREASED	0.29
676	ENSDARP0000082459	prmt5	prmt5-201	Protein arginine methyltransferase 5	Protein Synthesis	GQ INCREASED	0.29
677	ENSDARP00000116916	rps18	rps18-002	Small subunit ribosomal protein S18e	Protein Synthesis	GQ INCREASED	0.29
678	ENSDARP00000122082	rps18	rps18-003	Small subunit ribosomal protein S18e	Protein Synthesis	GQ INCREASED	0.29
679	ENSDARP0000052267	pltpnb	pltpnb-201	Phosphatidylinositol transfer protein, beta, like	Lipid metabolism	GQ INCREASED	0.29
680	ENSDARP00000124921	sept7b	Novel	Cytoskeleton proteins	Cell cycle, division, growth and fate	GQ INCREASED	0.29
681	ENSDARP0000068657	eif2a	eif2a-201	Eukaryotic translation initiation factor	Protein Synthesis	GQ INCREASED	0.29
682	ENSDARP00000125913	eif2a	eif2a-001	Eukaryotic translation initiation factor	Protein Synthesis	GQ INCREASED	0.29
683	ENSDARP00000115411	pdhb	pdhb-002	Pyruvate dehydrogenase (lipoamide) beta	Energy metabolism	GQ INCREASED	0.29
684	ENSDARP00000111558	pltpnb	pltpnb-202	Phosphatidylinositol transfer protein, beta, like	Lipid metabolism	GQ INCREASED	0.29
685	ENSDARP00000124765	glyctk	glyctk-002	Glycerate kinase	Energy metabolism	GQ INCREASED	0.29
686	ENSDARP00000109870	hdac10	hdac10-001	Histone deacetylase 10	Cell cycle, division, growth and fate	GQ INCREASED	0.29
687	ENSDARP00000067534	cap2	cap2-201	CAP, adenylate cyclase-associated protein, 2 (yeast)	Other	GQ INCREASED	0.29
688	ENSDARP00000106164	cltcb	cltcb-201	Clathrin, heavy polypeptide b	Protein degradation and synthesis inhibition	GQ INCREASED	0.28
689	ENSDARP00000105470	cltcb	cltcb-202	Clathrin, heavy polypeptide b	Protein degradation and synthesis inhibition	GQ INCREASED	0.28
690	ENSDARP00000119038	cltcb	cltcb-001	Clathrin, heavy polypeptide b	Protein degradation and synthesis inhibition	GQ INCREASED	0.28
691	ENSDARP0000077445	acad9	acad9-001	Acyl-CoA dehydrogenase family, member 9	Energy metabolism	GQ INCREASED	0.28
692	ENSDARP00000103810	prep	prep-001	Prolyl endopeptidase	Protein degradation and synthesis inhibition	GQ INCREASED	0.26
693	ENSDARP0000048675	prkar2aa	prkar2aa-001	Protein kinase, cAMP-dependent, regulatory, type II, alpha A	Apoptosis related	GQ INCREASED	0.26
694	ENSDARP0000046358	myh10	myh10-201	Myosin, heavy chain 10, non-muscle	Cell cycle, division, growth and fate	GQ INCREASED	0.26
695	ENSDARP00000125918	myh10	myh10-001	Myosin, heavy chain 10, non-muscle	Cell cycle, division, growth and fate	GQ INCREASED	0.26
696	ENSDARP0000007817	farsb	farsb-001	Phenylalanyl-tRNA synthetase, beta subunit	Protein Synthesis	GQ INCREASED	0.26
697	ENSDARP00000125771	myh10	myh10-002	Myosin, heavy chain 10, non-muscle	Cell cycle, division, growth and fate	GQ INCREASED	0.26
698	ENSDARP00000116604	selenbp1	selenbp1-001	Selenium binding protein 1	Protein Synthesis	GQ INCREASED	0.26
699	ENSDARP0000039986	pgm3	pgm3-001	Phosphoacetylglucosamine mutase	Energy metabolism	GQ INCREASED	0.26
700	ENSDARP0000023819	mccc2	mccc2-001	Methylcrotonoyl-CoA carboxylase 2 (beta)	Protein degradation and synthesis inhibition	GQ INCREASED	0.25
701	ENSDARP0000015404	ehd1a	ehd1a-201	EH domain-containing protein 1	Lipid metabolism	GQ INCREASED	0.25
702	ENSDARP0000057947	anxa11a	anxa11a-002	Annexin A11a	Immune system related	GQ INCREASED	0.24
703	ENSDARP00000092551	anxa11a	anxa11a-001	Annexin A11a	Immune system related	GQ INCREASED	0.24
704	ENSDARP0000052941	serpinh2	serpinh2	Serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	Other	GQ INCREASED	0.24
705	ENSDARP00000105167	serpinh2	serpinh2	Serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	Other	GQ INCREASED	0.24
706	ENSDARP00000125495	GBE1 (2 of 2)	GBE1 (2 of 2)-001	Glucan (1,4-alpha)-, branching enzyme 1	Energy metabolism	GQ INCREASED	0.24
707	ENSDARP0000086805	myh9b	myh9b-201	Myosin, heavy polypeptide 9b, non-muscle	Cell cycle, division, growth and fate	GQ INCREASED	0.24
708	ENSDARP00000114437	myh9b	myh9b-001	Myosin, heavy polypeptide 9b, non-muscle	Cell cycle, division, growth and fate	GQ INCREASED	0.23
709	ENSDARP0000068053	tes	tes-201	Testis derived transcript (3 LIM domains)	Cell cycle, division, growth and fate	GQ INCREASED	0.23
710	ENSDARP00000111043	supt16h	supt16h-203	Suppressor of Ty 16 homolog (S. cerevisiae) (FACT complex subunit SPT16)	Protein Synthesis	GQ INCREASED	0.22
711	ENSDARP0000039188	lmf2b	lmf2b-201	Lipase maturation factor 2b	Protein Synthesis	GQ INCREASED	0.22
712	ENSDARP00000100277	supt16h	supt16h-201	Suppressor of Ty 16 homolog (S. cerevisiae) (FACT complex subunit SPT16)	Protein Synthesis	GQ INCREASED	0.22
713	ENSDARP00000109077	supt16h	supt16h-202	Suppressor of Ty 16 homolog (S. cerevisiae) (FACT complex subunit SPT16)	Protein Synthesis	GQ INCREASED	0.22
714	ENSDARP0000014578	gpib	gpib-201	Glucose phosphate isomerase b	Energy metabolism	GQ INCREASED	0.22
715	ENSDARP0000089816	atp6v1h	atp6v1h-201	V-type H+-transporting ATPase subunit H	Energy metabolism	GQ INCREASED	0.22
716	ENSDARP00000113453	atp6v1h	atp6v1h-002	V-type H+-transporting ATPase subunit H	Energy metabolism	GQ INCREASED	0.22
717	ENSDARP0000068054	tes	tes-001	Testis derived transcript (3 LIM domains)	Cell cycle, division, growth and fate	GQ INCREASED	0.22
718	ENSDARP00000113128	arcn1b	arcn1b-002	Archain 1b	Other	GQ INCREASED	0.22
719	ENSDARP0000073441	cpvl	cpvl-001	Vitellogenin carboxypeptidase-like protein	Protein degradation and synthesis inhibition	GQ INCREASED	0.22
720	ENSDARP0000094422	sl:ch211-160d14.1	sl:ch211-160d14.1-001	Fascin	Cell cycle, division, growth and fate	GQ INCREASED	0.22
721	ENSDARP0000024886	atp6v1h	atp6v1h-001	V-type H+-transporting ATPase subunit H	Energy metabolism	GQ INCREASED	0.22
722	ENSDARP0000074155	nle1	nle1-002	Notchless homolog 1 (Drosophila)	Protein Synthesis	GQ INCREASED	0.22
723	ENSDARP00000122687	nle1	nle1-001	Notchless homolog 1 (Drosophila)	Protein Synthesis	GQ INCREASED	0.22
724	ENSDARP0000083458	lap3	lap3-001	Leucine aminopeptidase 3	Protein degradation and synthesis inhibition	GQ INCREASED	0.22
725	ENSDARP0000058889	ephx2	ephx2-001	Epoxide hydrolase 2, cytoplasmic	Lipid metabolism	GQ INCREASED	0.20
726	ENSDARP00000117022	cratb	cratb-001	Carnitine O-acetyltransferase b	Energy metabolism	GQ INCREASED	0.20
727	ENSDARP00000129034	eml2	eml2-001	Echinoderm microtubule associated protein like 2	Cell cycle, division, growth and fate	GQ INCREASED	0.20
728	ENSDARP0000008223	eml2	eml2-201	Echinoderm microtubule associated protein like 2	Cell cycle, division, growth and fate	GQ INCREASED	0.20
729	ENSDARP00000101418	GBE1 (2 of 2)	GBE1 (2 of 2)-201	Glucan (1,4-alpha)-, branching enzyme 1	Energy metabolism	GQ INCREASED	0.19
730	ENSDARP0000083382	fbxo10	fbxo10-001	F-box protein 10	Protein degradation and synthesis inhibition	GQ INCREASED	0.18
731	ENSDARP0000094289	cpne1	cpne1-202	Copine 1	Other	GQ INCREASED	0.18
732	ENSDARP00000121695	sl:ch211-93f2.1	Novel	Carboxylic ester hydrolase	REDOX/Detox related	GQ INCREASED	0.18
733	ENSDARP00000017582	zc3h15	zc3h15-001	Zinc finger CCHC-type containing 15	Protein Synthesis	GQ INCREASED	0.18
734	ENSDARP0000082086	cpne1	cpne1-201	Copine 1	Other	GQ INCREASED	0.18
735	ENSDARP0000007446	cox4i1	cox4i1-001	Cytochrome c oxidase subunit IV isoform 1	Energy metabolism	GQ INCREASED	0.17
736	ENSDARP0000035261	pfdn2	pfdn2-001	Prefoldin subunit 2	Protein Synthesis	GQ INCREASED	0.17
737	ENSDARP0000068644	BX322787.1	BX322787.1-201	ATP-binding cassette, sub-family F, member 2-like	Protein Synthesis	GQ INCREASED	0.17
738	ENSDARP00000119994	eno1a	eno1a-002	Enolase 1 a	Energy metabolism	GQ INCREASED	0.17
739	ENSDARP0000053867	aldh9a1b	aldh9a1b-001	Aldehyde dehydrogenase 9 family, member A1b	Lipid metabolism	GQ INCREASED	0.16

740	ENSDARP0000034052	pdcd4a	pdcd4a-201	Programmed cell death protein 4	Apoptosis related	GQ INCREASED	0.16
741	ENSDARP0000011311	arcn1a	arcn1a-001	Archain 1a	Other	GQ INCREASED	0.15
742	ENSDARP0000010190	RAP1GDS1	RAP1GDS1-201	RAP1, GTP-GDP dissociation stimulator 1	Other	GQ INCREASED	0.15
743	ENSDARP00000113140	larsb	larsb-001	Leucy-lRNA synthetase b	Protein Synthesis	GQ INCREASED	0.15
744	ENSDARP0000004838	rcc2	rcc2-001	Regulator of chromosome condensation 2	Cell cycle, division, growth and fate	GQ INCREASED	0.15
745	ENSDARP00000123019	zp3c	zp3c-001	Zona pellucida protein	Zona Pellucida proteins	GQ INCREASED	0.15
746	ENSDARP0000003359	larsb	larsb-201	Leucy-lRNA synthetase b	Protein Synthesis	GQ INCREASED	0.14
747	ENSDARP0000011011	eif3d	eif3d-201	Eukaryotic translation initiation factor	Protein Synthesis	GQ INCREASED	0.12
748	ENSDARP00000112626	oxcl1a	oxcl1a-003	3-oxoacid CoA transferase 1a	Energy metabolism	GQ INCREASED	0.12
749	ENSDARP00000116681	eif3d	eif3d-001	Eukaryotic translation initiation factor	Protein Synthesis	GQ INCREASED	0.12
750	ENSDARP00000056639	abcf2a	abcf2a-001	ATP-binding cassette, sub-family F (GCN20), member 2a	Protein Synthesis	GQ INCREASED	0.12
751	ENSDARP00000116165	cltcb	cltcb-003	Clathrin, heavy polypeptide b	Protein degradation and synthesis inhibition	GQ INCREASED	0.12
752	ENSDARP00000003738	eno1a	eno1a-001	Enolase 1 a	Energy metabolism	GQ INCREASED	0.12
753	ENSDARP00000047901	arcn1b	arcn1b-001	Archain 1b	Other	GQ INCREASED	0.12
754	ENSDARP00000020181	ehd1b	ehd1b-001	EH-domain containing 3	Protein degradation and synthesis inhibition	GQ INCREASED	0.11
755	ENSDARP00000051798	hdac1	hdac1-001	Histone deacetylase 1	Cell cycle, division, growth and fate	GQ INCREASED	0.11
756	ENSDARP00000095265	si:ch211-93f2.1	Novel	Carboxylic ester hydrolase-esterase lipase superfamily-drug metabolism	REDOX/Defox related	GQ INCREASED	0.10
757	ENSDARP000000021016	zgc:158620	Novel	Tubulin, beta 2A class IIa	Cell cycle, division, growth and fate	GQ UNIQUE	-
758	ENSDARP0000016957	rpl36	rpl36-001	Ribosomal protein L36	Protein Synthesis	GQ UNIQUE	-
759	ENSDARP00000124304	rpl36	rpl36-002	Ribosomal protein L36	Protein Synthesis	GQ UNIQUE	-
760	ENSDARP0000012767		aldh2.1-001	Aldehyde dehydrogenase 2 family (mitochondrial), tandem duplicate 2	Energy metabolism	GQ UNIQUE	-
761	ENSDARP00000118282	oxcl1a	oxcl1a-004	3-oxoacid CoA transferase 1a	Lipid metabolism	GQ UNIQUE	-
762	ENSDARP00000109625	tubb2	tubb2-001 (novel)	Beta tubulin	Cell cycle, division, growth and fate	GQ UNIQUE	-
763	ENSDARP00000108963	CABZ01032488.1	CABZ01032488.1-201	Aldehyde dehydrogenase super family	Energy metabolism	GQ UNIQUE	-
764	ENSDARP00000110851	FP102463.1	FP102463.1-201	Beta tubulin	Cell cycle, division, growth and fate	GQ UNIQUE	-
765	ENSDARP00000126192	eif3d	eif3d-004	Eukaryotic translation initiation factor 3, subunit D	Protein Synthesis	GQ UNIQUE	-
766	ENSDARP00000035541	ube2l3a	ube2l3a-201	Ubiquitin-conjugating enzyme E2L 3a	Cell cycle, division, growth and fate	GQ UNIQUE	-
767	ENSDARP00000054355	pam16	pam16-001	Presequence translocase-associated motor 16 homolog (S. cerevisiae)	Energy metabolism	GQ UNIQUE	-
768	ENSDARP00000072006	tuba1c	tuba1c-001	Tubulin alpha 1c	Cell cycle, division, growth and fate	GQ UNIQUE	-
769	ENSDARP00000016749	me2	me2-001	Malic enzyme 2, NAD(+)-dependent, mitochondrial	Energy metabolism	GQ UNIQUE	-
770	ENSDARP00000109682	me2	me2-201	Malic enzyme 2, NAD(+)-dependent, mitochondrial	Energy metabolism	GQ UNIQUE	-
771	ENSDARP00000127763	HIST1H2BA (9 of 9)	HIST1H2BA (9 of 9)-001	Histone	Cell cycle, division, growth and fate	GQ UNIQUE	-
772	ENSDARP00000115350	aldh9a1b	aldh9a1b-002	Aldehyde dehydrogenase 9 family, member A1b	Energy metabolism	GQ UNIQUE	-
773	ENSDARP00000088020	aldh2.2	aldh2.2-202	Aldehyde dehydrogenase 2 family (mitochondrial), tandem duplicate 2	Energy metabolism	GQ UNIQUE	-
774	ENSDARP00000088019	aldh2.2	aldh2.2-201	Aldehyde dehydrogenase 2 family (mitochondrial), tandem duplicate 2	Energy metabolism	GQ UNIQUE	-
775	ENSDARP00000105094	tuba1b	tuba1b-001	Tubulin alpha 1b	Cell cycle, division, growth and fate	GQ UNIQUE	-
776	ENSDARP00000083766	dak	dak-001	Dihydroxyacetone kinase 2 homolog (S. cerevisiae)	Energy metabolism	GQ UNIQUE	-
777	ENSDARP00000105448	pkma	pkma-202	Pyruvate kinase, muscle, a	Energy metabolism	GQ UNIQUE	-
778	ENSDARP00000105213	CABZ01112387.1	CABZ01112387.1-201	Myosin 9 like-myosin N super family	Cell cycle, division, growth and fate	GQ UNIQUE	-
779	ENSDARP00000009846	arf1	arf1-201	ADP-ribosylation factor 1	Cell cycle, division, growth and fate	GQ UNIQUE	-
780	ENSDARP00000102498	arf1	arf1-202	ADP-ribosylation factor 1	Cell cycle, division, growth and fate	GQ UNIQUE	-
781	ENSDARP00000128933	ppp5c	ppp5c-001	Protein phosphatase 5, catalytic subunit	Cell cycle, division, growth and fate	GQ UNIQUE	-
782	ENSDARP00000110687	LOC101884557	Novel	Myosin 9 like-myosin N super family	Cell cycle, division, growth and fate	GQ UNIQUE	-
783	ENSDARP00000124733	me2	me2-002	Malic enzyme 2, NAD(+)-dependent, mitochondrial	Energy metabolism	GQ UNIQUE	-
784	ENSDARP00000114018	prmt3	prmt3-002	Protein arginine methyltransferase 3	Protein Synthesis	GQ UNIQUE	-
785	ENSDARP00000003829	prmt3	prmt3-001	Protein arginine methyltransferase 3	Protein Synthesis	GQ UNIQUE	-
786	ENSDARP00000122171	rpl8	rpl8-002	Ribosomal protein L8	Protein Synthesis	GQ UNIQUE	-
787	ENSDARP00000104932	sh3d21	Novel	Uncharacterized protein--SH3 domain-containing protein 21	Cell cycle, division, growth and fate	GQ UNIQUE	-
788	ENSDARP00000058636	sh3d21	Novel	Uncharacterized protein--SH3 domain-containing protein 21	Cell cycle, division, growth and fate	GQ UNIQUE	-
789	ENSDARP00000062517	zgc:162356	zgc:162356-001	Glutathione S-transferase-glutathione metabolism-xenobiotics biodegradation and metabolism	Cell cycle, division, growth and fate	GQ UNIQUE	-
790	ENSDARP00000104897	dnlb	dnlb-202	Drebrin-like b	Endosome-Lysosome related	GQ UNIQUE	-
791	ENSDARP00000112697	sh3d21	Novel	Uncharacterized protein--SH3 domain-containing protein 21	Cell cycle, division, growth and fate	GQ UNIQUE	-
792	ENSDARP00000122208	ERAP1 (2 of 2)	ERAP1 (2 of 2)-201	Endoplasmic reticulum aminopeptidase 1	Immune system related	GQ UNIQUE	-
793	ENSDARP00000095260	cox4l2	cox4l2-001	Cytochrome c oxidase subunit IV isoform 2	Energy metabolism	GQ UNIQUE	-
794	ENSDARP00000066122	KPNA6	KPNA6-201	Karyopherin alpha 6 (importin alpha 7)	Protein Synthesis	GQ UNIQUE	-
795	ENSDARP00000117154	dnpep	dnpep-003	Aspartyl aminopeptidase	Protein degradation and synthesis inhibition	GQ UNIQUE	-
796	ENSDARP00000113894	hars	hars-002	Histidyl-tRNA synthetase	Protein Synthesis	GQ UNIQUE	-
797	ENSDARP00000051468	si:ch211-186e20.7	si:ch211-186e20.7-201	Serpin super family-alpha antitrypsin domain	Other	GQ UNIQUE	-
798	ENSDARP00000123705	si:ch211-186e20.7	si:ch211-186e20.7-001	Serpin super family-alpha antitrypsin domain	Other	GQ UNIQUE	-
799	ENSDARP00000114386	eno2	eno2-003	Enolase 2	Energy metabolism	GQ UNIQUE	-
800	ENSDARP00000117079	sh3d21	Novel	Uncharacterized protein--SH3 domain-containing protein 21	Cell cycle, division, growth and fate	GQ UNIQUE	-
801	ENSDARP00000124373	atp6v1h	atp6v1h-004	ATPase, H+ transporting, lysosomal, V1 subunit H	Endosome-Lysosome related	GQ UNIQUE	-
802	ENSDARP00000027911	dnlb	dnlb-201	Drebrin-like b	Endosome-Lysosome related	GQ UNIQUE	-
803	ENSDARP0000014921	zgc:92137	zgc:92137-201	alpha amylase	Energy metabolism	GQ UNIQUE	-
804	ENSDARP00000038975	dhdhl	dhdhl-001	Dihydrodiol dehydrogenase (dimeric), like	Energy metabolism	GQ UNIQUE	-
805	ENSDARP0000008466	hpx	hpx-201	Hemopexin	Other	GQ UNIQUE	-
806	ENSDARP00000111337	hpx	hpx-001	Hemopexin	Other	GQ UNIQUE	-
807	ENSDARP00000052498	gla	gla-201	Galactosidase, alpha	Lipid metabolism	GQ UNIQUE	-

808	ENSDARP0000075482	sb.cb252	sb.cb252-201	ES1 protein homolog, mitochondrial	Other	GQ UNIQUE	-
809	ENSDARP00000106738	larsa	larsa-201	Leucyl-tRNA synthetase a	Protein Synthesis	GQ UNIQUE	-
810	ENSDARP00000097448	trmt112	trmt112-001	TRNA methyltransferase 11-2 homolog (S. cerevisiae)	Protein Synthesis	GQ UNIQUE	-
811	ENSDARP00000114835	gla	gla-001	Galactosidase, alpha	Lipid metabolism	GQ UNIQUE	-
812	ENSDARP0000062263	sdhb	sdhb-201	Succinate dehydrogenase complex, subunit B, iron sulfur (lp)	Energy metabolism	GQ UNIQUE	-
813	ENSDARP0000019062	vars	vars-201	Valyl-tRNA synthetase	Protein Synthesis	GQ UNIQUE	-
814	ENSDARP00000120746	ces3	ces3-001	Carboxylesterase 3	Lipid metabolism	GQ UNIQUE	-
815	ENSDARP00000107172	ces3	ces3-203	Carboxylesterase 3	Lipid metabolism	GQ UNIQUE	-
816	ENSDARP00000021453	amy2a	amy2a-001	Amylase, alpha 2A, pancreatic	Energy metabolism	GQ UNIQUE	-
817	ENSDARP00000091190	lancl2	lancl2-201	LanC antibiotic synthetase component C-like 2 (bacterial)	Immune system related	GQ UNIQUE	-
818	ENSDARP00000114912	lancl2	lancl2-001	LanC antibiotic synthetase component C-like 2 (bacterial)	Immune system related	GQ UNIQUE	-
819	ENSDARP00000121084	dnpep	dnpep-002	Aspartyl aminopeptidase	Protein degradation and synthesis inhibition	GQ UNIQUE	-
820	ENSDARP0000046625	PRKAR2B	PRKAR2B-201	Protein kinase, cAMP-dependent, regulatory, type II, beta	Energy metabolism	GQ UNIQUE	-
821	ENSDARP00000023098	dlat	dlat-001	Dihydropyrimidine S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	Energy metabolism	GQ UNIQUE	-
822	ENSDARP00000091998	ddx39aa	ddx39aa-201	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39Aa	Cell cycle, division, growth and fate	GQ UNIQUE	-
823	ENSDARP00000115525	oxsr1b	oxsr1b-001	Oxidative-stress responsive 1b	Cell cycle, division, growth and fate	GQ UNIQUE	-
824	ENSDARP00000126065	sesn2	sesn2-003	Sestrin 2	Cell cycle, division, growth and fate	GQ UNIQUE	-
825	ENSDARP00000119784	zgc:165539	zgc:165539-003	Mucin 5Ac	Immune system related	GQ UNIQUE	-
826	ENSDARP00000117895	ITPA (2 of 2)	ITPA (2 of 2)-201	Inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	Cell cycle, division, growth and fate	GQ UNIQUE	-
827	ENSDARP00000123429	g3bp1	g3bp1-002	GTPase activating protein (SH3 domain) binding protein 1	Cell cycle, division, growth and fate	GQ UNIQUE	-
828	ENSDARP00000016959	carm1	carm1-001	Coactivator-associated arginine methyltransferase 1	Protein Synthesis	GQ UNIQUE	-
829	ENSDARP00000074674	itpa	itpa-001	Inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	Cell cycle, division, growth and fate	GQ UNIQUE	-
830	ENSDARP00000105903	anxa6	anxa6-203	Annexin A6	Endosome-Lysosome related	GQ UNIQUE	-
831	ENSDARP00000006047	ugg2a	ugg2a-001	UDP-glucose pyrophosphorylase 2a	Energy metabolism	GQ UNIQUE	-
832	ENSDARP00000076180	rab25a	rab25a-201	RAB25, member RAS oncogene family a	Oncogenesis related	GQ UNIQUE	-
833	ENSDARP00000008513	ddx39aa	ddx39aa-001	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39Aa	Cell cycle, division, growth and fate	GQ UNIQUE	-
834	ENSDARP00000093160	sesn2	sesn2-001	Sestrin 2	Cell cycle, division, growth and fate	GQ UNIQUE	-
835	ENSDARP00000087672	papl	papl-201	Iron/zinc purple acid phosphatase-like protein	Protein degradation and synthesis inhibition	GQ UNIQUE	-
836	ENSDARP00000114865	eef1da	eef1da-005	Elongation factor-1, delta, a	Protein Synthesis	GQ UNIQUE	-
837	ENSDARP00000122064	pold2	pold2-001	Polymerase (DNA directed), delta 2, regulatory subunit	Cell cycle, division, growth and fate	GQ UNIQUE	-
838	ENSDARP00000125677	sesn2	sesn2-002	Sestrin 2	Cell cycle, division, growth and fate	GQ UNIQUE	-
839	ENSDARP00000041675	tph1a	tph1a-201	Tryptophan hydroxylase 1 (tryptophan 5-monooxygenase) a	Protein Synthesis	GQ UNIQUE	-
840	ENSDARP00000112644	sh3d21	Novel	SH3 domain-containing protein 21	Cell cycle, division, growth and fate	GQ UNIQUE	-
841	ENSDARP00000067158	tph1a	tph1a-202	Tryptophan hydroxylase 1 (tryptophan 5-monooxygenase) a	Protein Synthesis	GQ UNIQUE	-
842	ENSDARP00000113340	pold2	pold2-002	Polymerase (DNA directed), delta 2, regulatory subunit	Cell cycle, division, growth and fate	GQ UNIQUE	-
843	ENSDARP00000125959	carm1	carm1-003	Coactivator-associated arginine methyltransferase 1	Protein Synthesis	GQ UNIQUE	-
844	ENSDARP00000052682	c3c	c3c-001	Complement component c3c	Immune system related	GQ UNIQUE	-
845	ENSDARP00000083043	rangap1a	rangap1a-001	RAN GTPase activating protein 1a	Cell cycle, division, growth and fate	GQ UNIQUE	-
846	ENSDARP00000112996	phex	phex-002	Phosphate regulating gene with homologues to endopeptidases on the X chromosome	Protein degradation and synthesis inhibition	GQ UNIQUE	-
847	ENSDARP00000009876	memo1	memo1-001	Mediator of cell motility 1	Cell cycle, division, growth and fate	GQ UNIQUE	-
848	ENSDARP00000025917	ppp6c	ppp6c-001	Protein phosphatase 6, catalytic subunit	Cell cycle, division, growth and fate	GQ UNIQUE	-
849	ENSDARP00000023871	flj13639	flj13639-201	Uncharacterized protein--short chain dehydrogenase/reductase	Other	GQ UNIQUE	-
850	ENSDARP00000113500	ndufaf5	ndufaf5-001	NADH dehydrogenase (ubiquinone) complex 1, assembly factor 5	Energy metabolism	GQ UNIQUE	-
851	ENSDARP00000104359	si:ch211-165b10.3	si:ch211-165b10.3-201	Uncharacterized protein	Other	GQ UNIQUE	-
852	ENSDARP00000098664	ME1 (2 of 2)	ME1 (2 of 2)-201	Malic enzyme 1, NADP(+)-dependent, cytosolic	Energy metabolism	GQ UNIQUE	-
853	ENSDARP00000124689	nmt1a	nmt1a-002	N-myristoyltransferase 1a	Other	GQ UNIQUE	-
854	ENSDARP00000128976	si:ch211-165b10.3	si:ch211-165b10.3-001	Uncharacterized protein	Other	GQ UNIQUE	-
855	ENSDARP00000076538	PPP2R5C (2 of 2)	PPP2R5C (2 of 2)-201	Protein phosphatase 2, regulatory subunit B., gamma	Cell cycle, division, growth and fate	GQ UNIQUE	-
856	ENSDARP00000026827	anxa6	anxa6-201	Annexin A6	Endosome-Lysosome related	GQ UNIQUE	-
857	ENSDARP00000081541	EIF4G1 (1 of 3)	EIF4G1 (1 of 3)-201	Eukaryotic translation initiation factor 4 gamma, 1	Protein Synthesis	GQ UNIQUE	-
858	ENSDARP00000081554	EIF4G1 (1 of 3)	EIF4G1 (1 of 3)-002	Eukaryotic translation initiation factor 4 gamma, 1	Protein Synthesis	GQ UNIQUE	-
859	ENSDARP00000098745	nomo	nomo-201	Nodal modulator	Cell cycle, division, growth and fate	GQ UNIQUE	-
860	ENSDARP00000128647	nomo	nomo-001	Nodal modulator	Cell cycle, division, growth and fate	GQ UNIQUE	-
861	ENSDARP00000010925	ddx39ab	ddx39ab-001	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39Ab	Cell cycle, division, growth and fate	GQ UNIQUE	-
862	ENSDARP00000052354	ddx39b	ddx39b-001	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39Ab	Cell cycle, division, growth and fate	GQ UNIQUE	-
863	ENSDARP00000069703	me1	me1-201	Malic enzyme 1, NADP(+)-dependent, cytosolic	Energy metabolism	GQ UNIQUE	-
864	ENSDARP00000012808	pah	pah-001	Phenylalanine hydroxylase	Protein degradation and synthesis inhibition	GQ UNIQUE	-
865	ENSDARP00000042296	kdelc1	kdelc1-001	KDEL (Lys-Asp-Glu-Leu) containing 1	Protein Synthesis	GQ UNIQUE	-
866	ENSDARP00000047072	oxsr1a	oxsr1a-001	Oxidative-stress responsive 1a	Cell cycle, division, growth and fate	GQ UNIQUE	-
867	ENSDARP00000055010	PDILT	PDILT-001	Protein disulfide isomerase-like, testis expressed	Protein Synthesis	GQ UNIQUE	-
868	ENSDARP00000066974	impdh1b	impdh1b-002	Inosine 5,-phosphate dehydrogenase 1b	Cell cycle, division, growth and fate	GQ UNIQUE	-
869	ENSDARP00000074184	oxct1b	oxct1b-001	3-oxoacid CoA transferase 1b	Lipid metabolism	GQ UNIQUE	-
870	ENSDARP00000066972	impdh1b	impdh1b-001	Inosine 5,-phosphate dehydrogenase 1b	Cell cycle, division, growth and fate	GQ UNIQUE	-
871	ENSDARP00000092803	kpnas5	kpnas5-001	Karyopherin alpha 5 (importin alpha 6)	Protein Synthesis	GQ UNIQUE	-
872	ENSDARP00000019185	impdh1a	impdh1a-001	Inosine 5,-phosphate dehydrogenase 1a	Cell cycle, division, growth and fate	GQ UNIQUE	-
873	ENSDARP00000125968	usp7	usp7-001	Ubiquitin specific peptidase 7 (herpes virus-associated)	Cell cycle, division, growth and fate	GQ UNIQUE	-
874	ENSDARP00000002502	usp7	usp7-201	Ubiquitin specific peptidase 7 (herpes virus-associated)	Cell cycle, division, growth and fate	GQ UNIQUE	-
875	ENSDARP00000096118	anxa6	anxa6-202	Annexin A6	Endosome-Lysosome related	GQ UNIQUE	-

876	ENSDARP00000124518	anxa6	anxa6-001	Annexin A6	Endosome-Lysosome related	GQ UNIQUE	-
877	ENSDARP00000014963	ppp2r5cb	ppp2r5cb-201	Protein phosphatase 2, regulatory subunit B, gamma b	Cell cycle, division, growth and fate	GQ UNIQUE	-
878	ENSDARP000000101961	ppp2r5cb	ppp2r5cb-202	Protein phosphatase 2, regulatory subunit B, gamma b	Cell cycle, division, growth and fate	GQ UNIQUE	-
879	ENSDARP00000103928	ppp2r5cb	ppp2r5cb-001	Protein phosphatase 2, regulatory subunit B, gamma b	Cell cycle, division, growth and fate	GQ UNIQUE	-
880	ENSDARP00000012056	ctps1b	ctps1b-001	CTP synthase 1b	Cell cycle, division, growth and fate	GQ UNIQUE	-
881	ENSDARP00000028051	lmnl3	lmnl3-001	Lamin L3	Cell cycle, division, growth and fate	GQ UNIQUE	-
882	ENSDARP00000070709	ctps1b	ctps1b-201	CTP synthase 1b	Cell cycle, division, growth and fate	GQ UNIQUE	-
883	ENSDARP00000092744	me1	me1-002	Malic enzyme 1, NADP(+)-dependent, cytosolic	Energy metabolism	GQ UNIQUE	-
884	ENSDARP000000113885	me1	me1-001	Malic enzyme 1, NADP(+)-dependent, cytosolic	Energy metabolism	GQ UNIQUE	-
885	ENSDARP000000120790	kpna1	kpna1-001	Karyopherin alpha 1 (importin alpha 5)	Protein Synthesis	GQ UNIQUE	-
886	ENSDARP00000091935	impdh1a	impdh1a-201	Inosine 5-phosphate dehydrogenase 1a	Cell cycle, division, growth and fate	GQ UNIQUE	-
887	ENSDARP00000059197	PARP14	PARP14-201	Poly (ADP-ribose) polymerase family, member 14	Apoptosis related	GQ UNIQUE	-
888	ENSDARP00000016922	aglb	aglb-001	Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase b	Energy metabolism	GQ UNIQUE	-
889	ENSDARP00000098492	zfat	zfat-201	Zinc finger and AT hook domain containing	Protein Synthesis	GQ UNIQUE	-
890	ENSDARP000000127519	zfat	zfat-001	Zinc finger and AT hook domain containing	Protein Synthesis	GQ UNIQUE	-
891	ENSDARP00000025533	tlm1	tlm1-201	Talin 1	Cell cycle, division, growth and fate	GQ UNIQUE	-
892	ENSDARP00000072597	tlm1	tlm1-001	Talin 1	Cell cycle, division, growth and fate	GQ UNIQUE	-

**S2 Table. Proteins differentially regulated in the Multiple Samples Experiment.** List of the 274 proteins from the Multiple Samples Experiment that were considered to be differentially regulated between egg quality groups and whose distribution among various functional categories is illustrated in Fig 2b. These include proteins detected only in poor quality eggs (PQ UNIQUE, n=93), proteins in poor quality eggs with N-SC increased  $\geq 2$ -fold relative to values for good quality eggs (PQ INCREASED, n=58), proteins detected only in good quality eggs (GQ UNIQUE, n=90), and proteins in good quality eggs with N-SC increased  $\geq 2$ -fold relative to values for poor quality eggs (GQ INCREASED, n=32). For each protein, the Ensembl Protein ID and associated gene, transcript and protein name, functional category (see Fig 2b), regulation (UNIQUE or INCREASED), fold-difference in N-SC between egg quality groups (if available), and fraction in which the protein was originally detected (LMW, low molecular weight; HMW, high molecular weight) is shown. Color shading corresponds to that used to designate functional categories in Fig 2.

ENSEMBL Protein ID	Associated Gene Name	Associated Transcript Name	Protein Full Name	Functional Category	Regulation	Fold Difference	Fraction
1	si:ch211-161h7.6	si:ch211-161h7.6-002	cst14a.2	Other	PQ UNIQUE	-	LMW
2	si:ch211-161h7.6	si:ch211-161h7.6-001	cst14a.2	Other	PQ UNIQUE	-	LMW
3	dap1b	dap1b-201	Death associated protein 1b	Apoptosis related	PQ UNIQUE	-	LMW
4	dap1b	dap1b-202	Death associated protein b-apoptotic signaling pathway	Apoptosis related	PQ UNIQUE	-	LMW
5	rab7	rab7-001	RAB7, member RAS oncogene family	Endosome-Lysosome related	PQ UNIQUE	-	LMW
6	si:dkeyp-20e4.8	si:dkeyp-20e4.8-001	Uncharacterized protein	Other	PQ UNIQUE	-	LMW
7	rpl23	rpl23-001	Ribosomal protein L23	Protein synthesis	PQ UNIQUE	-	LMW
8	rpl30	rpl30-002	Ribosomal protein L30	Protein synthesis	PQ UNIQUE	-	LMW
9	rpl30	rpl30-001	Ribosomal protein L30	Protein synthesis	PQ UNIQUE	-	LMW
10	Rab7-like, rab7b,	Rab7-like, rab7b,	Rab7-like, rab7b	Endosome-Lysosome related	PQ UNIQUE	-	LMW
11	Rab7-like	Rab7-like	Rab7-like	Endosome-Lysosome related	PQ UNIQUE	-	LMW
12	apom	apom-002	Apolipoprotein M	Immune system related	PQ UNIQUE	-	LMW
13	zgc:100918	Novel transcript	Uncharacterized protein-Rab7-like, ras-related, protein	Endosome-Lysosome related	PQ UNIQUE	-	LMW
14	zgc:100918	Novel transcript	Uncharacterized protein-Rab7a-like, ras-related, protein	Endosome-Lysosome related	PQ UNIQUE	-	LMW
15	apom	apom-003	Apolipoprotein M	Immune system related	PQ UNIQUE	-	LMW
16	rab11a	rab11a-001	RAB11a, member RAS oncogene family, like	Endosome-Lysosome related	PQ UNIQUE	-	LMW
17	apom	apom-001	Apolipoprotein M	Immune system related	PQ UNIQUE	-	LMW
18	ACTC1 (2 of 2)	ACTC1 (2 of 2)-001	Actin, alpha, cardiac muscle 1a	Cell cycle, division, growth and fate	PQ UNIQUE	-	LMW
19	si:ch211-226h8.8	si:ch211-226h8.8-201	Uncharacterized protein containing SUEL type lectin domain	Lectins	PQ UNIQUE	-	LMW
20	fkbp1aa	fkbp1aa-001	FK506 binding protein 1Aa	Protein synthesis	PQ UNIQUE	-	LMW
21	fkbp1aa	fkbp1aa-003	FK506 binding protein 1Aa	Protein synthesis	PQ UNIQUE	-	LMW
22	fkbp1aa	fkbp1aa-002	FK506 binding protein 1Aa	Protein synthesis	PQ UNIQUE	-	LMW
23	sri	sri-001	Sorcin	Protein degradation and synthesis inhibition	PQ UNIQUE	-	LMW
24	si:ch211-226h8.8	si:ch211-226h8.8-001	Uncharacterized protein-Gal lectin superfamily	Lectins	PQ UNIQUE	-	LMW
25	zgc:172218	Novel transcript	Uncharacterized protein containing 3SUEL type lectin domains	Lectins	PQ UNIQUE	-	LMW
26	si:ch211-226h8.11	si:ch211-226h8.11-001	L-rhamnose-binding lectin CSL3-like isoform X1	Lectins	PQ UNIQUE	-	LMW
27	ITIH4	ITIH4-201	Inter-alpha-trypsin inhibitor heavy chain family member 4	Other	PQ UNIQUE	-	LMW
28	snrpd2	snrpd2-001	Small nuclear ribonucleoprotein D2 polypeptide	Protein synthesis	PQ UNIQUE	-	LMW
29	rpl31	rpl31-201	Ribosomal protein L31	Protein synthesis	PQ UNIQUE	-	LMW
30	rpl31	rpl31-002	Ribosomal protein L31	Protein synthesis	PQ UNIQUE	-	LMW
31	rpl31	rpl31-001	Ribosomal protein L31	Protein synthesis	PQ UNIQUE	-	LMW
32	snx3	snx3-003	Sorting nexin 3	Endosome-Lysosome related	PQ UNIQUE	-	LMW
33	actb2	actb2-002	Actin, beta 2	Cell cycle, division, growth and fate	PQ UNIQUE	-	LMW
34	actb1	actb1-002	Actin, beta 1	Cell cycle, division, growth and fate	PQ UNIQUE	-	LMW
35	CABZ01044980.1	CABZ01044980.1-201	Zona pellucida sperm-binding protein 3-like precursor	Zona Pellucida proteins	PQ UNIQUE	-	LMW
36	park7	park7-002	Parkinson protein 7	REDOX/Detox related	PQ UNIQUE	-	LMW
37	snx3	snx3-001	Sorting nexin 3	Endosome-Lysosome related	PQ UNIQUE	-	LMW
38	cp	cp-002	Ceruloplasmin	REDOX/Detox related	PQ UNIQUE	-	LMW
39	cp	cp-003	Ceruloplasmin	REDOX/Detox related	PQ UNIQUE	-	LMW
40	ube2nb	ube2nb-001	Ubiquitin-conjugating enzyme E2Nb	Protein degradation and synthesis inhibition	PQ UNIQUE	-	LMW
41	lect2l	lect2l-001	Leukocyte cell-derived chemotaxin 2 like	Immune system related	PQ UNIQUE	-	LMW
42	cp	cp-202	Ceruloplasmin	REDOX/Detox related	PQ UNIQUE	-	LMW
43	cdh1	cdh1-001	Cadherin 1, type 1, E-cadherin (epithelial)	Cell cycle, division, growth and fate	PQ UNIQUE	-	LMW
44	MFAP4 (12 of 14)	MFAP4 (12 of 14)-201	Microfibrillar-associated protein 4	Cell cycle, division, growth and fate	PQ UNIQUE	-	LMW
45	cdh1	cdh1-201	Cadherin 1, type 1, E-cadherin (epithelial)	Cell cycle, division, growth and fate	PQ UNIQUE	-	LMW
46	cp	cp-201	Ceruloplasmin	REDOX/Detox related	PQ UNIQUE	-	LMW
47	CU469531.2	CU469531.2-201	Small GTPase mediated signal transduction-protein transport	Other	PQ UNIQUE	-	LMW
48	cdc42	cdc42-001	Cell division cycle 42	Cell cycle, division, growth and fate	PQ UNIQUE	-	LMW
49	zgc:162356	zgc:162356-001	Glutathione S-transferase rho	REDOX/Detox related	PQ UNIQUE	-	LMW
50	acta1a	acta1a-001	Actin alpha 1 a skeletal muscle	Cell cycle, division, growth and fate	PQ UNIQUE	-	LMW
51	actc1b	actc1b-201	Actin, alpha, cardiac muscle 1b	Cell cycle, division, growth and fate	PQ UNIQUE	-	LMW
52	acta1b	acta1b-001	Actin, alpha 1b, skeletal muscle	Cell cycle, division, growth and fate	PQ UNIQUE	-	LMW
53	ywhaqb	ywhaqb-001	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide b	REDOX/Detox related	PQ UNIQUE	-	LMW



54	ENSDARP0000062382	ywhaqa	ywhaqa-001	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide b	REDOX/Detox related	PQ UNIQUE	-	LMW
55	ENSDARP0000074935	ywhag1	ywhag1-001	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide 1	Cell cycle, division, growth and fate	PQ UNIQUE	-	LMW
56	ENSDARP0000096898	ywhag2	ywhag2-001	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide 2	Cell cycle, division, growth and fate	PQ UNIQUE	-	LMW
57	ENSDARP0000040421	bhmt	bhmt-201	Betaine-homocysteine methyltransferase	Other	PQ UNIQUE	-	LMW
58	ENSDARP00000104071	f2	f2-002	Coagulation factor II (thrombin)	Immune system related	PQ UNIQUE	-	LMW
59	ENSDARP0000052324	f2	f2-001	Coagulation factor II (thrombin)	Immune system related	PQ UNIQUE	-	LMW
60	ENSDARP0000015293	cp	cp-001	Ceruloplasmin	REDOX/Detox related	PQ UNIQUE	-	LMW
61	ENSDARP00000109575	si:ch1073-263o8.2	si:ch1073-263o8.2-201	Uncharacterized protein	Other	PQ UNIQUE	-	LMW
62	ENSDARP00000125992	si:ch1073-263o8.2	si:ch1073-263o8.2-001	Uncharacterized protein	Other	PQ UNIQUE	-	LMW
63	ENSDARP00000102472	vtg4	vtg4-202	Vitellogenin 4	Vitellogenins	PQ UNIQUE	-	LMW
64	ENSDARP00000103251	qdprb2	qdprb2-201	Quinoid dihydropteridine reductase b2	REDOX/Detox related	PQ UNIQUE	-	LMW
65	ENSDARP00000104702	qdprb2	qdprb2-001	Quinoid dihydropteridine reductase b2	REDOX/Detox related	PQ UNIQUE	-	LMW
66	ENSDARP00000005402	zgc:173556	zgc:173556-201	Zona pellucida protein superfamily	Zona Pellucida proteins	PQ UNIQUE	-	HMW
67	ENSDARP00000010482	ybx1	ybx1-001	Y box binding protein 1	Protein synthesis	PQ UNIQUE	-	HMW
68	ENSDARP00000016831	cct6a	cct6a-201	Chaperonin containing TCP1, subunit 6A (zeta 1)	Protein synthesis	PQ UNIQUE	-	HMW
69	ENSDARP00000059040	h1m	h1m-201	Linker histone H1M	Cell cycle, division, growth and fate	PQ UNIQUE	-	HMW
70	ENSDARP00000061743	zp3a.1	zp3a.1-001	Zona pellucida glycoprotein 3a, tandem duplicate 1	Zona Pellucida proteins	PQ UNIQUE	-	HMW
71	ENSDARP00000067534	cap2	cap2-201	CAP, adenylate cyclase-associated protein, 2 (yeast)	Cell cycle, division, growth and fate	PQ UNIQUE	-	HMW
72	ENSDARP00000068662	zp3.2	zp3.2-202	Zona pellucida glycoprotein 3, tandem duplicate 2	Zona Pellucida proteins	PQ UNIQUE	-	HMW
73	ENSDARP00000068670	zgc:173556	zgc:173556-203	Zona pellucida protein superfamily	Zona Pellucida proteins	PQ UNIQUE	-	HMW
74	ENSDARP00000095894	si:dkey-90I23.2	Novel transcript	L-rhamnose-binding lectin CSL3-like isoform X2	Lectins	PQ UNIQUE	-	HMW
75	ENSDARP00000099884	ZP2 (3 of 4)	ZP2 (3 of 4)-201	Zona pellucida glycoprotein 2 (sperm receptor)	Zona Pellucida proteins	PQ UNIQUE	-	HMW
76	ENSDARP00000101517	ybx1	ybx1-201	Y box binding protein 1	Protein synthesis	PQ UNIQUE	-	HMW
77	ENSDARP00000105815	CU695117.1	CU695117.1-201	Zinc finger MYM-type protein 1	Protein synthesis	PQ UNIQUE	-	HMW
78	ENSDARP00000105815	zgc:173556	zgc:173556-001	Zona pellucida glycoprotein 3.1	Zona Pellucida proteins	PQ UNIQUE	-	HMW
79	ENSDARP00000107790	zp3a.1	zp3a.1-201	Zona pellucida glycoprotein 3a, tandem duplicate 1	Zona Pellucida proteins	PQ UNIQUE	-	HMW
80	ENSDARP00000107948	CU467646.1	CU467646.1-201	Mucin-5B-like isoform X5	Other	PQ UNIQUE	-	HMW
81	ENSDARP00000109119	zp3.2	zp3.2-201	Zona pellucida protein superfamily	Zona Pellucida proteins	PQ UNIQUE	-	HMW
82	ENSDARP00000109275	CU929506.1	CU929506.1-201	Zinc finger MYM-type protein 1	Protein synthesis	PQ UNIQUE	-	HMW
83	ENSDARP00000112608	cct6a	cct6a-002	Chaperonin containing TCP1, subunit 6A (zeta 1)	Protein synthesis	PQ UNIQUE	-	HMW
84	ENSDARP00000116487	zgc:165539	zgc:165539-002	Mucin-5AC	Other	PQ UNIQUE	-	HMW
85	ENSDARP00000118006	cct6a	cct6a-001	Chaperonin containing TCP1, subunit 6A (zeta 1)	Protein synthesis	PQ UNIQUE	-	HMW
86	ENSDARP00000118276	si:dkey-90I23.1	Novel transcript	SUEL type lectin domain	Lectins	PQ UNIQUE	-	HMW
87	ENSDARP0000021016	tubb2	Novel transcript	Tubulin beta 2	Cell cycle, division, growth and fate	PQ UNIQUE	-	HMW
88	ENSDARP00000055379	tubb5	tubb5-201	Tubulin beta 5	Cell cycle, division, growth and fate	PQ UNIQUE	-	HMW
89	ENSDARP00000095074	cnp	cnp-201	2',3'-cyclic nucleotide 3' phosphodiesterase	Cell cycle, division, growth and fate	PQ UNIQUE	-	HMW
90	ENSDARP00000102472	vtg4	vtg4-202	Vitellogenin 4	Vitellogenins	PQ UNIQUE	-	HMW
91	ENSDARP00000109625	tubb2	Novel transcript	Tubulin beta 2A chain	Cell cycle, division, growth and fate	PQ UNIQUE	-	HMW
92	ENSDARP00000110851	FP102463.1	FP102463.1-201	Tubulin	Cell cycle, division, growth and fate	PQ UNIQUE	-	HMW
93	ENSDARP00000119055	zgc:123194	zgc:123194-001	Tubulin	Cell cycle, division, growth and fate	PQ UNIQUE	-	HMW
94	ENSDARP00000062142	ARF5 (1 of 2)	ARF5 (1 of 2)-001	ADP-ribosylation factor 5	Endosome-Lysosome related	PQ INCREASED	7.06	LMW
95	ENSDARP00000094243	arf5	arf5-201	ADP-ribosylation factor 5	Endosome-Lysosome related	PQ INCREASED	7.06	LMW
96	ENSDARP00000116010	vtg7	vtg7-002	Vitellogenin 7	Vitellogenins	PQ INCREASED	7.00	LMW
97	ENSDARP00000115259	actb1	actb1-004	Actin beta 1	Cell cycle, division, growth and fate	PQ INCREASED	6.85	LMW
98	ENSDARP00000112639	actb1	actb1-005	Actin, beta 1	Cell cycle, division, growth and fate	PQ INCREASED	6.81	LMW
99	ENSDARP00000111487	rpl22	rpl22-001	Ribosomal protein L22	Protein synthesis	PQ INCREASED	5.90	LMW
100	ENSDARP00000067606	arf4a	arf4a-202	ADP-ribosylation factor 4a	Cell cycle, division, growth and fate	PQ INCREASED	5.16	LMW
101	ENSDARP00000067603	arf4a	arf4a-201	ADP-ribosylation factor 4a	Cell cycle, division, growth and fate	PQ INCREASED	5.10	LMW
102	ENSDARP00000067677	zgc:110339	zgc:110339-001	Uncharacterized	REDOX/Detox related	PQ INCREASED	4.24	LMW
103	ENSDARP00000046181	gstm3	gstm3-001	Glutathione S-transferase M3 (brain)	REDOX/Detox related	PQ INCREASED	3.20	LMW
104	ENSDARP00000054986	actb1	actb1-001	Actin beta 1	Cell cycle, division, growth and fate	PQ INCREASED	3.13	LMW
105	ENSDARP00000055193	actb2	actb2-007	Actin beta 2	Cell cycle, division, growth and fate	PQ INCREASED	3.13	LMW
106	ENSDARP00000122263	actb2	actb2-001	Actin beta 2	Cell cycle, division, growth and fate	PQ INCREASED	3.13	LMW
107	ENSDARP00000116310	ube2l3b	ube2l3b-002	Ubiquitin-conjugating enzyme E2L 3b	Protein degradation and synthesis inhibition	PQ INCREASED	3.07	LMW
108	ENSDARP00000035541	ube2l3a	ube2l3a-201	Ubiquitin-conjugating enzyme E2L 3a	Protein degradation and synthesis inhibition	PQ INCREASED	3.06	LMW
109	ENSDARP00000008064	ube2l3b	ube2l3b-003	Ubiquitin-conjugating enzyme E2L 3b	Protein degradation and synthesis inhibition	PQ INCREASED	3.05	LMW
110	ENSDARP00000090376	ube2l3b	ube2l3b-001	Ubiquitin-conjugating enzyme E2L 3b	Protein degradation and synthesis inhibition	PQ INCREASED	3.05	LMW
111	ENSDARP00000032643	zgc:56530	zgc:56530-001	MGC174082 protein-mRNA	Other	PQ INCREASED	3.04	LMW
112	ENSDARP00000035513	sumo3a	sumo3a-001	Small ubiquitin-related modifier 3-like	Cell cycle, division, growth and fate	PQ INCREASED	2.73	LMW
113	ENSDARP00000052255	sumo3b	sumo3b-001	Small ubiquitin-related modifier	Cell cycle, division, growth and fate	PQ INCREASED	2.73	LMW
114	ENSDARP00000108738	sumo3a	sumo3a-201	Small ubiquitin-related modifier 3-like	Cell cycle, division, growth and fate	PQ INCREASED	2.73	LMW
115	ENSDARP00000010242	sumo2b	sumo2b-201	Small ubiquitin-related modifier 2	Cell cycle, division, growth and fate	PQ INCREASED	2.71	LMW

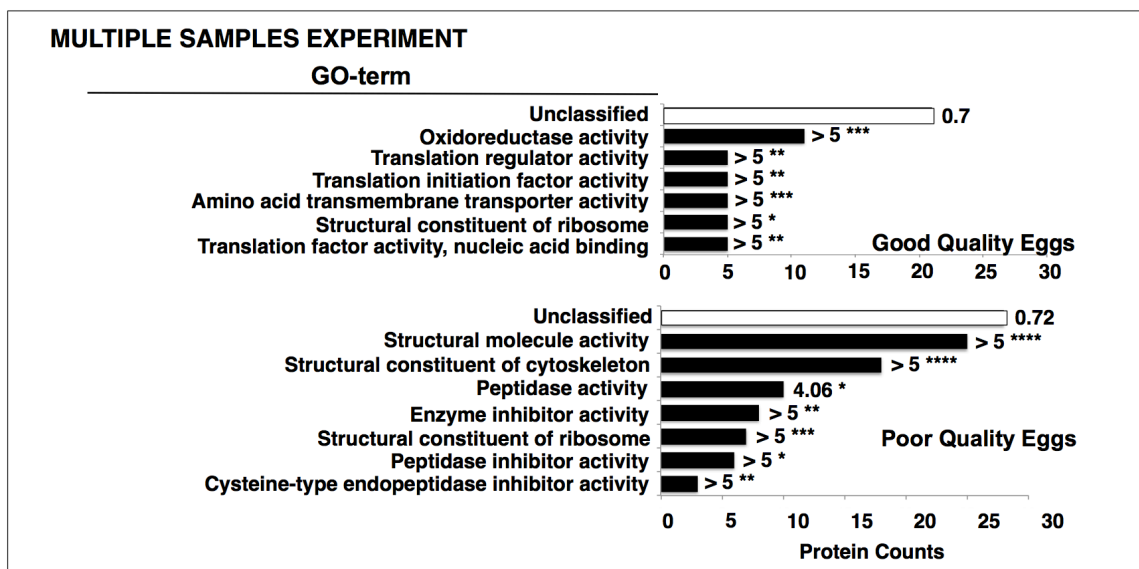
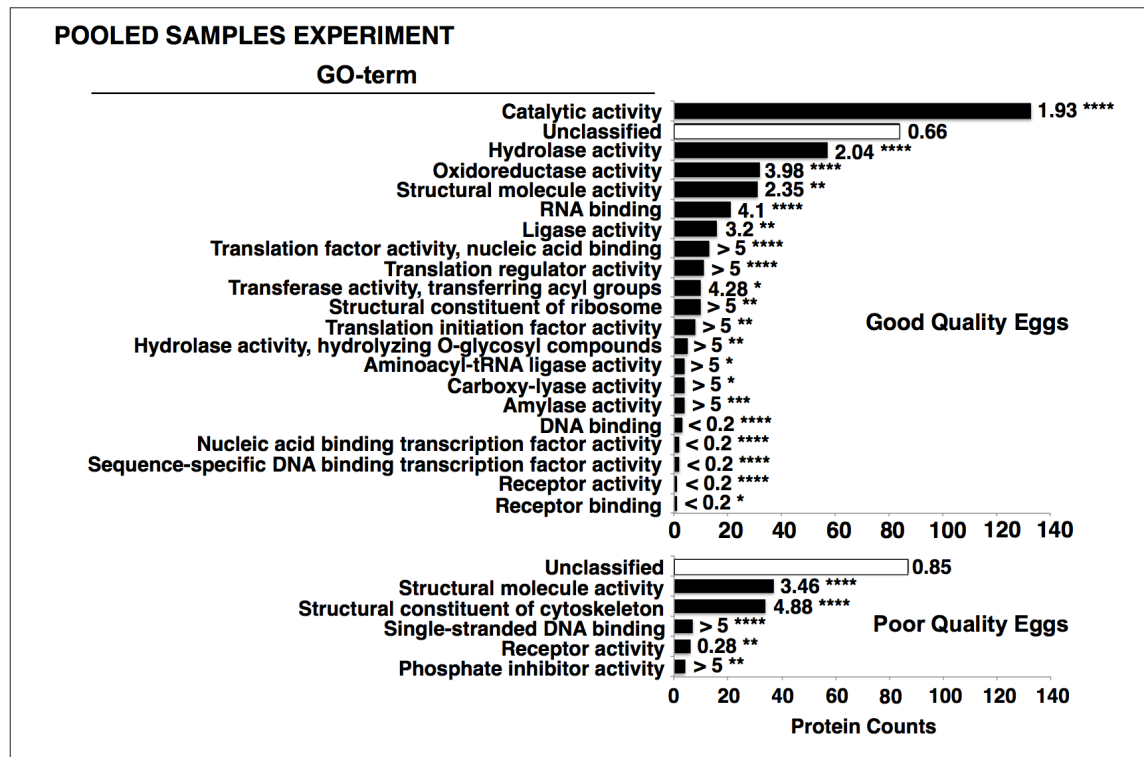
116	ENSDARP0000006628	sumo2b	sumo2b-001	Small ubiquitin-related modifier 2	Cell cycle, division, growth and fate	PQ INCREASED	2.71	LMW
117	ENSDARP0000006783	ctf2	ctf2-001	Cofilin	Cell cycle, division, growth and fate	PQ INCREASED	2.69	LMW
118	ENSDARP00000062369	actc1a	actc1a-001	Actin, alpha, cardiac muscle 1a	Cell cycle, division, growth and fate	PQ INCREASED	2.54	LMW
119	ENSDARP00000066429	acta2	acta2-201	Actin, alpha 2, smooth muscle, aorta	Cell cycle, division, growth and fate	PQ INCREASED	2.54	LMW
120	ENSDARP00000075110	CH211-260D9.2-001	Novel transcript	Actin, novel	Cell cycle, division, growth and fate	PQ INCREASED	2.54	LMW
121	ENSDARP00000100195	ACTC1 (2 of 2)	ACTC1 (2 of 2)-002	Actin alpha 1 (ACTA1)-like	Cell cycle, division, growth and fate	PQ INCREASED	2.54	LMW
122	ENSDARP00000100434	si:ch73-187m15.4	Novel transcript	Actin, alpha, cardiac muscle 1a, novel	Cell cycle, division, growth and fate	PQ INCREASED	2.54	LMW
123	ENSDARP0000009096	rp12	rp12-001	Ribosomal protein L12	Protein synthesis	PQ INCREASED	2.43	LMW
124	ENSDARP00000124371	acta2	acta2-001	Actin, alpha 2, smooth muscle, aorta	Cell cycle, division, growth and fate	PQ INCREASED	2.35	LMW
125	ENSDARP00000069198	ncls	ncls-201	Nothepsin	Protein degradation and synthesis inhibition	PQ INCREASED	2.27	LMW
126	ENSDARP00000119104	dut	dut-005	dUTP pyrophosphatase	Cell cycle, division, growth and fate	PQ INCREASED	2.20	LMW
127	ENSDARP00000122542	ddx41	ddx41-002	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	Cell cycle, division, growth and fate	PQ INCREASED	2.03	LMW
128	ENSDARP00000122730	ddx41	ddx41-001	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	Cell cycle, division, growth and fate	PQ INCREASED	2.03	LMW
129	ENSDARP00000118860	si:ch1073-75o15.4	si:ch1073-75o15.4-001	SUEL type lectin domain	Lectins	PQ INCREASED	1.94	LMW
130	ENSDARP00000121416	si:ch1073-75o15.4	si:ch1073-75o15.4-002	L-rhamnose-binding lectin CSL1-like isoform X1	Lectins	PQ INCREASED	1.93	LMW
131	ENSDARP00000120984	si:ch211-145c1.1	si:ch211-145c1.1-001	Gal lectin superfamily, L-rhamnose-binding lectin CSL3	Lectins	PQ INCREASED	6.88	HMW
132	ENSDARP00000093515	si:ch211-145c1.1	si:ch211-145c1.1-002	Gal lectin superfamily, L-rhamnose-binding lectin CSL3	Lectins	PQ INCREASED	6.85	HMW
133	ENSDARP00000020578	cap1	cap1-001	Adenylyl cyclase-associated protein	Cell cycle, division, growth and fate	PQ INCREASED	3.78	HMW
134	ENSDARP00000005460	c3b	c3b-201	Complement component c3b	Immune system related	PQ INCREASED	3.13	HMW
135	ENSDARP00000108724	c3b	c3b-001	Complement component c3b	Immune system related	PQ INCREASED	3.13	HMW
136	ENSDARP00000076290	pdia4	pdia4-201	Protein disulfide-isomerase A4	Protein synthesis	PQ INCREASED	2.99	HMW
137	ENSDARP00000027102	nap11i	nap11i-201	Nucleosome assembly protein 1, like 1	Cell cycle, division, growth and fate	PQ INCREASED	2.76	HMW
138	ENSDARP00000104033	A2ML1 (7 of 12)	A2ML1 (7 of 12)-201	Alpha-2-macroglobulin-like 1	Immune system related	PQ INCREASED	2.50	HMW
139	ENSDARP00000121031	hspa8	hspa8-003	Heat shock protein 8	Protein synthesis	PQ INCREASED	2.47	HMW
140	ENSDARP00000100695	A2ML1 (7 of 12)	A2ML1 (7 of 12)-001	Alpha-2-macroglobulin-like 1	Immune system related	PQ INCREASED	2.43	HMW
141	ENSDARP00000100381	A2ML1 (7 of 12)	A2ML1 (7 of 12)-203	Alpha-2-macroglobulin-like 1	Immune system related	PQ INCREASED	2.38	HMW
142	ENSDARP00000100196	A2ML1 (7 of 12)	A2ML1 (7 of 12)-202	Alpha-2-macroglobulin-like 1	Immune system related	PQ INCREASED	2.37	HMW
143	ENSDARP00000124860	nap14a	nap14a-002	Nucleosome assembly protein 1, like 1	Cell cycle, division, growth and fate	PQ INCREASED	2.25	HMW
144	ENSDARP00000094479	nap14a	nap14a-001	Nucleosome assembly protein 1, like 2	Cell cycle, division, growth and fate	PQ INCREASED	2.24	HMW
145	ENSDARP00000103384	prmt1	prmt1-001	Protein arginine methyltransferase 1	Cell cycle, division, growth and fate	PQ INCREASED	2.14	HMW
146	ENSDARP00000027115	taldo1	taldo1-201	Transaldolase	Energy metabolism	PQ INCREASED	2.00	HMW
147	ENSDARP00000067816	chia.3	chia.3-001	Chitinase, acidic.3	Immune system related	PQ INCREASED	2.00	HMW
148	ENSDARP00000103361	si:ch211-14a17.7	si:ch211-14a17.7-201	Zona pellucida protein superfamily	Zona Pellucida proteins	PQ INCREASED	2.00	HMW
149	ENSDARP00000116459	si:ch211-14a17.7	si:ch211-14a17.7-001	Zona pellucida protein superfamily	Zona Pellucida proteins	PQ INCREASED	2.00	HMW
150	ENSDARP00000003107	cct7	cct7-001	Chaperonin containing TCP1, subunit 7	Protein synthesis	PQ INCREASED	2.00	HMW
151	ENSDARP00000020361	gcat	gcat-001	Glycine C-acetyltransferase	Protein synthesis	PQ INCREASED	2.00	HMW
152	ENSDARP00000090833	prdx4	prdx4-001	Peroxiredoxin 4	REDOX/Detox related	GQ INCREASED	0.50	LMW
153	ENSDARP00000094194	vtg3	vtg3-202	Vitellogenin 3	Vitellogenins	GQ INCREASED	0.50	LMW
154	ENSDARP00000072678	vtg7	vtg7-201	Vitellogenin 7	Vitellogenins	GQ INCREASED	0.50	LMW
155	ENSDARP00000114558	vtg7	vtg7-001	Vitellogenin 7	Vitellogenins	GQ INCREASED	0.50	LMW
156	ENSDARP00000116066	celsr3	celsr3-002	Cadherin, EGF LAG seven-pass G-type receptor 3	Other	GQ INCREASED	0.50	LMW
157	ENSDARP00000118276	si:dkey-90I23.1	Novel transcript	SUEL type lectin domain	Lectins	GQ INCREASED	0.50	LMW
158	ENSDARP00000063876	prdx6	prdx6-001	Peroxiredoxin 6	REDOX/Detox related	GQ INCREASED	0.50	LMW
159	ENSDARP00000096079	si:ch211-226h8.4	si:ch211-226h8.4-001	SUEL type lectin domain	Lectins	GQ INCREASED	0.49	LMW
160	ENSDARP00000115012	vtg4	vtg4-001	Vitellogenin 4	Vitellogenins	GQ INCREASED	0.49	LMW
161	ENSDARP00000050237	vtg1	vtg1-001	Vitellogenin 1	Vitellogenins	GQ INCREASED	0.49	LMW
162	ENSDARP00000101309	vtg4	vtg4-201	Vitellogenin 4	Vitellogenins	GQ INCREASED	0.49	LMW
163	ENSDARP00000072738	vtg1	vtg1-201	Vitellogenin 1	Vitellogenins	GQ INCREASED	0.48	LMW
164	ENSDARP00000072790	vtg2	vtg2-201	Vitellogenin 2	Vitellogenins	GQ INCREASED	0.47	LMW
165	ENSDARP00000096034	vtg2	vtg2-202	Vitellogenin 2	Vitellogenins	GQ INCREASED	0.47	LMW
166	ENSDARP00000120934	prdx3	prdx3-002	Peroxiredoxin 3	REDOX/Detox related	GQ INCREASED	0.45	LMW
167	ENSDARP00000123406	si:dkeyp-46h3.8	si:dkeyp-46h3.8-001	SUEL type lectin domain	Lectins	GQ INCREASED	0.44	LMW
168	ENSDARP00000115568	si:dkeyp-46h3.8	si:dkeyp-46h3.8-201	SUEL type lectin domain	Lectins	GQ INCREASED	0.44	LMW
169	ENSDARP00000096443	crp6	crp6-001	C-reactive protein 6	Immune system related	GQ INCREASED	0.43	LMW
170	ENSDARP00000113089	dut	dut-003	dUTP pyrophosphatase	Cell cycle, division, growth and fate	GQ INCREASED	0.41	LMW
171	ENSDARP00000122570	dut	dut-002	dUTP pyrophosphatase	Cell cycle, division, growth and fate	GQ INCREASED	0.40	LMW
172	ENSDARP00000108320	dut	dut-001	dUTP pyrophosphatase-deoxyundine triphosphatase	Cell cycle, division, growth and fate	GQ INCREASED	0.40	LMW
173	ENSDARP00000023863	rpe	rpe-001	Ribulose-5-phosphate-3-epimerase	Energy metabolism	GQ INCREASED	0.40	LMW
174	ENSDARP00000048374	stmn4	stmn4-001	Stathmin-like 4	Cell cycle, division, growth and fate	GQ INCREASED	0.39	LMW
175	ENSDARP00000113219	stmn4	stmn4-002	Stathmin-like 4	Cell cycle, division, growth and fate	GQ INCREASED	0.39	LMW
176	ENSDARP00000023158	vtg3	vtg3-201	Vitellogenin 3	Vitellogenins	GQ INCREASED	0.38	LMW
177	ENSDARP00000120407	si:ch211-250e5.16	si:ch211-250e5.16-001	SUEL type lectin domain	Lectins	GQ INCREASED	0.36	LMW

178	ENSDARP00000128406	vtg3	vtg3-001	Vitellogenin 3	Vitellogenins	GQ INCREASED	0.36	LMW
179	ENSDARP0000032532	ran	ran-003	GTP-binding nuclear protein Ran-Ras related nuclear protein	Cell cycle, division, growth and fate	GQ INCREASED	0.35	LMW
180	ENSDARP00000108629	ran	ran-001	RAN, member RAS oncogene family	Cell cycle, division, growth and fate	GQ INCREASED	0.35	LMW
181	ENSDARP00000121831	ran	ran-002	RAN, member RAS oncogene family	Cell cycle, division, growth and fate	GQ INCREASED	0.35	LMW
182	ENSDARP00000090756	glo1	glo1-001	Glyoxalase 1-Lactoylglutathione lyase	Energy metabolism	GQ INCREASED	0.34	LMW
183	ENSDARP00000117771	EIF5A2	EIF5A2-004	Translation initiation factor	Protein synthesis	GQ INCREASED	0.33	LMW
184	ENSDARP00000073095	EIF5A2	EIF5A2-001	Translation initiation factor	Protein synthesis	GQ INCREASED	0.33	LMW
185	ENSDARP00000117947	EIF5A2	EIF5A2-002	Translation initiation factor	Protein synthesis	GQ INCREASED	0.33	LMW
186	ENSDARP00000120991	EIF5A2	EIF5A2-003	Translation initiation factor	Protein synthesis	GQ INCREASED	0.33	LMW
187	ENSDARP00000117883	si:dkey-8816.3	si:dkey-8816.3-001	Low-density lipoprotein receptor-related protein 2 isoform X5	Lipid metabolism	GQ INCREASED	0.30	LMW
188	ENSDARP00000056381	crp3	crp3-201	C-reactive protein 2	Immune system related	GQ INCREASED	0.23	LMW
189	ENSDARP00000104927	crp3	crp3-202	C-reactive protein 3	Immune system related	GQ INCREASED	0.23	LMW
190	ENSDARP00000116589	crp3	crp3-001	C-reactive protein 3	Immune system related	GQ INCREASED	0.23	LMW
191	ENSDARP00000053425	pfn2l	pfn2l-001	Profilin 2 like	Cell cycle, division, growth and fate	GQ INCREASED	0.16	LMW
192	ENSDARP00000113417	pfn2l	pfn2l-002	Profilin 2 like	Cell cycle, division, growth and fate	GQ INCREASED	0.16	LMW
193	ENSDARP00000128438	pfn2l	pfn2l-003	Profilin 2 like	Cell cycle, division, growth and fate	GQ INCREASED	0.16	LMW
194	ENSDARP00000089804	zgc:136254	zgc:136254-001	Fish egg lectin like isoform X1	Endosome-Lysosome related	GQ INCREASED	0.16	LMW
195	ENSDARP00000129497	zgc:136254	zgc:136254-201	Fish egg lectin like isoform X1	Endosome-Lysosome related	GQ INCREASED	0.16	LMW
196	ENSDARP00000070002	ALDH6A1	ALDH6A1-001	Aldehyde dehydrogenase 6 family, member A1	Energy metabolism	GQ INCREASED	0.55	HMW
197	ENSDARP00000116781	si:dkey-152b24.6	si:dkey-152b24.6-001	1-phosphatidylinositol phosphodiesterase-like	Lipid metabolism	GQ INCREASED	0.54	HMW
198		si:ch1073-13h15.3	si:ch1073-13h15.3-001	Putative all-trans-retinol 13,14-reductase	Other	GQ INCREASED	0.54	HMW
199	ENSDARP00000024082	ATIC	ATIC-001	5-aminimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	Cell cycle, division, growth and fate	GQ INCREASED	0.54	HMW
200	ENSDARP00000008576	A2ML1 (1 of 12)	A2ML1 (1 of 12)-001	Alpha-2-macroglobulin-like 1	Immune system related	GQ INCREASED	0.53	HMW
201	ENSDARP00000069178	si:ch1073-13h15.3	si:ch1073-13h15.3-201	Putative all-trans-retinol 13,14-reductase	Other	GQ INCREASED	0.53	HMW
202	ENSDARP0000014978	HSP90AB1	HSP90AB1-001	Heat shock protein 90, alpha (cytosolic), class B member 1	Protein synthesis	GQ INCREASED	0.50	HMW
203	ENSDARP00000025538	RANBP1	RANBP1-001	RAN binding protein 1	Other	GQ INCREASED	0.50	HMW
204	ENSDARP00000060204	TUFM	TUFM-001	Elongation factor Tu	Protein synthesis	GQ INCREASED	0.50	HMW
205	ENSDARP00000101406	RANBP1	RANBP1-201	RAN binding protein 1	Other	GQ INCREASED	0.50	HMW
206	ENSDARP00000104512	HSP90AB1	HSP90AB1-201	Heat shock protein 90, alpha (cytosolic), class B member 1	Protein synthesis	GQ INCREASED	0.50	HMW
207	ENSDARP00000025702	TFA	TFA-201	Transferrin a	Immune system related	GQ INCREASED	0.49	HMW
208	ENSDARP0000012767	ALDH2.1	ALDH2.1-001	Aldehyde dehydrogenase 2, tandem duplicate 1	Lipid metabolism	GQ INCREASED	0.49	HMW
209	ENSDARP00000100241	TFA	TFA-001	Transferrin a	Immune system related	GQ INCREASED	0.49	HMW
210	ENSDARP00000062351	SLC25A6 (1 of 2)	SLC25A6 (1 of 2)-201	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	Cell cycle, division, growth and fate	GQ INCREASED	0.46	HMW
211	ENSDARP00000096509	SLC25A6 (1 of 2)	SLC25A6 (1 of 2)-001	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	Cell cycle, division, growth and fate	GQ INCREASED	0.46	HMW
212	ENSDARP00000008085	SETB	SETB-001	SET translocation (myeloid leukemia-associated) B	Cell cycle, division, growth and fate	GQ INCREASED	0.46	HMW
213	ENSDARP00000066176	TUBA2	TUBA2-001	Tubulin alpha 2	Cell cycle, division, growth and fate	GQ INCREASED	0.45	HMW
214	ENSDARP00000022077	SLC25A6	SLC25A6-001	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	Cell cycle, division, growth and fate	GQ INCREASED	0.45	HMW
215	ENSDARP00000030881	SLC25A4	SLC25A4-001	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	Cell cycle, division, growth and fate	GQ INCREASED	0.45	HMW
216	ENSDARP00000058383	GAPDH8	GAPDH8-001	Glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	Energy metabolism	GQ INCREASED	0.45	HMW
217	ENSDARP00000120922	DCR1	DCR1-001	2,4-dienoyl CoA reductase 1, mitochondrial	Energy metabolism	GQ INCREASED	0.45	HMW
218	ENSDARP00000023429	ALDH2.2	ALDH2.2-001	Aldehyde dehydrogenase 2, tandem duplicate 1	Energy metabolism	GQ INCREASED	0.45	HMW
219	ENSDARP00000088020	ALDH2.2	ALDH2.2-202	Aldehyde dehydrogenase 2, tandem duplicate 1	Energy metabolism	GQ INCREASED	0.45	HMW
220	ENSDARP00000088019	ALDH2.2	ALDH2.2-201	Aldehyde dehydrogenase 2, tandem duplicate 1	Energy metabolism	GQ INCREASED	0.44	HMW
221	ENSDARP00000117350	GALE	GALE-001	UDP-galactose 4-epimerase	Energy metabolism	GQ INCREASED	0.42	HMW
222	ENSDARP00000110334	GALE	GALE-201	UDP-galactose 4-epimerase	Energy metabolism	GQ INCREASED	0.41	HMW
223	ENSDARP00000073345	A2ML1 (1 of 12)	A2ML1 (1 of 12)-201	Alpha-2-macroglobulin-like 1	Immune system related	GQ INCREASED	0.40	HMW
224	ENSDARP00000116143	ESD	ESD-002	Esterase D/fornylglutathione hydrolase	Other	GQ INCREASED	0.37	HMW
225	ENSDARP00000118149	ESD	ESD-003	Esterase D/fornylglutathione hydrolase	Other	GQ INCREASED	0.37	HMW
226	ENSDARP00000024121	ESD	ESD-001	Esterase D/fornylglutathione hydrolase	Other	GQ INCREASED	0.36	HMW
227	ENSDARP00000114456	VDAC2	VDAC2-001	Voltage-dependent anion channel 2	Cell cycle, division, growth and fate	GQ INCREASED	0.34	HMW
228	ENSDARP00000111790	VDAC2	VDAC2-201	Voltage-dependent anion channel 2	Cell cycle, division, growth and fate	GQ INCREASED	0.34	HMW
229	ENSDARP00000114537	PGK1	PGK1-003	Phosphoglycerate kinase 1	Energy metabolism	GQ INCREASED	0.34	HMW
230	ENSDARP00000119690	AKR1A1B	AKR1A1B-004	Aldo-keto reductase family 1, member A1a (aldehyde reductase)	Lipid metabolism	GQ INCREASED	0.32	HMW
231	ENSDARP00000113696	AKR1A1B	AKR1A1B-005	Aldo-keto reductase family 1, member A1a (aldehyde reductase)	Lipid metabolism	GQ INCREASED	0.32	HMW
232	ENSDARP00000120539	AKR1A1B	AKR1A1B-006	Aldo-keto reductase family 1, member A1a (aldehyde reductase)	Lipid metabolism	GQ INCREASED	0.32	HMW
233	ENSDARP00000096504	SLC25A5	SLC25A5-001	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	Cell cycle, division, growth and fate	GQ INCREASED	0.30	HMW
234	ENSDARP00000040408	PPA1B	PPA1B-001	Phosphotyrosine phosphohistidine inorganic pyrophosphate phosphatase	Energy metabolism	GQ INCREASED	0.28	HMW
235	ENSDARP00000034804	ST13	ST13-201	Suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	Protein synthesis	GQ INCREASED	0.28	HMW
236	ENSDARP00000112549	ST13	ST13-001	Suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	Protein synthesis	GQ INCREASED	0.28	HMW
237	ENSDARP00000070807	PGK1	PGK1-001	Phosphoglycerate kinase 1	Energy metabolism	GQ INCREASED	0.27	HMW
238	ENSDARP00000124008	ALDH6A1	ALDH6A1-003	Aldehyde dehydrogenase 6 family, member A1	Energy metabolism	GQ INCREASED	0.25	HMW
239	ENSDARP00000123894	ALDH6A1	ALDH6A1-002	Aldehyde dehydrogenase 6 family, member A1	Energy metabolism	GQ INCREASED	0.25	HMW

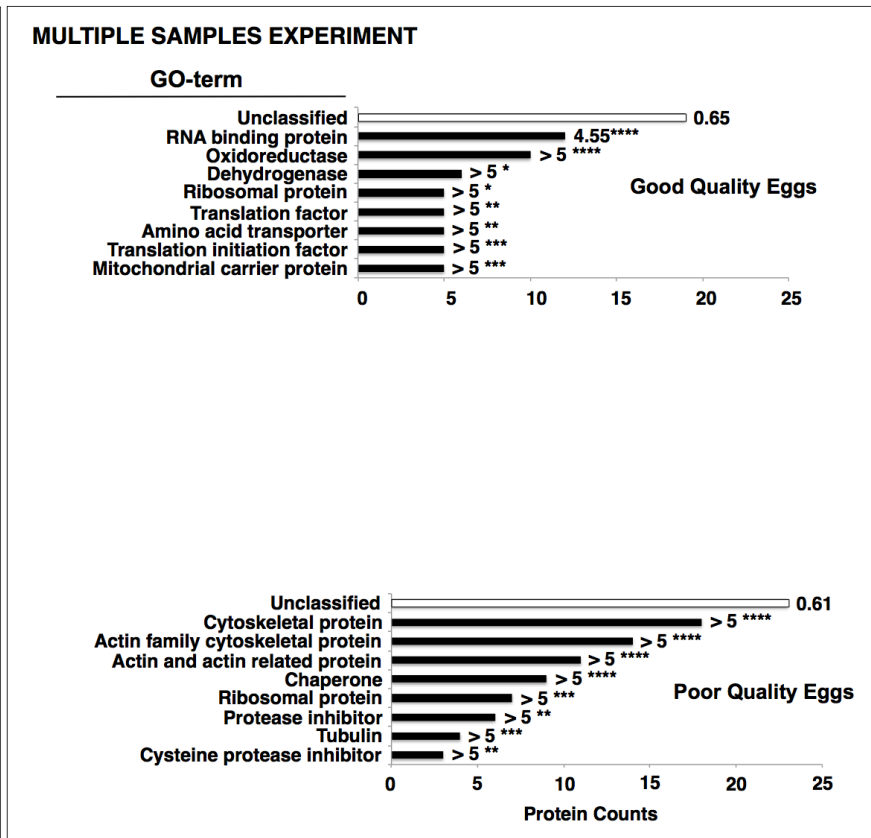
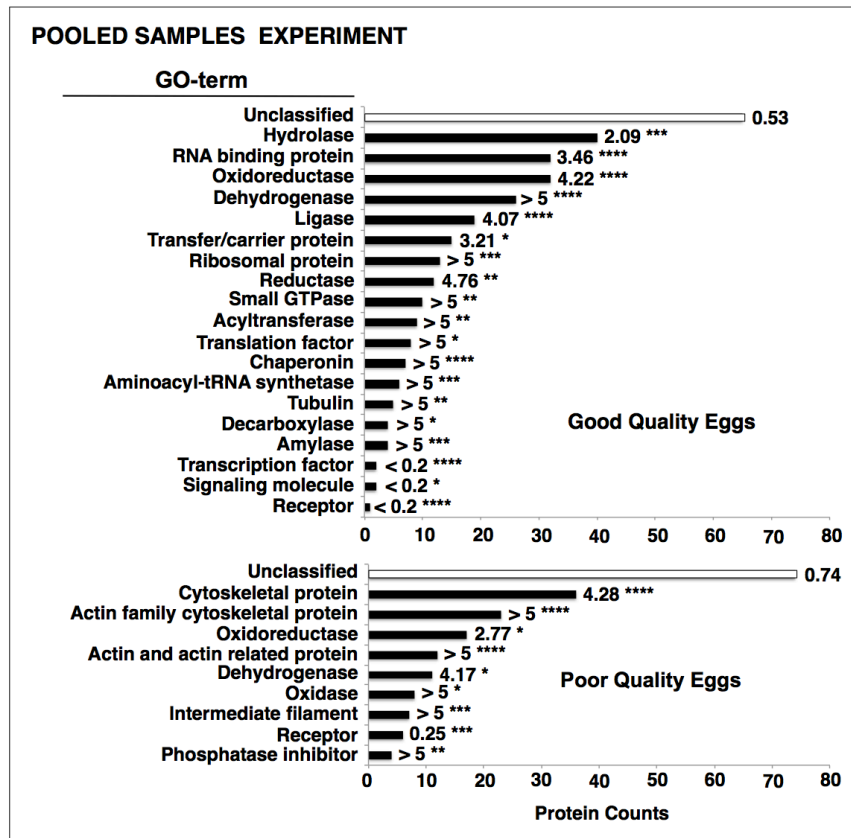
240	ENSDARP0000070667	zgc:171779	zgc:171779-201	Zona pellucida superfamily	Cell cycle, division, growth and fate	GQ INCREASED	0.24	HMW
241	ENSDARP0000006510	pgm1	pgm1-001	Phosphoglucomutase 1	Energy metabolism	GQ INCREASED	0.10	HMW
242	ENSDARP00000113349	KRT23 (1 of 2)	KRT23 (1 of 2)-003	Keratin 17	Cell cycle, division, growth and fate	GQ UNIQUE	-	LMW
243	ENSDARP00000089806	si:ch211-251f6.7	si:ch211-251f6.7-201	Fish egg lectin like precursor	Lectins	GQ UNIQUE	-	LMW
244	ENSDARP00000113985	si:ch211-251f6.7	si:ch211-251f6.7-001	Fish egg lectin like precursor	Lectins	GQ UNIQUE	-	LMW
245	ENSDARP00000115840	dut	dut-004	Deoxyuridine triphosphatase	Cell cycle, division, growth and fate	GQ UNIQUE	-	LMW
246	ENSDARP00000059013	zgc:173443	zgc:173443-001	Fish egg lectin like precursor	Lectins	GQ UNIQUE	-	LMW
247	ENSDARP00000034555	cycsb	cycsb-001	cytochrome c, somatic b	Energy metabolism	GQ UNIQUE	-	LMW
248	ENSDARP00000037864	glrx	glrx-001	Glutaredoxin (thioltransferase)	Protein synthesis	GQ UNIQUE	-	LMW
249	ENSDARP00000076087	glrx	glrx-201	Glutaredoxin (thioltransferase)	Protein synthesis	GQ UNIQUE	-	LMW
250	ENSDARP00000120838	glrx	glrx-002	Glutaredoxin (thioltransferase)	Protein synthesis	GQ UNIQUE	-	LMW
251	ENSDARP00000121692	gstm3	gstm3-002	Glutathione S transferase M3 (brain)	REDOX/Detox related	GQ UNIQUE	-	LMW
252	ENSDARP00000051749	si:rp71-45k5.4	si:rp71-45k5.4-001	Proteasome subunit alpha 2	Protein degradation and synthesis inhibition	GQ UNIQUE	-	LMW
253	ENSDARP00000128459	si:rp71-45k5.4	si:rp71-45k5.4-202	Proteasome subunit alpha 2	Protein degradation and synthesis inhibition	GQ UNIQUE	-	LMW
254	ENSDARP00000058679	psma2	psma2-201	Proteasome subunit alpha 2	Protein degradation and synthesis inhibition	GQ UNIQUE	-	LMW
255	ENSDARP00000127697	si:rp71-45k5.4	si:rp71-45k5.4-201	Proteasome subunit alpha 2	Protein degradation and synthesis inhibition	GQ UNIQUE	-	LMW
256	ENSDARP00000075482	sb.cb252	sb.cb252-201	ES1 protein homolog, mitochondrial	Energy metabolism	GQ UNIQUE	-	LMW
257	ENSDARP00000027268	gspt1l	gspt1l-001	G1 to S phase transition 1, like	Protein synthesis	GQ UNIQUE	-	HMW
258	ENSDARP00000039367	prmt1	prmt1-002	Protein arginine methyltransferase 1	Cell cycle, division, growth and fate	GQ UNIQUE	-	HMW
259	ENSDARP00000052324	f2	f2-001	Coagulation factor II, thrombin	Immune system related	GQ UNIQUE	-	HMW
260	ENSDARP00000057644	qsox1	qsox1-001	Quiescin Q6 sulfhydryl oxidase 1	Protein synthesis	GQ UNIQUE	-	HMW
261	ENSDARP00000096969	psmc5	psmc5-001	Proteasome (prosome, macropain) 26S subunit, ATPase, 5	Protein synthesis	GQ UNIQUE	-	HMW
262	ENSDARP00000104071	f2	f2-002	Coagulation factor II, thrombin	Immune system related	GQ UNIQUE	-	HMW
263	ENSDARP00000105266	zgc:152830	zgc:152830-201	Peptidase M17 superfamily	Protein degradation and synthesis inhibition	GQ UNIQUE	-	HMW
264	ENSDARP00000108730	ifa	ifa-202	Transferrin a	Immune system related	GQ UNIQUE	-	HMW
265	ENSDARP00000110443	BX323793.2	BX323793.2-201	1-phosphatidylinositol phosphodiesterase-like	Lipid metabolism	GQ UNIQUE	-	HMW
266	ENSDARP00000114109	si:dkey-152b24.7	si:dkey-152b24.7-201	1-phosphatidylinositol phosphodiesterase-like	Lipid metabolism	GQ UNIQUE	-	HMW
267	ENSDARP00000112306	pycr1b	pycr1b-201	Pyroline-5-carboxylate reductase 1b	Protein degradation and synthesis inhibition	GQ UNIQUE	-	HMW
268	ENSDARP00000116484	gspt1l	gspt1l-002	G1 to S phase transition 1, like	Protein synthesis	GQ UNIQUE	-	HMW
269	ENSDARP00000116563	si:dkey-152b24.7	si:dkey-152b24.7-001	1-phosphatidylinositol phosphodiesterase-like	Lipid metabolism	GQ UNIQUE	-	HMW
270	ENSDARP00000117331	nasp	nasp-002	Nuclear autoantigenic sperm protein (histone-binding)	Protein synthesis	GQ UNIQUE	-	HMW
271	ENSDARP00000118947	gale	gale-002	UDP-galactose-4-epimerase	Energy metabolism	GQ UNIQUE	-	HMW
272	ENSDARP00000127771	zgc:152830	zgc:152830-001	Peptidase M17 superfamily	Protein degradation and synthesis inhibition	GQ UNIQUE	-	HMW
273	ENSDARP00000128522	ifa	ifa-003	Transferrin a	Immune system related	GQ UNIQUE	-	HMW
274	ENSDARP00000017776	A2ML1 (10 of 12)	A2ML1 (10 of 12)-201	Alpha-2-macroglobulin-like 1	Lipid metabolism	GQ UNIQUE	-	HMW

**S3 Table. Enrichment of PANTHER pathways with differentially regulated proteins.** Results of overrepresentation binomial tests [27] for enrichment of PANTHER pathways with proteins showing a  $\geq 2$ -fold difference in N-SC between egg quality groups, or unique to an egg quality group, in the Pooled Samples Experiment (top) and in the Multiple Samples Experiment (bottom). Only statistically significant results ( $p \leq 0.05$  after Bonferroni correction for multiple tests) are reported. Numbers of mapped and unmapped proteins are given in **Fig 3 and Fig 5**.

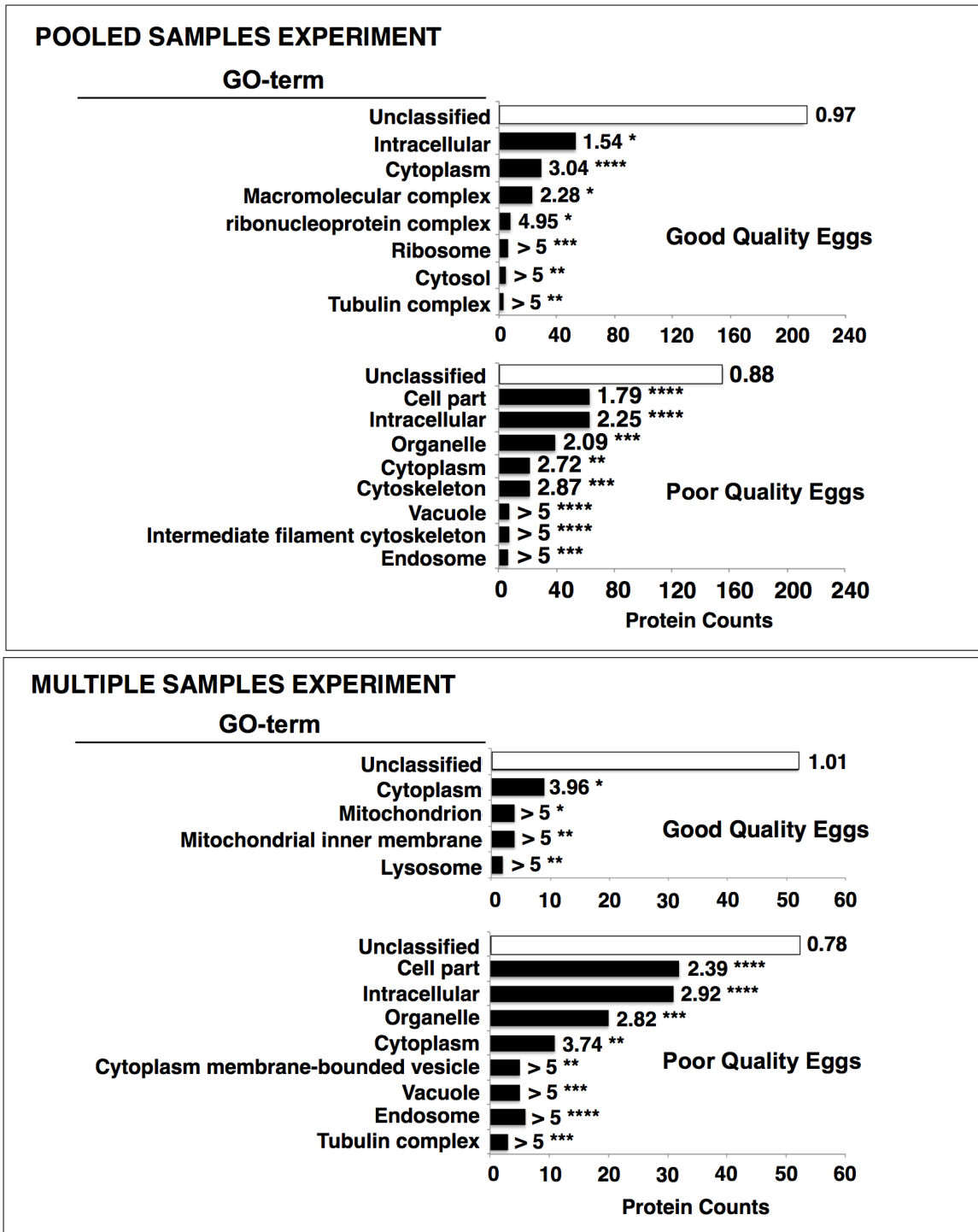
<b>PANTHER Overrepresentation Test</b>		PANTHER version 11.0 Released 2016				
Analyzed List: <i>Danio rerio</i> (input - differentially regulated proteins)		Reference List: <i>Danio rerio</i> (all genes in database)				
<b>POOLED SAMPLES EXPERIMENT</b>		<b>POOR QUALITY EGGS</b>				
<b>PANTHER Pathways</b>	REFLIST (27187)	Input (194)	Input (expected)	Input (over/under)	Input (fold Enrichment)	Input (P-value)
Cytoskeletal regulation by Rho GTPase (P00016)	120	12	0.86	+	14.01	1.67E-08
Parkinson disease (P00049)	112	11	0.8	+	13.76	1.22E-07
Huntington disease (P00029)	183	13	1.31	+	9.96	1.69E-07
Cadherin signaling (P00012)	183	12	1.31	+	9.19	1.79E-06
FGF signaling (P00021)	160	10	1.14	+	8.76	4.69E-05
Nicotinic acetylcholine receptor signaling (P00044)	141	8	1.01	+	7.95	1.46E-03
EGF receptor signaling (P00018)	174	9	1.24	+	7.25	8.46E-04
Alzheimer disease-presenilin (P00004)	166	8	1.18	+	6.75	4.65E-03
Integrin signaling (P00034)	219	9	1.56	+	5.76	5.10E-03
Wnt signaling (P00057)	388	13	2.77	+	4.7	8.32E-04
Inflammation mediated by chemokine /cytokine signaling (P00031)	353	10	2.52	+	3.97	3.94E-02
Unclassified (UNCLASSIFIED)	24075	146	171.79	-	0.85	0.00E+00
		<b>GOOD QUALITY EGGS</b>				
<b>PANTHER Pathways</b>	REFLIST (27187)	Input (251)	Input (expected)	Input (over/under)	Input (fold Enrichment)	Input (P-value)
Pyruvate metabolism (P02772)	15	6	0.14	+	43.33	1.26E-06
De novo purine biosynthesis (P02738)	33	4	0.3	+	13.13	4.22E-02
Unclassified (UNCLASSIFIED)	24075	188	222.27	-	0.85	0.00E+00
<b>MULTIPLE SAMPLES EXPERIMENT</b>		<b>POOR QUALITY EGGS</b>				
<b>PANTHER Pathways</b>	REFLIST (27187)	Input (74)	Input (expected)	Input (over/under)	Input (fold Enrichment)	Input (P-value)
Cytoskeletal regulation by Rho GTPase (P00016)	120	15	0.33	+	45.92	1.03E-18
Huntington disease (P00029)	183	17	0.5	+	34.13	2.92E-19
Nicotinic acetylcholine receptor signaling pathway (P00044)	141	10	0.38	+	26.06	1.14E-09
Alzheimer disease-presenilin pathway (P00004)	166	11	0.45	+	24.35	1.98E-10
Cadherin signaling pathway (P00012)	183	11	0.5	+	22.08	5.57E-10
Parkinson disease (P00049)	112	6	0.3	+	19.68	1.09E-04
Integrin signaling pathway (P00034)	219	7	0.6	+	11.74	3.78E-04
Inflammation med. by chemokine & cytokine signaling (P00031)	353	10	0.96	+	10.41	7.02E-06
Wnt signaling pathway (P00057)	388	9	1.06	+	8.52	1.80E-04
Unclassified (UNCLASSIFIED)	24075	43	65.53	-	0.66	0.00E+00
		<b>GOOD QUALITY EGGS</b>				
<b>PANTHER Pathways</b>	REFLIST (27187)	Input (60)	Input (expected)	Input (over/under)	Input (fold Enrichment)	Input (P-value)
5-Hydroxytryptamine degradation (P04372)	19	3	0.04	+	71.54	1.73E-03
Unclassified (UNCLASSIFIED)	24075	43	53.13	-	0.81	0.00E+00



**S1 Fig. Enrichment of Molecular Function GO terms with differentially regulated proteins.** Results of over-representation binomial tests [27] for enrichment of Molecular Function GO terms (PANTHER GO-Slim) with proteins up-regulated in good and poor quality zebrafish eggs. **Top Panel.** Pooled Samples Experiment. **Bottom Panel.** Multiple Samples Experiment. Horizontal bars indicate the number of proteins attributed to each GO term for which statistically significant results ( $p \leq 0.05$  after Bonferroni correction for multiple tests) were observed. Numbers next to the bars indicate the fold-enrichment with proteins attributed to each term and the number of asterisks indicates the significance level of the enrichment, as follows  $p \leq 0.05$  (\*),  $p \leq 0.01$  (\*\*),  $p \leq 0.001$  (\*\*\*), and  $p \leq 0.0001$  (\*\*\*\*).



**S2 Fig. Enrichment of Protein Class GO terms with differentially regulated proteins.** Results of over-representation binomial tests [27] for enrichment of Protein Class GO terms (PANTHER GO-Slim) with proteins up-regulated in good and poor quality zebrafish eggs. **Left Panel.** Pooled Samples Experiment. **Right Panel.** Multiple Samples Experiment. Horizontal bars indicate the number of proteins attributed to each GO term for which statistically significant results ( $p \leq 0.05$  after Bonferroni correction for multiple tests) were observed. Numbers next to the bars indicate the fold-enrichment with proteins attributed to each term and the number of asterisks indicates the significance level of the enrichment, as follows  $p \leq 0.05$  (\*),  $p \leq 0.01$  (\*\*),  $p \leq 0.001$  (\*\*\*), and  $p \leq 0.0001$  (\*\*\*\*).



**S3 Fig. Enrichment of Cellular Component GO terms with differentially regulated proteins.** Results of over-representation binomial tests [27] for enrichment of Cellular Component GO terms (PANTHER GO-Slim) with proteins up-regulated in good and poor quality zebrafish eggs. **Top Panel.** Pooled Samples Experiment. **Bottom Panel.** Multiple Samples Experiment. Horizontal bars indicate the number of proteins attributed to each GO term for which statistically significant results ( $p \leq 0.05$  after Bonferroni correction for multiple tests) were observed. Numbers next to the bars indicate the fold-enrichment with proteins attributed to each term and the number of asterisks indicates the significance level of the enrichment, as follows  $p \leq 0.05$  (\*),  $p \leq 0.01$  (\*\*),  $p \leq 0.001$  (\*\*\*), and  $p \leq 0.0001$  (\*\*\*\*).



**S4 Fig. Diagrams of PANTHER pathways enriched with differentially regulated proteins.** Proteins showing a  $\geq 2$ -fold difference in N-SC between egg quality groups, or unique to an egg quality group, in the Pooled Samples Experiment and/or the Multiple Samples Experiment are mapped to the PANTHER pathways in which they were found to be overrepresented (see **S3 Table**). Pathways are presented as follows:

**Panel a.** Cytoskeletal regulation by Rho GTPase pathway (PANTHER pathway P00016)

**Panel b.** Parkinson disease pathway (PANTHER pathway P00049)

**Panel c.** Huntington's disease pathway (PANTHER pathway P00029)

**Panel d.** Cadherin signaling pathway (PANTHER pathway P00012)

**Panel e.** FGF signaling pathway (PANTHER pathway P00021)

**Panel f.** Nicotinic acetylcholine receptor signaling pathway (PANTHER pathway P00044)

**Panel g.** EGF receptor signaling pathway (PANTHER pathway P00018)

**Panel h.** Alzheimer's disease-presenilin pathway (PANTHER pathway P00004)

**Panel i.** Integrin signaling pathway (PANTHER pathway P00034)

**Panel j.** Wnt signaling pathway (PANTHER pathway P00057).

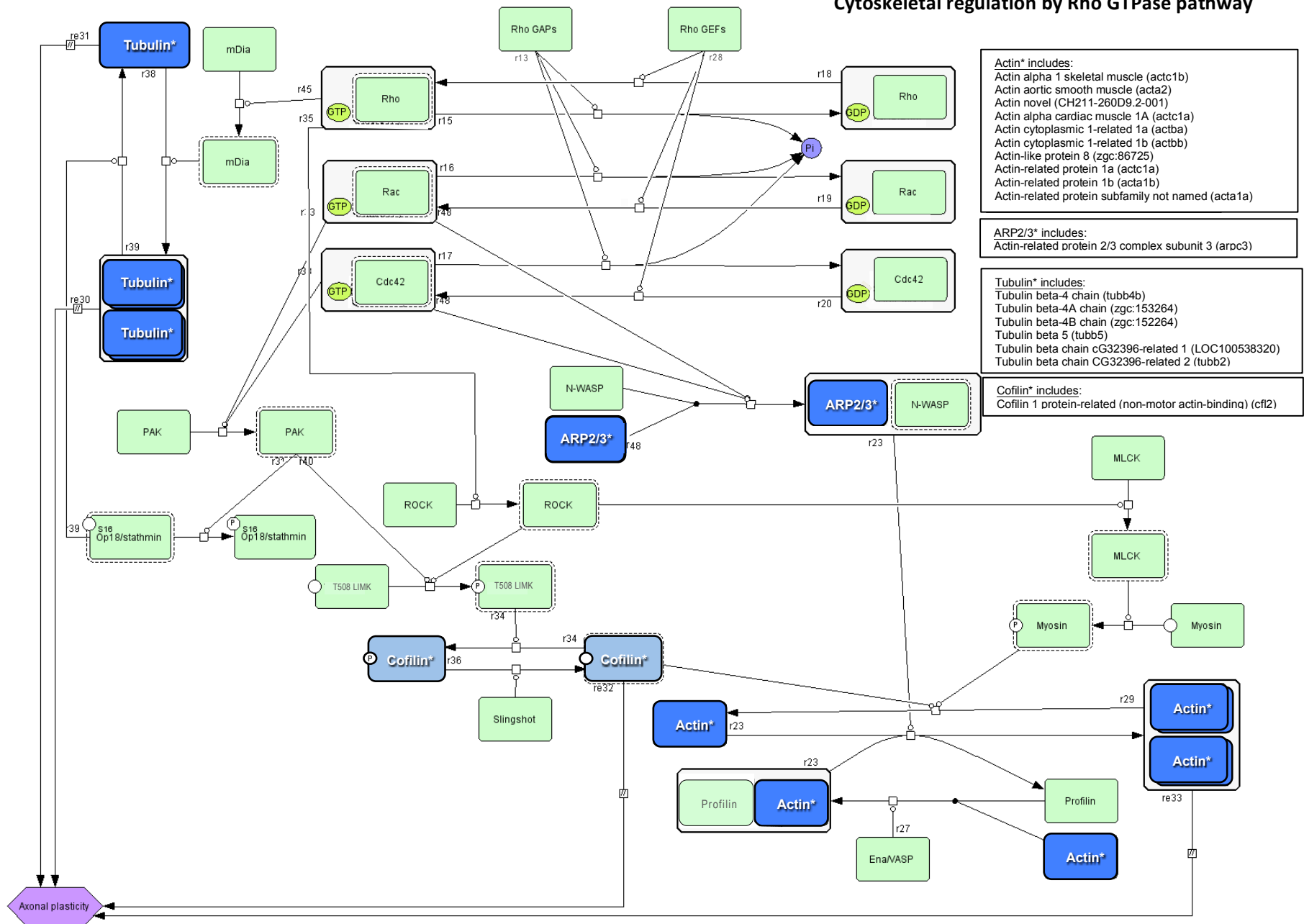
**Panel k.** Inflammation mediated by chemokine & cytokine signaling pathway (PANTHER pathway P00031)

**Panel l.** Pyruvate metabolism pathway (PANTHER pathway P02772)

**Panel m.** De novo purine biosynthesis (PANTHER pathway P02738)

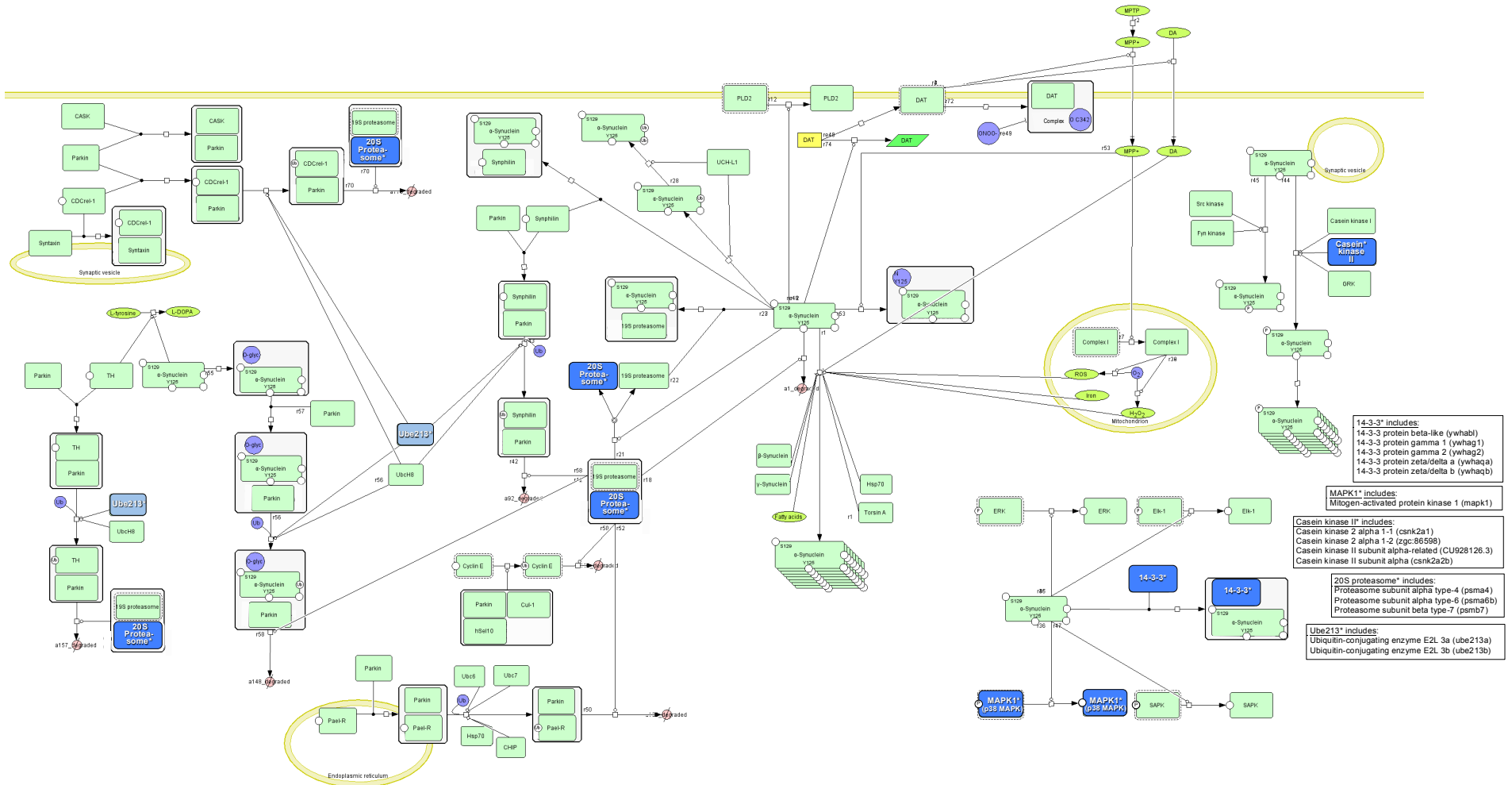
**Panel n.** 5-Hydroxytryptamine degradation (PANTHER pathway P04372)

## Cytoskeletal regulation by Rho GTPase pathway

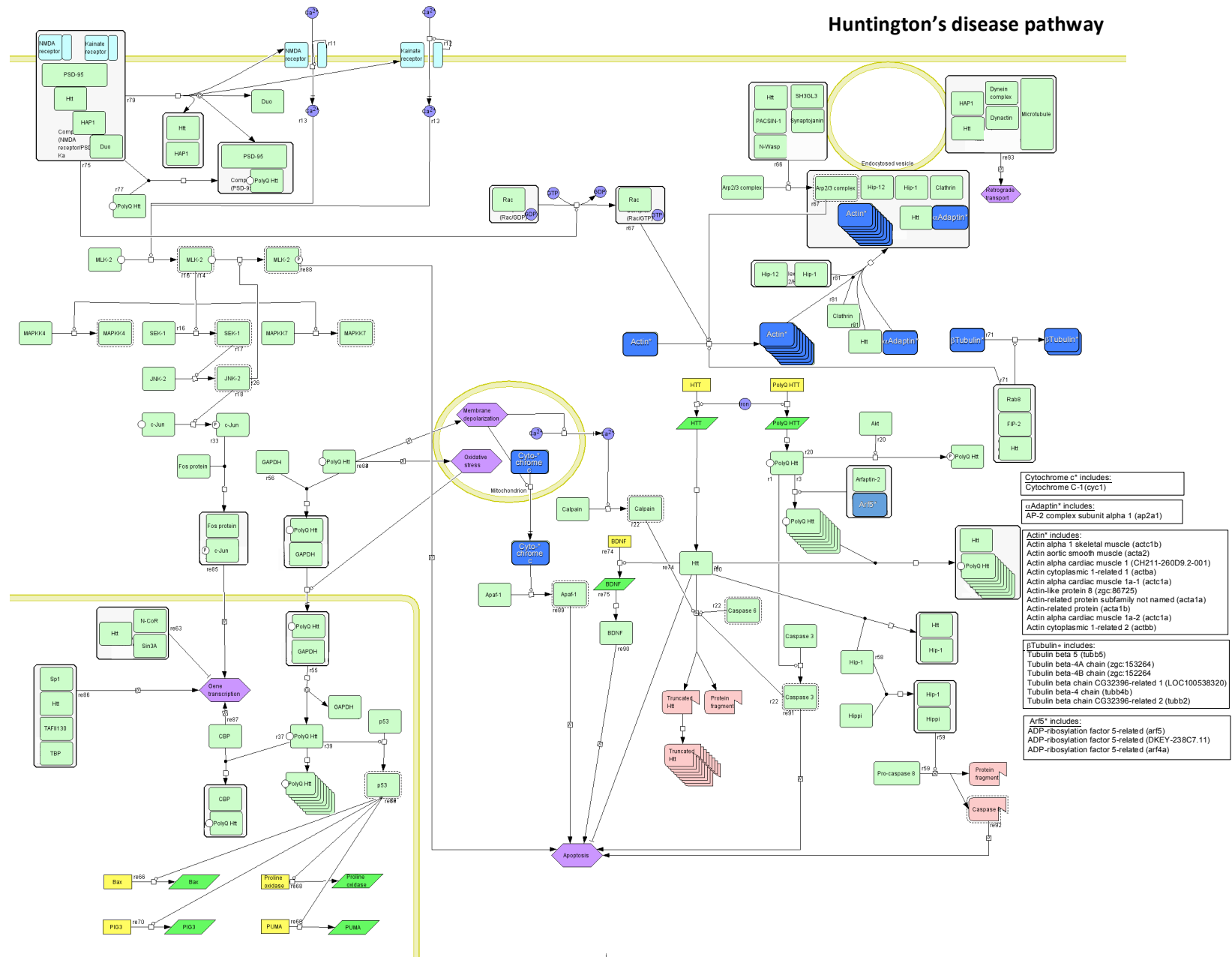


**Panel a.** Proteins up-regulated  $\geq 2$ -fold in poor quality zebrafish eggs, or unique to poor quality eggs, mapped to the Cytoskeletal regulation by Rho GTPase pathway (PANTHER pathway P00016) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by blue boxes with white text and are individually named in open boxes to the upper right with corresponding transcript names in parentheses. Dark blue boxes indicate mapped proteins from the Pooled Samples Experiment and light blue boxes indicate additional mapped proteins from the Multiple Samples Experiment. The mapped zebrafish proteins include actins (Actin\*), actin-related protein 2/3 complex subunit 3 (ARP2/3\*), tubulins (Tubulin\*), and cofilin 1 protein-related protein.

## Parkinson disease pathway

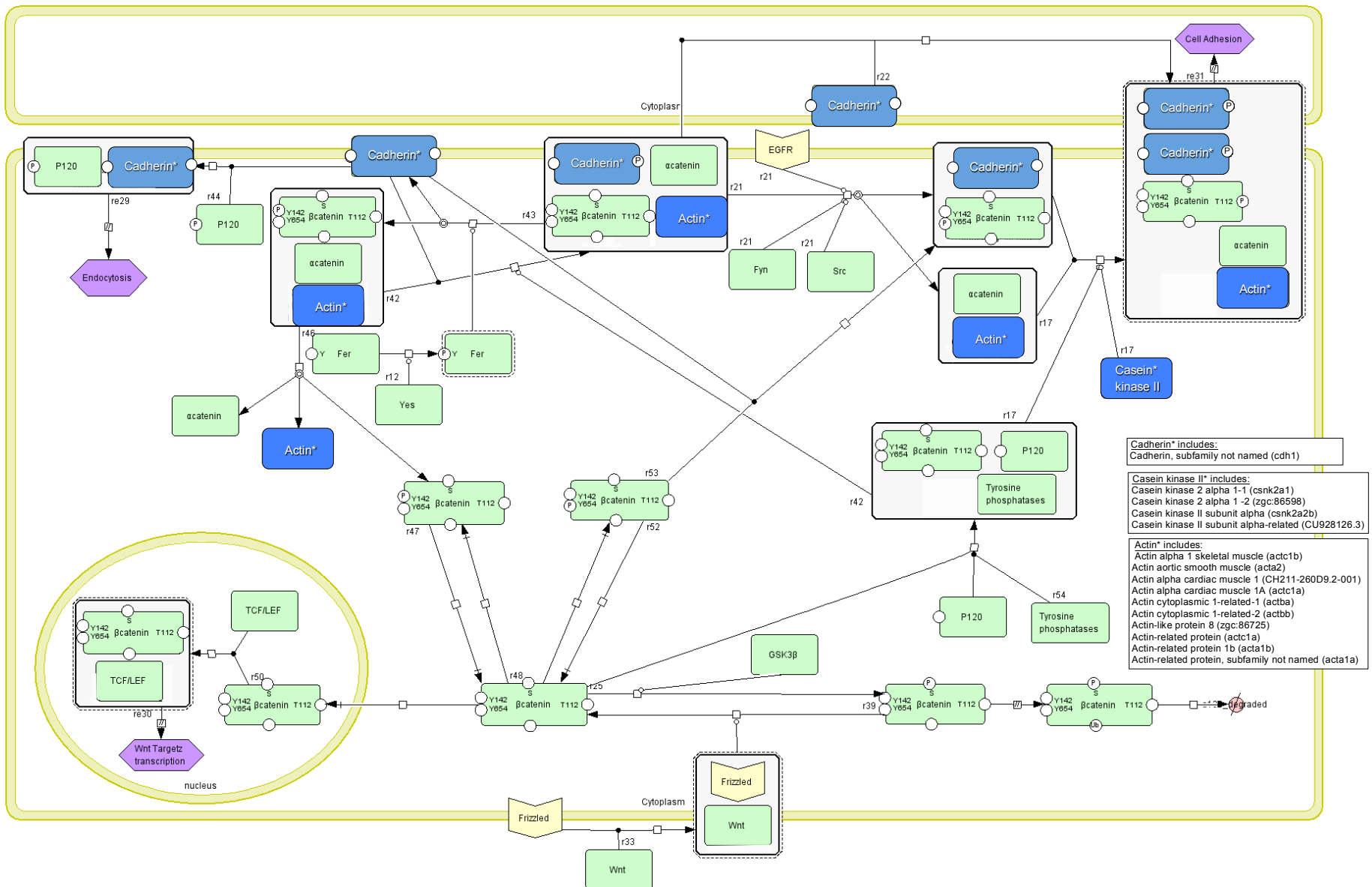


**Panel b.** Proteins up-regulated  $\geq 2$ -fold in poor quality zebrafish eggs, or unique to poor quality eggs, mapped to the Parkinson disease pathway (PANTHER pathway P00049) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by blue boxes with white text and are individually named in open boxes to the lower right with corresponding transcript names in parentheses. Dark blue boxes indicate mapped proteins from the Pooled Samples Experiment and light blue boxes indicate additional mapped proteins from the Multiple Samples Experiment. The mapped zebrafish proteins include 20S-proteasome components (20S proteasome\*), variants of ubiquitin-conjugating enzyme E2L 3B (Ube213\*), mitogen-activated kinase 1 (MAPK1\*), variants of casein kinase II (Casein kinase II\*), and 14-3-3 chaperone proteins (14-3-3\*).

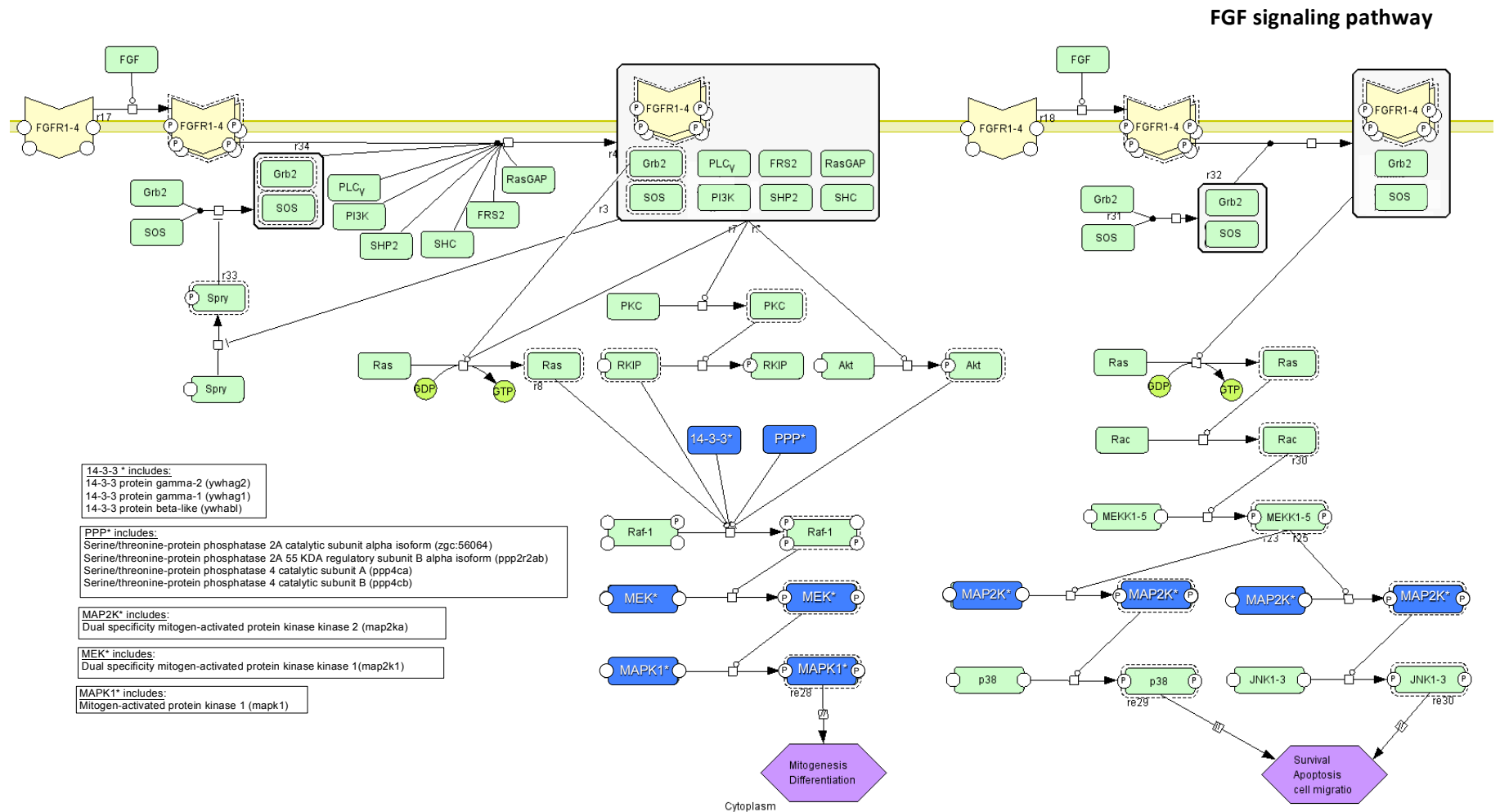


**Panel c.** Proteins up-regulated  $\geq 2$ -fold in poor quality zebrafish eggs, or unique to poor quality eggs, mapped to the Huntington's disease pathway (Panther pathway P00029) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by blue boxes with white text and are individually named in open boxes to the lower right with corresponding transcript names in parentheses. Dark blue boxes indicate mapped proteins from the Pooled Samples Experiment and light blue boxes indicate additional mapped proteins from the Multiple Samples Experiment. Aside from mitochondrial cytochrome c and variants of ADP-ribosylation factor 5, all of these zebrafish proteins are actins, tubulins or  $\alpha$ -adaptin involved in clathrin-mediated endocytosis, a major activity in growing oocytes.

## Cadherin signaling pathway

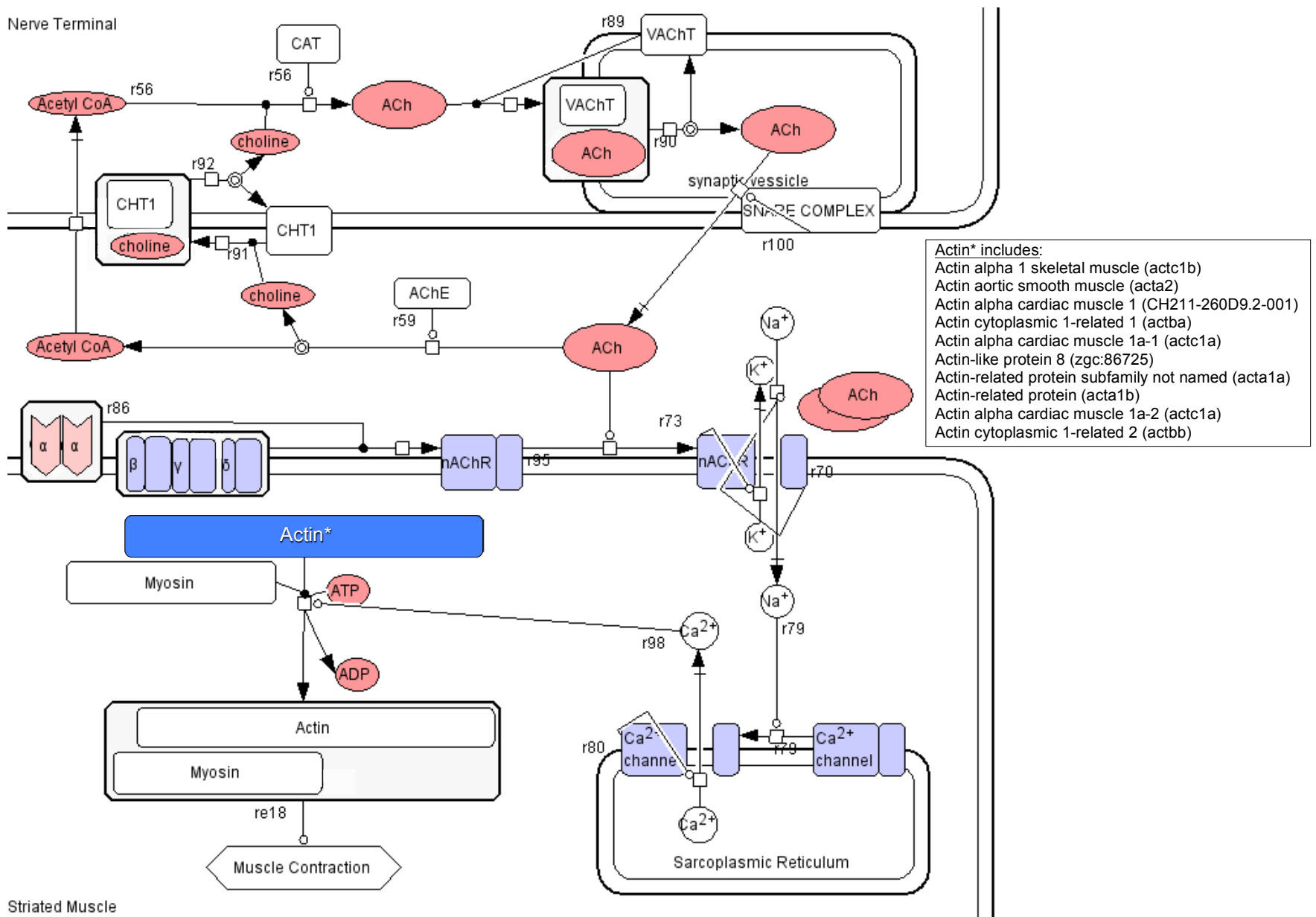


**Panel d.** Proteins upregulated  $\geq 2$ -fold in poor quality zebrafish eggs, or unique to poor quality eggs, mapped to the Cadherin signaling pathway (Panther pathway P00012) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by blue boxes with white text and are individually named in open boxes on the lower right with corresponding transcript names in parentheses. Dark blue boxes indicate mapped proteins from the Pooled Samples Experiment and light blue boxes indicate additional mapped proteins from the Multiple Samples Experiment. The mapped zebrafish proteins are all actins (Actin\*), variants of casein kinase II (Casein kinase II\*) or cadherin 1 (Cadherin\*).

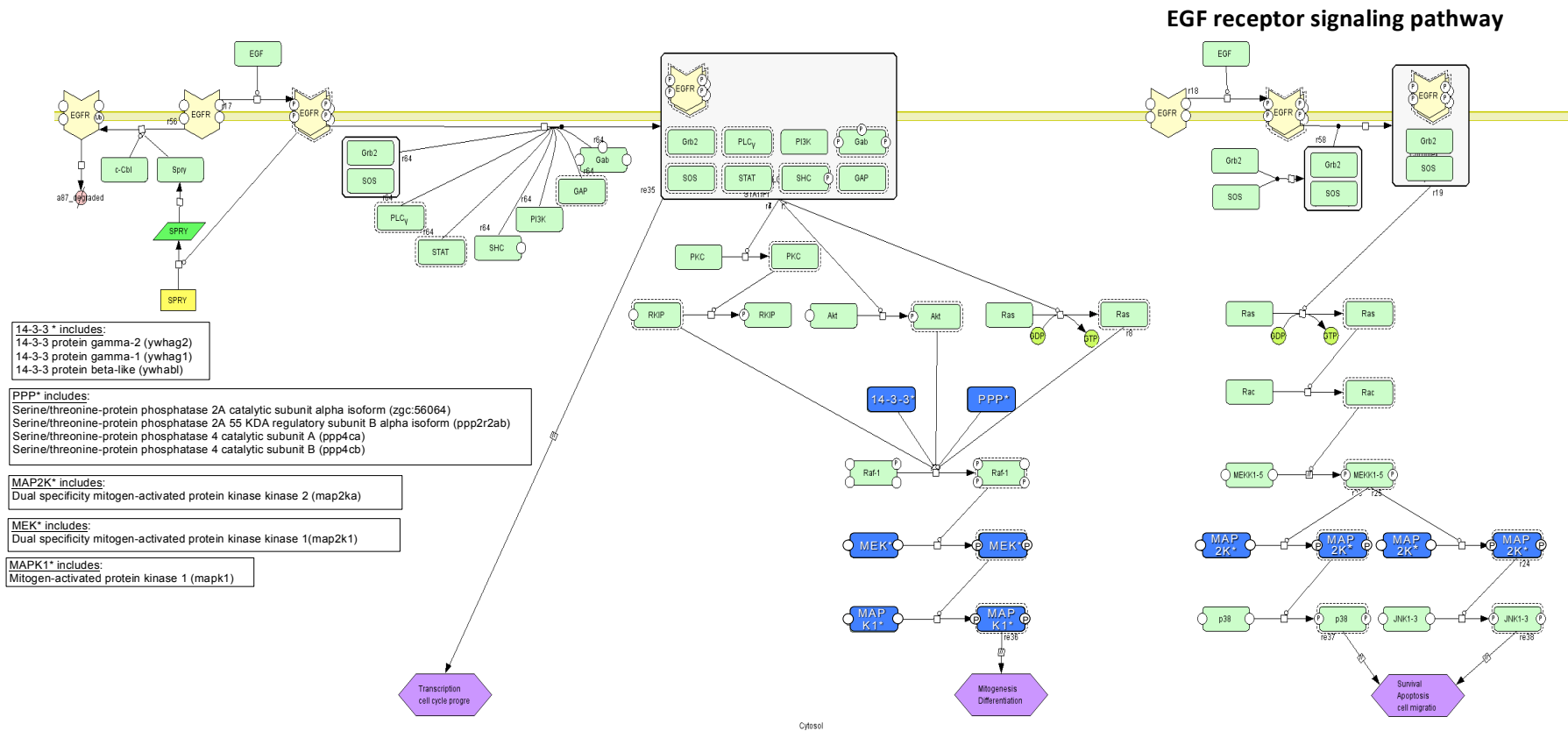


**Panel e.** Proteins up-regulated  $\geq 2$ -fold in poor quality zebrafish eggs, or unique to poor quality eggs, mapped to the FGF signaling pathway (Panther pathway P00021) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by blue boxes with white text and are individually named in open boxes on the lower left with corresponding transcript names in parentheses. The dark blue boxes indicate mapped proteins from the Pooled Samples Experiment. The mapped zebrafish proteins are all 14-3-3 chaperone proteins (14-3-3\*), variants of serine/threonine protein phosphatase (PPP\*), variants of dual specificity mitogen-activated protein kinase kinase (MEK\* and MAP2K\*), or mitogen-activated protein kinase 1 (MAPK1\*) and all were also mapped to the EGF signaling pathway (see **S4 Fig Panel g**).

## Nicotinic acetylcholine receptor signaling pathway



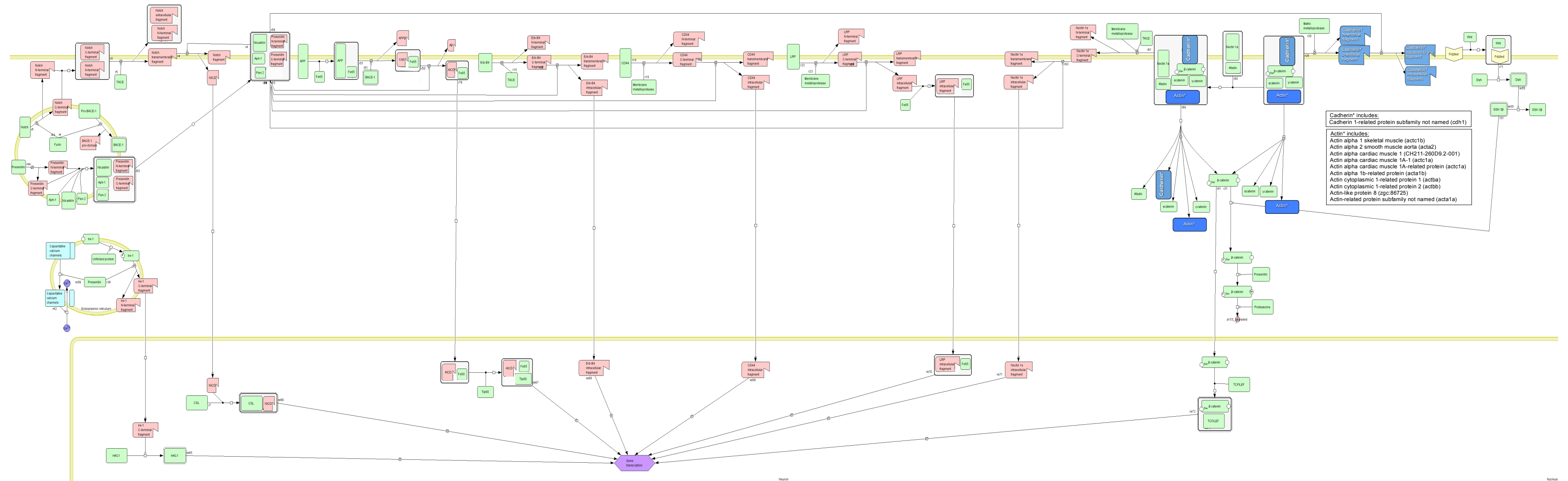
**Panel f.** Proteins up-regulated  $\geq 2$ -fold in poor quality zebrafish eggs, or unique to poor quality eggs, mapped to the Nicotinic acetylcholine receptor signaling pathway (Panther pathway P00044) in which they were found to be overrepresented (see **S3 Table**). The mapped zebrafish proteins from the Pooled Samples Experiment and the Multiple Samples Experiment are indicated by the blue box with white text and are individually named in open boxes on the right with corresponding transcript names in parentheses. Experiment. The mapped zebrafish proteins are all actins (Actin\*).



**Panel g.** Proteins up-regulated  $\geq 2$ -fold in poor quality zebrafish eggs, or unique to poor quality eggs, mapped to the EGF receptor signaling pathway (Panther pathway P00018) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by the blue boxes with white text and are individually named in open boxes on the left with corresponding transcript names in parentheses. The dark blue boxes indicate mapped proteins from the Pooled Samples Experiment. The mapped zebrafish proteins are all 14-3-3 chaperone proteins (14-3-3\*), variants of serine/threonine protein phosphatase (PPP\*), variants of dual specificity mitogen-activated protein kinase kinase (MEK\* and MAP2K\*), or mitogen-activated protein kinase 1 (MAPK1\*) and all were also mapped to the FGF signaling pathway (see **S4 Fig Panel e**).

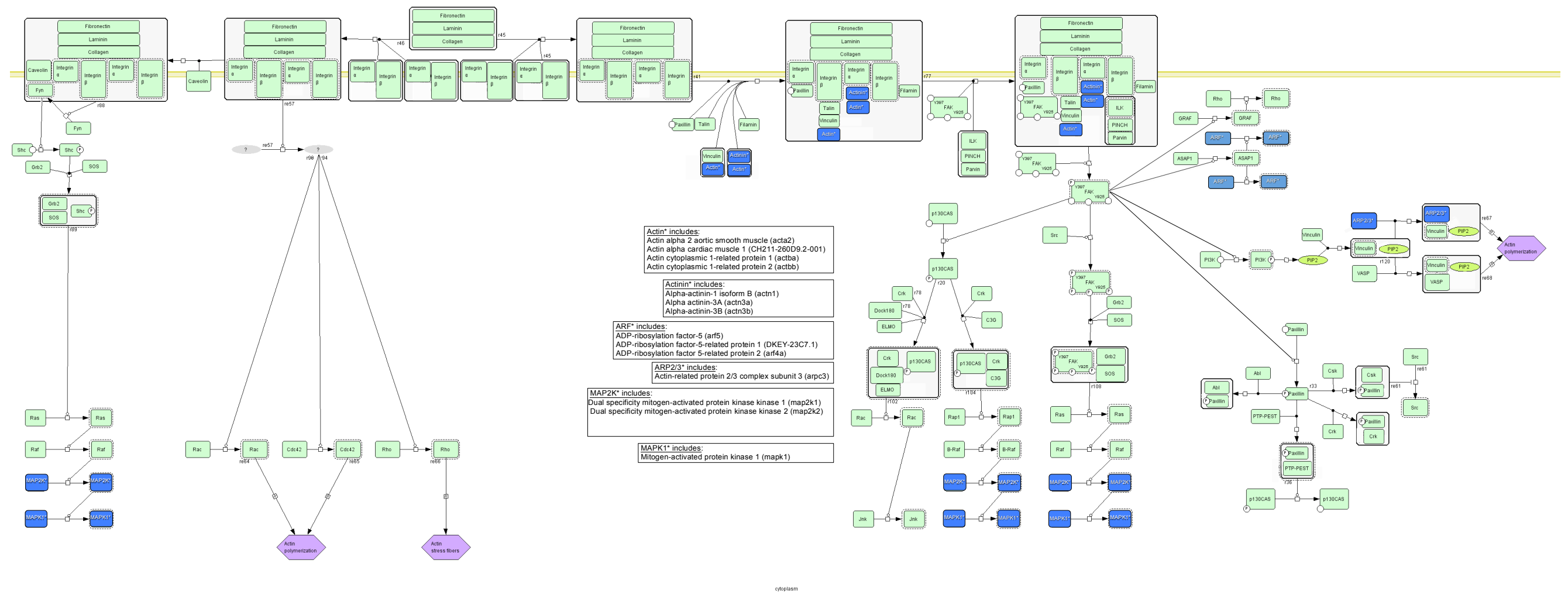


Alzheimer's disease-presenilin pathway

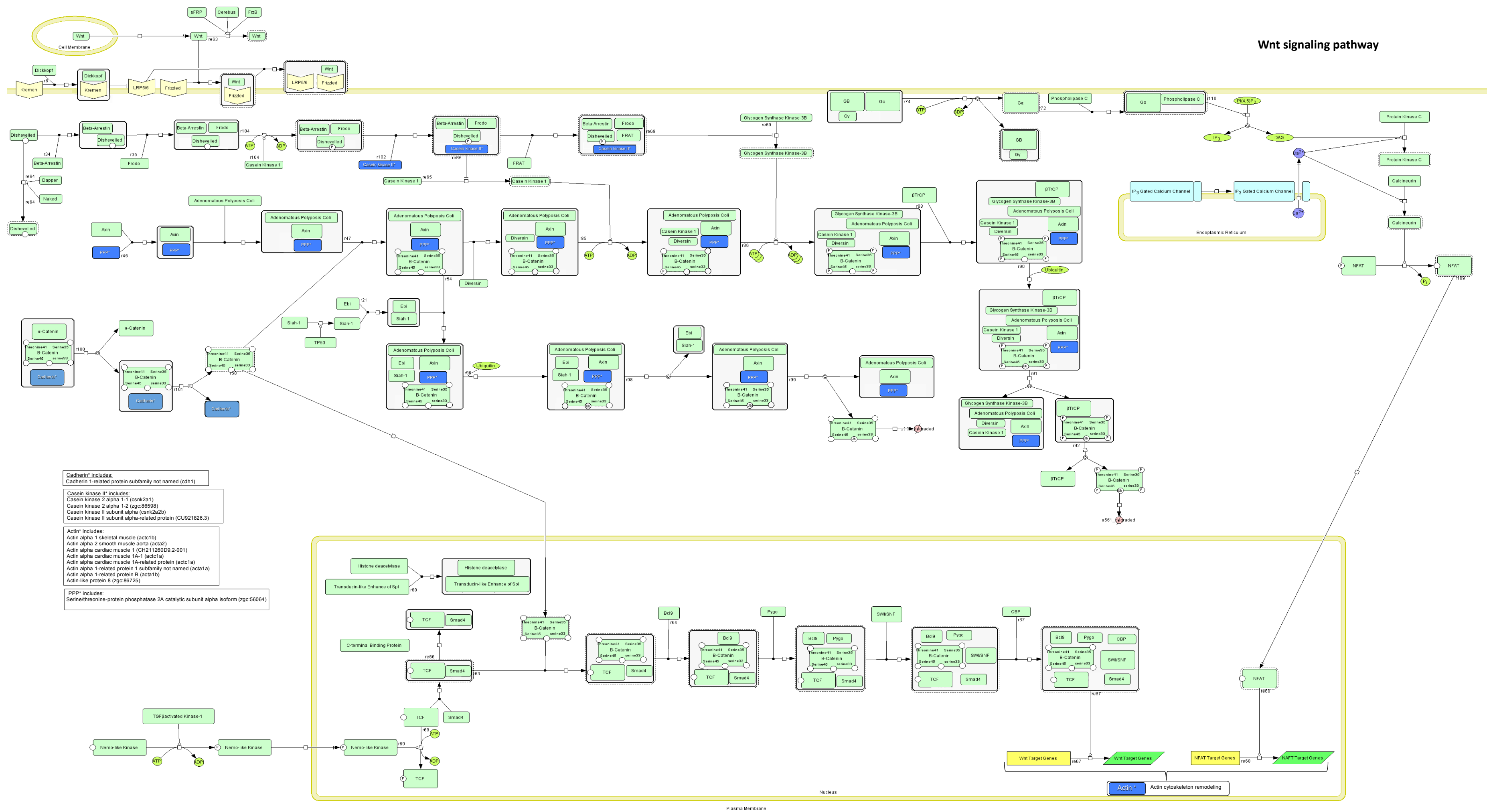


**Panel h.** Proteins up-regulated  $\geq 2$ -fold in poor quality zebrafish eggs, or unique to poor quality eggs, mapped to the Alzheimer's disease-presenilin pathway (Panther pathway P00004) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by blue boxes with white text and are individually named in open boxes on the upper right with corresponding transcript names in parentheses. Dark blue boxes indicate mapped proteins from the Pooled Samples Experiment and light blue shapes indicate mapped proteins from the Multiple Samples Experiment. The mapped zebrafish proteins are all actins (Actin\*) or cadherin (Cadherin\*).

## Integrin signaling pathway

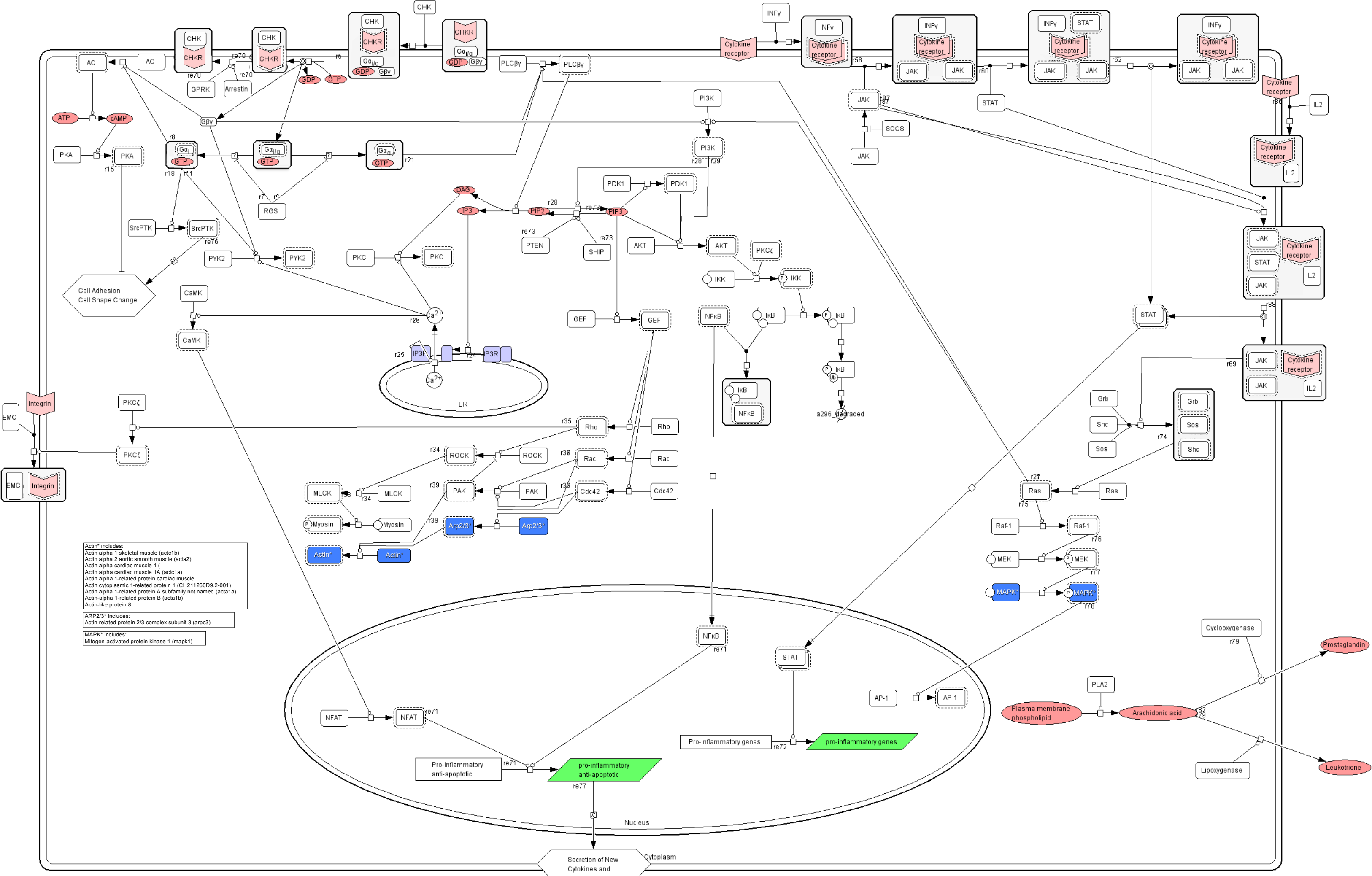


**Panel i.** Proteins up-regulated  $\geq 2$ -fold in poor quality zebrafish eggs, or unique to poor quality eggs, mapped to the Integrin signaling pathway (Panther pathway P00034) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by blue boxes with white text and are individually named in open boxes in the center with corresponding transcript names in parentheses. Dark blue boxes indicate mapped proteins from the Pooled Samples Experiment and light blue boxes indicate additional mapped proteins from the Multiple Samples Experiment. The mapped zebrafish proteins are actins (Actin\*), actin-related proteins (ARP2/3\*), actinins (Actinin\*), ADP-ribosylation factor-5 variants (ARF\*), dual-specificity mitogen-activated protein kinases (MAP2K\*), or mitogen-activated protein kinase 1 (MAPK1\*).



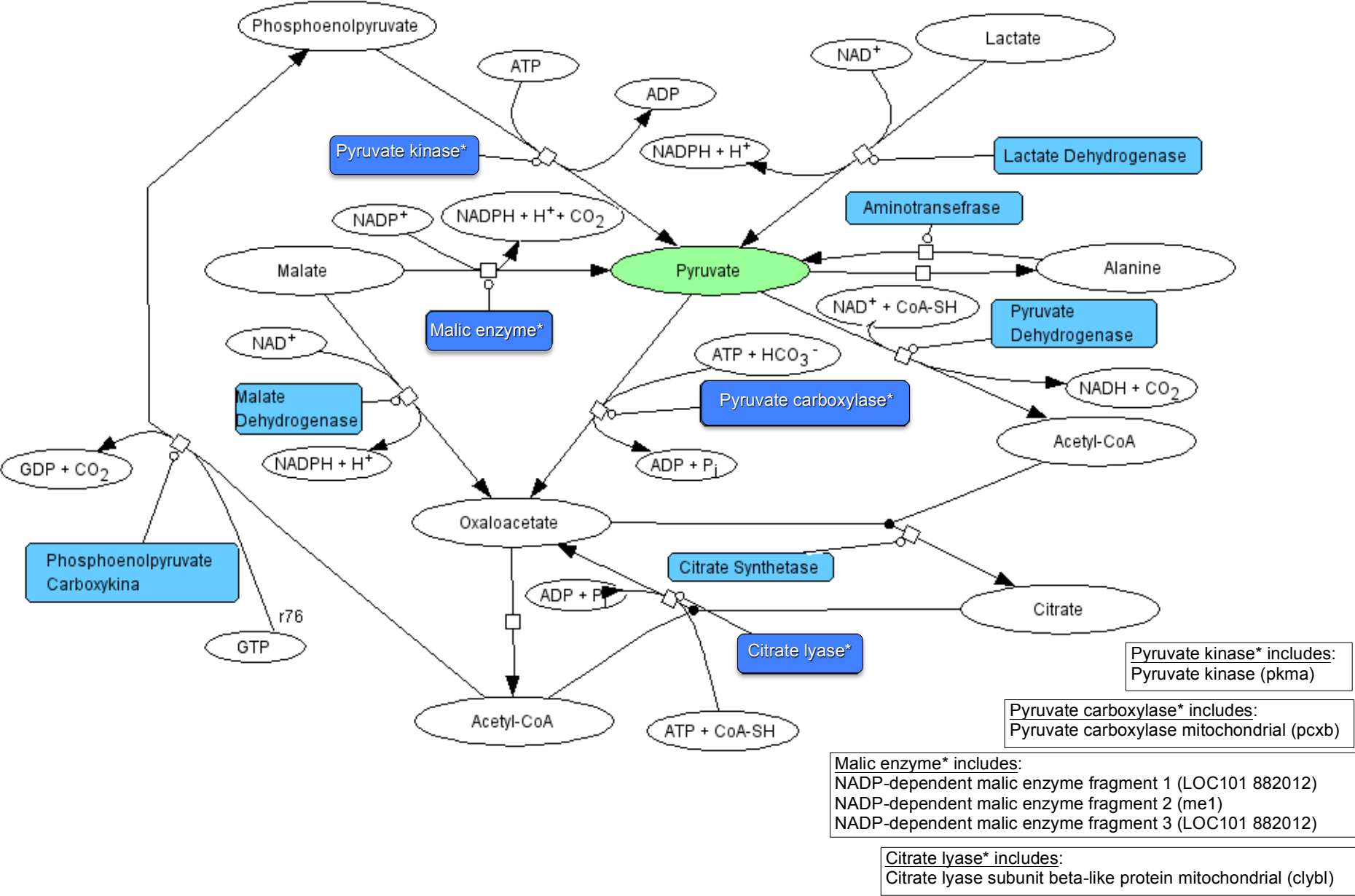
**Panel j.** Proteins up-regulated  $\geq 2$ -fold in poor quality zebrafish eggs, or unique to poor quality eggs, mapped to the Wnt signaling pathway (Panther pathway P00057) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by the blue boxes with white text and are individually named in open boxes on the left with corresponding transcript names in parentheses. The dark blue boxes indicate mapped proteins from the Pooled Samples Experiment and the light blue boxes indicate mapped proteins from the Multiple Samples Experiment. The mapped zebrafish proteins are cadherin-1-related protein (Cadherin\*), variants of casein kinase II (Casein kinase II\*), actins (Actin\*) or Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform (PPP\*).

Inflammation mediated by chemokine and cytokine signaling pathway



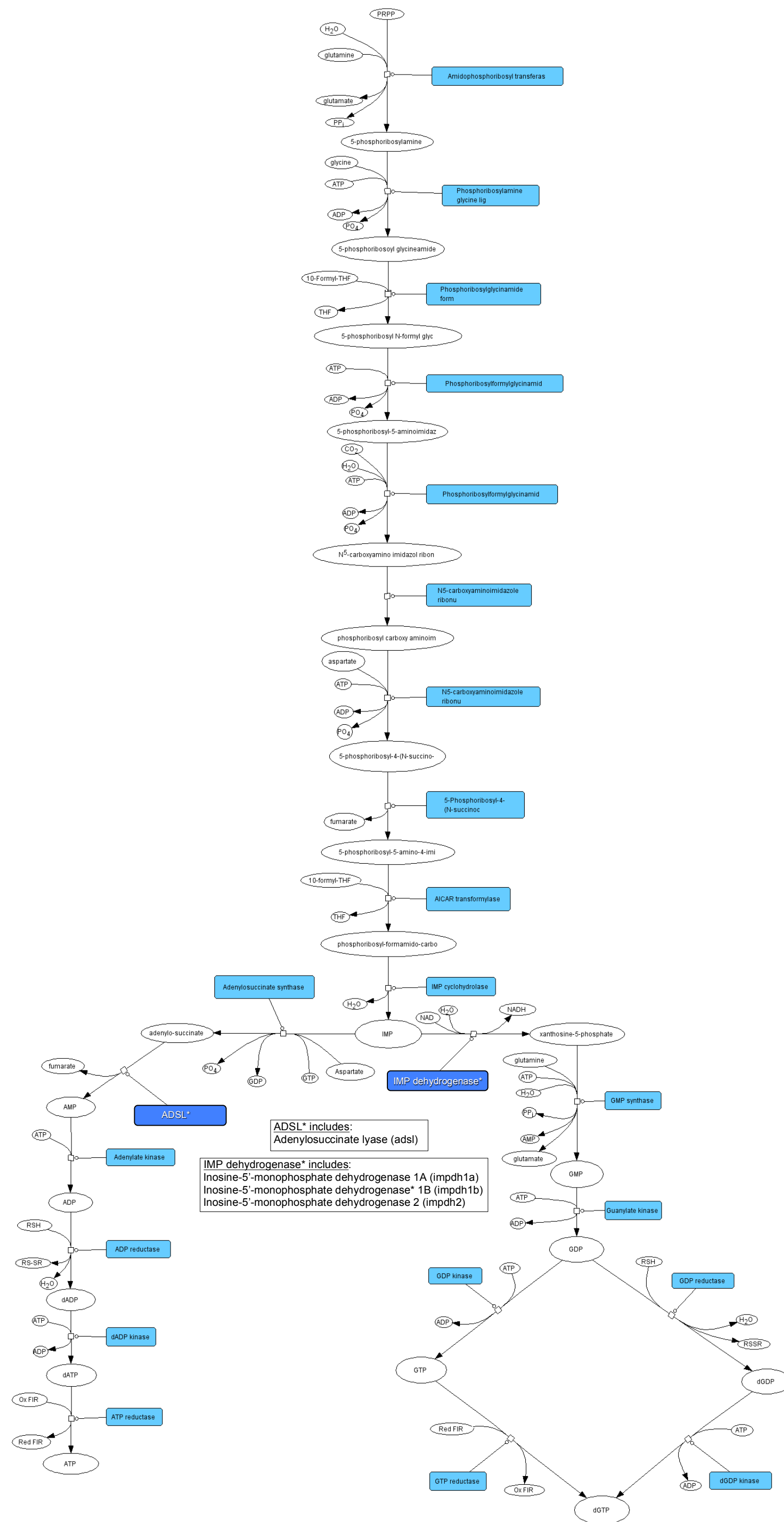
**Panel k.** Proteins up-regulated ≥ 2-fold in poor quality zebrafish eggs, or unique to poor quality eggs, mapped to Inflammation mediated by chemokine and cytokine signaling pathway (Panther pathway P00031) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by blue boxes with white text and are individually named in open boxes at the lower left with corresponding transcript names in parentheses. Dark blue boxes indicate mapped proteins from the Pooled Samples Experiment and the Multiple Samples Experiment. The mapped zebrafish proteins are actins (Actin\*), actin-related protein 2/3 complex subunit 3 (Arp2/3\*) and mitogen-activated protein kinase (MAPK\*)

**Pyruvate metabolism pathway**



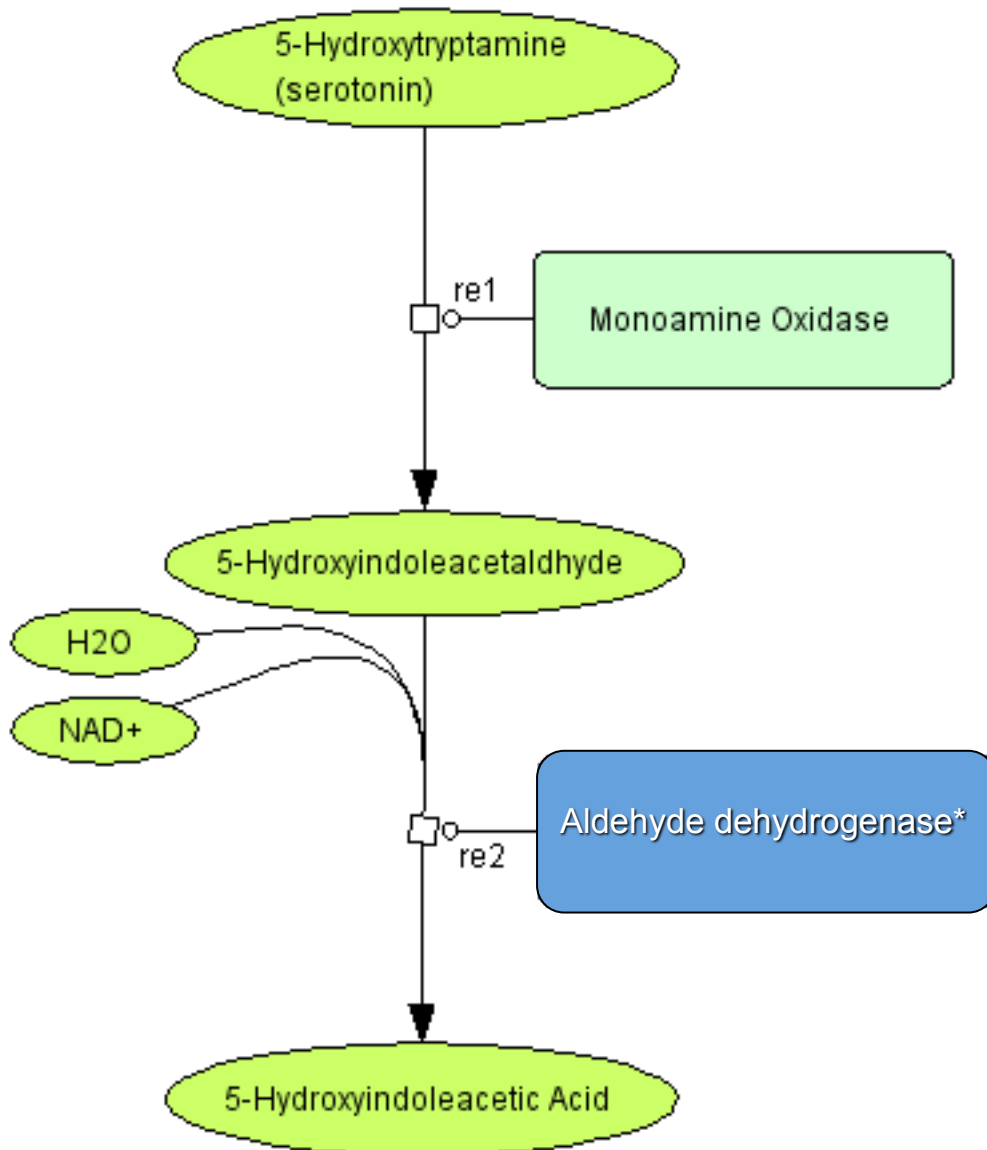
**Panel I.** Proteins up-regulated  $\geq 2$ -fold in good quality zebrafish eggs, or unique to good quality eggs, in the Pooled Samples Experiment mapped to the Pyruvate metabolism pathway (Panther pathway P02772) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by the dark blue boxes with white text and are individually named in open boxes on the lower right with corresponding transcript names in parentheses. The mapped zebrafish proteins are pyruvate kinase (Pyruvate kinase\*), Pyruvate carboxylase (Pyruvate carboxylase\*), malic enzyme fragments (Malic enzyme\*) and citrate lyase subunit beta-like protein (Citrate lyase).

### De novo purine biosynthesis



**Panel m.** Proteins upregulated  $\geq 2$ -fold in good quality zebrafish eggs, or unique to good quality eggs, in the Pooled Samples Experiment mapped to De novo purine biosynthesis (Panther pathway P02738) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by the dark blue boxes with white text and are individually named in open boxes in the lower center with corresponding transcript names in parentheses. The mapped zebrafish proteins are adenylosuccinate lyase (ADSL\*) and various forms of Inosine-5'-monophosphate dehydrogenase (IMP dehydrogenase\*)

## 5-Hydroxytryptamine degradation



Aldehyde dehydrogenase\* includes:  
Aldehyde dehydrogenase 2.1 (aldh2.1)  
Aldehyde dehydrogenase 2.2 (aldh2.2)  
Aldehyde dehydrogenase 2-like (aldh2l)

**Panel n.** Proteins up-regulated  $\geq 2$ -fold in good quality zebrafish eggs, or unique to good quality eggs, in the Pooled Samples Experiment or the Multiple Samples Experiment mapped to 5-Hydroxytryptamine degradation (Panther pathway P04372) in which they were found to be overrepresented (see **S3 Table**). The zebrafish proteins are indicated by the blue box with white text and are individually named in open boxes on the lower right with corresponding transcript names in parentheses. The mapped zebrafish proteins are all variants of aldehyde dehydrogenase (Aldehyde dehydrogenase\*).