Supporting Information

Global transcriptome profiling reveals molecular mechanisms of metal tolerance in a chronically exposed wild population of brown trout.

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Supplemental Experimental Section

Sample collection
Eggs and sperm were stripped from five female and two male brown trout obtained from a trout farm and mixed to facilitate fertilisation. Fertilised eggs were incubated at 8±1 °C on gravel beds in flow-through de-chlorinated tap water. Embryos were collected at 10 developmental stages identified according to [16], as follows: unfertilised eggs (0 days post fertilisation (dpf)), blastula (2 dpf), gastrula (6 dpf), early somitogenesis (10 dpf), late somitogenesis (14 dpf), early organogenesis (21 dpf), mid organogenesis (31 dpf), late organogenesis (41 dpf), hatched alevins (51 dpf) and swim-up fry just prior to commencement of feeding (70 dpf). All embryos were snap frozen in liquid nitrogen then stored at -80 °C prior to RNA extraction.

For collection of adult tissues, five brown trout from the River Hayle at Relubbus in Cornwall (N 50° 8.476774', W 5° 24.661446') and 10 brown trout from the control site, the relatively un-impacted River Teign at Gidleigh Park in Devon (N 50° 40.568816', W 3° 52.407188') were caught by electric fishing on the 19th September 2010 and 11th October 2010 respectively. The fish were humanely killed with a lethal dose of benzocaine (0.5 g L⁻¹; Sigma-Aldrich) and individual tissues (gill, liver, heart, spleen, stomach, intestine, gonad, head kidney, trunk kidney, eye, brain, pituitary, muscle, skin and caudal fin) were dissected and transported on dry ice to the University of Exeter where they were stored at -80 °C prior to RNA extraction or analysis of metal content.

RNA extraction, cDNA Library preparation and sequencing
Total RNA was extracted from all individual wild fish tissues and from individual embryos using TRI reagent (Sigma-Aldrich) according to the manufacturer’s instructions. The isopropanol precipitation step was modified by addition of a high salt solution (0.8 M sodium citrate, 1.2 M NaCl) to remove proteoglycon and polysaccharide contamination [1] during the embryo extractions. The concentration and purity of the resulting RNA was assessed using absorbance measurements at 260 nm and by monitoring the 230/260 and 260/280 nm absorbance ratios, using a NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies, Wilmington, USA). The integrity of the RNA was further assessed by gel electrophoresis (1% agarose). Equal amounts of total RNA from five embryos were pooled for each developmental stage, before these were combined into a single embryonic sample for sequencing. For the adult fish, equal amounts of total RNA from individual fish tissues were pooled into 12 samples for sequencing to form the following pools: gill, trunk kidney, liver and gut (consisting of stomach and intestine) from both Hayle and Teign fish; ovary and testis from Teign fish (from mature and maturing fish only); and mixed remaining tissues from the Hayle and from the Teign trout (Table S2). This strategy was adopted to allow for comparisons of transcript abundance between the Hayle and Teign fish for tissues hypothesised to be involved in metal tolerance (gill, gut, kidney and liver), and to maximise the likelihood of sequencing genes specific for each tissue. All RNA samples were treated with DNase and cleaned up on Qiagen RNaseasy MinElute columns, then quality and concentration were determined using an Agilent 2100 Bioanalyzer (Agilent Technologies, Inc., USA). All RNA input to library construction was of high quality with a RIN > 8. cDNA libraries were prepared from each
RNA sample using the Illumina TruSeq RNA Sample Preparation kit, and according to the manufacturer’s instructions. The single embryonic cDNA library was sequenced in one lane of the Illumina GAIIx Genome Analyzer generating 100 bp paired-end reads. All cDNA libraries constructed from the wild fish were multiplexed 12x and sequenced in another single lane, generating 76 bp paired-end reads. The average insert size of the multiplexed libraries was 153 bp, and of the embryonic library was 142 bp.

**Bioinformatics**

The FASTX-Toolkit ([http://hannonlab.cshl.edu/fastx_toolkit](http://hannonlab.cshl.edu/fastx_toolkit)) was used to clip remaining Illumina adapter sequences from the sequence reads and to trim the first 12 bp at the 5’ end to remove bias caused by random hexamer priming [2]. Quality trimming of the 3’ end of the reads using a sliding window at the first base with a quality Phred score of < 20 was performed ([http://wiki.bioinformatics.ucdavis.edu/index.php/Trim.slidingWindow.pl](http://wiki.bioinformatics.ucdavis.edu/index.php/Trim.slidingWindow.pl)) and reads shorter than 30 bp were discarded from the dataset. Paired reads were separated from orphan reads for each of the adult tissue and embryonic libraries, using the script from [https://github.com/lexnederbragt/denovo-assembly-tutorial/blob/master/scripts/pair_up_reads.py](https://github.com/lexnederbragt/denovo-assembly-tutorial/blob/master/scripts/pair_up_reads.py). All 'forward' reads (read 1) and 'reverse' reads (read 2) of the adult tissue libraries were pooled into 2 separate fastq files and interleaved using the shuffleSequences_fastq.pl script provided by the Velvet package in preparation for assembly. Similarly, interleaved fastq files were created for the embryonic tissue library.

The interleaved paired and orphan sequences for adult tissues and embryos were assembled **de novo** using Velvet (version 1.2.08; [3]) and Oases (version 0.2.08; [4]). An initial assembly was created using a k-mer of 73 and using the following parameters for Oases: ins_length 50 - ins_length_sd 200. Subsequently, assemblies were created using k-mers ranging from 65 to 41 (with steps of 8), such that the transcripts generated by the previous assembly were used as a – long input for the next assembly. The resulting transcripts of the final assembly (the brown trout transcriptome) were then annotated using Blast and all available Ensembl cDNA sequences for zebrafish (*Danio rerio*), medaka (*Oryzias latipes*), nile tilapia (*Oreochromis niloticus*), stickleback (*Gasterosteus aculeatus*), human and mouse (Release 69; October 2012), (non-human) vertebrate RefSeq RNA and protein sequences and EST sequences (Database of 2012-11-09). In addition, transcripts were also annotated using the Blast service at the Bioportal, University of Oslo, using the non-redundant nucleotides (nt) and proteins (nr) databases [5]. The resulting blast outputs were parsed using the blast2table.pl script from [ftp://ftp.genome.ou.edu/pub/programs/Blast2table](ftp://ftp.genome.ou.edu/pub/programs/Blast2table) keeping only the top hits with an e-value cut off < 1e^{-15}. Annotations were assigned in the following preferential order: zebrafish, medaka, nile tilapia, stickleback, human, mouse (Ensembl cDNA), RefSeq vertebrates RNA, nt, RefSeq vertebrates proteins, and nr. When no annotation could be found, the transcript ID was given.

Gene expression was determined in the gill, gut, kidney and liver of fish inhabiting the metal-contaminated river Hayle and the reference river Teign using RSEM [6]. To reduce the redundancy of the dataset, accession numbers of the various annotations were used as gene ID and the
transcript names generated by Oases were used as transcript IDs. Reads were mapped against the brown trout reference transcriptome (generated using the --no_polyA parameter) and using default settings. Subsequent analyses in RSEM were conducted using a selection of scripts provided as part of the Trinity assembly package (version r2012-10-05; [7], following the differential expression analysis pipeline described on http://trinityrnaseq.sourceforge.net/analysis/diff_expression_analysis.html. Statistical differences in gene expression levels between tissues of the 2 rivers were calculated using edgeR [8]. Genes were considered differentially expressed when FDR < 0.1 (Benjamini-Hochberg correction). Hierarchical clustering was performed on all differentially expressed genes (> 2-fold and FDR < 0.1) between Teign and Hayle brown trout using the analyze_diff_expr.pl script provided by Trinity [6]. Hierarchical trees were generated using the Euclidean distance metric and complete linkage clustering. A 4-way Venn diagram showing overlapping differentially-expressed genes was produced using VennDiagram [9] in R/Bioconductor.

All analyses were carried out on a local server running under the NEBC Bio-Linux 7 environment [10] unless stated otherwise.

RT-QPCR validation of gene expression profiles in Hayle and Teign fish

Validation of the quantification of gene expression in Teign and Hayle fish was conducted using real time quantitative PCR (RT-QPCR) for five transcripts (mtb, gpx1b, cat, slc40a1 and arpc3), in gill, gut, kidney and liver samples from all individual fish. Primers for each target gene were designed with Beacon Designer 3.0 software (Premier Biosoft International, Paulo Alto, CA) using the transcript sequences assembled during this project. Specificity of primer sets throughout the range of detection was confirmed by the observation of single amplification products of the expected size and Tm, and optimised by performing a standard curve for each primer pair as described by Filby and Tyler [11]. Over the detection range, the linear correlation ($R^2$) between the mean Ct and the logarithm of the cDNA dilution was $>0.99$ in each case, and efficiencies were between 1.943- 2.134. The sequences, PCR product sizes, annealing temperatures and PCR efficiencies for each primer pair are shown in Table S3. cDNA was synthesised according to manufacturer's instructions from 2 µg of total RNA treated with RQ1 DNase (Promega, Southampton, UK), using random hexamers (MWG-Biotech) and M-MLV reverse transcriptase (Promega). cDNA was diluted (1:2) then RT-QPCR was performed using an iCycler iQ Real-time Detection System (Bio-Rad Laboratories, Hercules, CA) with SYBR Green chemistry as described by Filby and Tyler [11]. A template-minus negative control was run in triplicate on each plate to verify the absence of cDNA contamination. Efficiency-corrected relative expression levels were determined by normalizing to the control gene, Actin-related protein 2/3 complex 3 (arp⁰3). To select an appropriate control gene, we examined our assembly to find transcripts where expression levels were high and consistent between Hayle and Teign fish for all tissues. A comparison between the expression ratios (Hayle/Teign) in the gill, gut, kidney and liver for arpc3 and other candidate control genes is presented in Table S3a.
References

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Table S1 - Metal concentrations in the river Hayle and river Teign. Mean values, and range of values, are presented from data collected at monthly intervals by the Environment Agency monitoring programme throughout the year between 1990-1996 and 2010-2012 for the river Hayle, and from 1991-2012 (zinc only) and 1991-1995 (all other metals) for the river Teign. The data contained in this table was kindly provided by the UK Environment Agency.

|       | River Hayle (Relubbus) |                     | River Teign (Gidleigh Park) |                     |
|-------|------------------------|---------------------|-----------------------------|---------------------|
|       | Total metal (µg/L)     | Filtered metal (µg/L) | Total metal (µg/L)           | Filtered metal (µg/L) |
| Zinc  | 638.9 (404-858)        | 599.2 (390-780)     | 10.4 (2-204)                | 4.7 (2-12)           |
| Copper| 42.3 (24-193)          | 34.9 (17-86.5)      | <1 (<1)                     | -                   |
| Iron  | 199.2 (60-2690)        | 80.5 (34-210)       | 172.0 (50-760)              | 128.9 (60-280)       |
| Arsenic| 8.4 (1.1-101)         | 4.5 (0.4-8)         | 1.2 (0.6-5.4)               | 1.0 (0.5-2.4)        |
| Cadmium| 1.4 (0.9-4)           | 1.3 (0.9-1.6)       | <0.2 (<0.2)                 | <0.2 (<0.2)          |
| Nickel| 27.1 (18-39)           | 25.8 (17.6-37.4)    | 1.0 (1)                     | 1.3 (1-2)            |
| Lead  | <2 (<1-12)             | <2 (<2)             | <1 (<1)                     | <1 (<1)              |
**Table S2** - Description of cDNA libraries sequenced. Mixed tissue samples from the Hayle and the Teign contained equal amounts of RNA from the heart, spleen, head kidney, eye, brain, pituitary, muscle, skin and caudal fin.

| Sample no. | Sample description | Lane no. | Read characteristics |
|------------|--------------------|----------|----------------------|
| 1          | Embryonic (10 developmental stages pooled) | 1        | 100 bp paired end    |
| 2          | Teign Mixed Tissue | 2        | 76 bp paired end (multiplexed) |
| 3          | Hayle Mixed Tissue | 2        | 76 bp paired end (multiplexed) |
| 4          | Hayle Gill         | 2        | 76 bp paired end (multiplexed) |
| 5          | Hayle Gut          | 2        | 76 bp paired end (multiplexed) |
| 6          | Hayle Kidney       | 2        | 76 bp paired end (multiplexed) |
| 7          | Hayle Liver        | 2        | 76 bp paired end (multiplexed) |
| 8          | Teign Gill         | 2        | 76 bp paired end (multiplexed) |
| 9          | Teign Gut          | 2        | 76 bp paired end (multiplexed) |
| 10         | Teign Kidney       | 2        | 76 bp paired end (multiplexed) |
| 11         | Teign Liver        | 2        | 76 bp paired end (multiplexed) |
| 12         | Teign Ovary        | 2        | 76 bp paired end (multiplexed) |
| 13         | Teign Testis       | 2        | 76 bp paired end (multiplexed) |
Table S3a – Fold changes in expression level quantified by RNA-seq of potential control genes for RT-QPCR analysis.

| Gene                                           | Fold change (Hayle/Teign) in expression | Gill  | Gut  | Kidney | Liver |
|------------------------------------------------|----------------------------------------|-------|------|--------|-------|
| Actin-related protein 2/3 complex 3            | arpc3                                  | 1.25  | 1.17 | 0.97   | 1.10  |
| Ribosomal protein L8                           | rpl8                                   | 0.92  | 0.61 | 0.49   | 0.77  |
| Ribosomal protein L7                           | rpl7                                   | 1.25  | 1.27 | 0.75   | 2.04  |
| Beta Actin                                     | bactin                                 | 1.25  | 1.18 | 0.72   | 1.41  |
| Glucose-6-phosphate dehydrogenase              | g6pdh                                  | 1.67  | 1.53 | 0.75   | 1.49  |
| Glyceraldehyde-3-phosphate dehydrogenase       | gapdh                                  | 0.58  | 0.95 | 1.75   | 0.61  |

Table S3b – Target genes, primers and assay details for RT-QPCR analysis.

| Target Gene          | Forward Primer (5'-3') | Reverse Primer (5'-3') | Product size (bp) | Ta (°C) | PCR efficiency |
|----------------------|------------------------|------------------------|-------------------|---------|----------------|
| Actin-related protein 2/3 complex 3            | arpc3                  | CCAGCAACAAGCAGGAAGAC  | ACGGTACACACGCTCAG | 83      | 58.5           | 96.2 %        |
| Ferroportin          | slc401a                | GGCACTAGAGCAGCAAGTCTC | GACAGGACAGCAGCAGC | 162     | 58.5           | 113.4 %       |
| Metallothionein b    | mtb                    | ACCAGTGTGAAAGCAAG      | GTACAGTCATAGGGAATG | 155     | 55.0           | 109.9 %       |
| Glutathione peroxidise 1b | gpx1b             | GCCAGTCACTTTCCCCAAAG | GAGAGCCTTTCAACGTTAT | 200     | 55.0           | 94.3 %        |
| Catalase             | cat                    | CGGCTCTCACCACTCAAG     | GTCTCGGATGGCGTAGTC | 148     | 57.0           | 102.9 %       |
Figure S1: Cluster diagrams displaying the concentration of each metal in individual fish from the river Hayle (h1-h5) and river Teign (t1-t10), illustrating the similarity of distribution profiles of metals in each tissue. Values given are log transformed metal concentrations (µg/g).
Table S4 - Summary statistics of raw sequencing reads, numbers of reads retained after adaptor removal and quality filtering and retained for input into transcriptome assembly as either paired reads or orphans. 1 and 2 refer to the forward and reverse reads in each paired-end sequence read.

| Sample              | No. raw reads | Adaptors removed | Quality Filtered | No. Paired reads | No. orphans |
|---------------------|---------------|------------------|------------------|------------------|-------------|
|                     | Read 1        | Read 2           | Read 1           | Read 2           | Read 1      | Read 2      |
| Hayle Gill          | 2,936,116     | 2,936,116        | 2,680,643        | 2,683,739        | 2,455,767   | 2,520,215   | 2,156,170   | 2,156,170   | 299,597    | 364,045    |
| Hayle Gut           | 3,198,880     | 3,198,880        | 2,912,539        | 2,916,540        | 2,659,209   | 2,724,901   | 2,321,001   | 2,321,001   | 338,208    | 403,900    |
| Hayle Kidney        | 3,587,826     | 3,587,826        | 3,272,885        | 3,276,952        | 2,996,962   | 3,090,315   | 2,637,910   | 2,637,910   | 359,052    | 452,405    |
| Hayle Liver         | 3,648,593     | 3,648,593        | 3,329,308        | 3,334,596        | 3,043,407   | 3,124,718   | 2,669,069   | 2,669,069   | 374,338    | 455,649    |
| Hayle Mixed Tissue  | 2,541,870     | 2,541,870        | 2,303,275        | 2,305,787        | 2,099,076   | 2,156,734   | 1,825,364   | 1,825,364   | 273,712    | 331,370    |
| Teign Gill          | 3,489,607     | 3,489,607        | 3,186,023        | 3,189,248        | 2,912,245   | 2,993,566   | 2,555,857   | 2,555,857   | 356,388    | 437,709    |
| Teign Gut           | 3,418,757     | 3,418,757        | 3,115,427        | 3,118,565        | 2,850,298   | 2,930,476   | 2,500,343   | 2,500,343   | 349,955    | 430,133    |
| Teign Kidney        | 3,147,358     | 3,147,358        | 2,875,181        | 2,877,401        | 2,637,264   | 2,710,844   | 2,321,788   | 2,321,788   | 315,476    | 389,056    |
| Teign Liver         | 3,855,726     | 3,855,726        | 3,523,064        | 3,527,418        | 3,215,926   | 3,300,338   | 2,818,972   | 2,818,972   | 396,954    | 481,366    |
| Teign Ovary         | 2,591,346     | 2,591,346        | 2,364,740        | 2,368,163        | 2,166,788   | 2,198,275   | 1,886,219   | 1,886,219   | 280,569    | 312,056    |
| Teign Testis        | 3,540,738     | 3,540,738        | 3,228,934        | 3,235,082        | 2,942,162   | 3,028,973   | 2,577,349   | 2,577,349   | 364,813    | 451,624    |
| Teign Mixed Tissue  | 3,415,701     | 3,415,701        | 3,099,156        | 3,106,756        | 2,820,832   | 2,907,199   | 2,460,718   | 2,460,718   | 360,114    | 446,481    |
| Total Adult Tissues | 39,372,518    | 39,372,518       | 35,891,175       | 35,940,247       | 32,799,936  | 33,686,554  | 28,730,760  | 28,730,760  | 4,069,176  | 4,955,794  |
| Embryonic           | 34,411,228    | 34,411,228       | 30,970,124       | 29,448,455       | 30,829,882  | 29,311,104  | 27,162,593  | 27,162,593  | 3,667,289  | 2,148,511  |
| TOTAL               | 73,783,746    | 73,783,746       | 66,861,299       | 65,388,702       | 63,629,818  | 62,997,658  | 55,893,353  | 55,893,353  | 7,736,465  | 7,104,305  |
**Table S5** - Number of transcripts in the final transcriptome assembly and relative expression levels for each tissue. Expression is presented as Fragments Per Kilobase of Exon Per Million Fragments Mapped (FPKM).

| Expression level (FPKM) | H Gill | T Gill | H Gut | T Gut | H Kidney | T Kidney | H Liver | T Liver |
|-------------------------|--------|--------|-------|-------|----------|----------|---------|---------|
| ≤ 1                     | 1194   | 1472   | 2825  | 2626  | 1874     | 1314     | 5348    | 4893    |
| 1-10                    | 30608  | 33783  | 27904 | 29047 | 34121    | 28273    | 24208   | 23809   |
| 10-100                  | 13587  | 13758  | 8790  | 8992  | 12834    | 13911    | 4431    | 4306    |
| 100-1000                | 1094   | 1068   | 953   | 978   | 1039     | 1122     | 603     | 656     |
| > 1000                  | 117    | 116    | 86    | 110   | 96       | 155      | 102     | 130     |
| **Total transcripts**   | 46600  | 50197  | 40558 | 41753 | 49964    | 44775    | 34693   | 33794   |
| **expressed**           |        |        |       |       |          |          |         |         |
| **Transcripts not**     | 50083  | 46486  | 56125 | 54930 | 46719    | 51908    | 61991   | 62889   |
| **expressed**           |        |        |       |       |          |          |         |         |
Table S6 - Comparison between the fold differences in expression levels for selected transcripts generated based on the global analysis (RNA-Seq) and on the individual gene quantification (RT-QPCR). Values presented are mean expression of transcripts for the Hayle population relative to Teign (Hayle; n=5, Teign; n=10). Fold differences in expression measured using RNA-Seq are in blue, and those obtained by RT-QPCR are in red. Asterisks indicate a significant difference in expression between the two populations.

| Gene  | Gill | Gut | Kidney | Liver |
|-------|------|-----|--------|-------|
| slc40a1 | 1.2 | 0.7 | 4.3 | 1.2 |
|       | 7.7 | 0.8 | 0.5 | 1.3 |
| mtb   | 8.2 * | 7.7 * | 2.2 | 5.6 * |
|       | 9.8 * | 5.7 * | 7.1 | 14.7 * |
| gpx1b | 2.5 | 1.3 | 0.48 | 1.6 |
|       | 0.8 | 9.1 | 0.8 | 1.5 |
| cat   | 1.1 | 1.2 | 0.4 | 0.9 |
|       | 0.2 | 1.2 | 1.2 | 0.2 |
Figure S2- Heatmaps illustrating changes in gene expression for all differentially expressed genes (> 2-fold and FDR < 0.1) between Teign and Hayle brown trout, in the four separate tissues. Hierarchical trees were generated using the Euclidean distance metric and complete linkage clustering.
Table S7- Gene Ontology Terms over-represented in the lists of differentially expressed genes between Hayle and Teign fish for each tissue. Values presented are the number and percentage of genes in the tissue-specific gene lists associated with each term and the P-values associated with this over-representation. This analysis was conducted using the Database for Annotation, Visualisation and Integrated Discovery (DAVID v6.7; [12]), using our whole brown trout transcriptome assembly as a background.

### GUT

| Category       | Term                                | Count | %   | P-Value | Bonferroni | Benjamini | FDR     | Fisher Exact |
|----------------|-------------------------------------|-------|-----|---------|------------|-----------|---------|             |
| GOTERM_BP_FAT  | Proteolysis                         | 11    | 7.10| 8.90E-06| 7.50E-04  | 7.50E-04  | 9.60E-03| 1.60E-06    |
| GOTERM_BP_FAT  | platelet activation                 | 2     | 1.30| 2.00E-02| 8.10E-01  | 5.70E-01  | 1.90E+01| 1.60E-04    |
| GOTERM_BP_FAT  | cell activation                     | 2     | 1.3 | 5.80E-02| 9.90E-01  | 8.10E-01  | 4.70E+01| 1.70E-03    |
| GOTERM_BP_FAT  | Coagulation                         | 2     | 1.3 | 6.50E-02| 1.00E+00  | 7.60E-01  | 5.20E+01| 2.10E-03    |
| GOTERM_BP_FAT  | Hemostasis                          | 2     | 1.3 | 6.50E-02| 1.00E+00  | 7.60E-01  | 5.20E+01| 2.10E-03    |
| GOTERM_BP_FAT  | regulation of body fluid levels     | 2     | 1.3 | 6.50E-02| 1.00E+00  | 7.60E-01  | 5.20E+01| 2.10E-03    |
| GOTERM_BP_FAT  | blood coagulation                   | 2     | 1.3 | 6.50E-02| 1.00E+00  | 7.60E-01  | 5.20E+01| 2.10E-03    |
| GOTERM_BP_FAT  | protein polymerization              | 2     | 1.3 | 9.50E-02| 1.00E+00  | 8.10E-01  | 6.60E+01| 4.60E-03    |
| GOTERM_CC_FAT  | extracellular space                 | 5     | 3.2 | 1.30E-05| 3.70E-04  | 3.70E-04  | 1.10E-02| 3.80E-07    |
| GOTERM_CC_FAT  | extracellular region                | 8     | 5.2 | 1.20E-04| 3.50E-03  | 1.70E-03  | 1.00E-01| 2.00E-05    |
| GOTERM_CC_FAT  | extracellular region part           | 5     | 3.2 | 1.10E-03| 3.00E-02  | 1.00E-02  | 8.90E-01| 1.00E-04    |
| GOTERM_CC_FAT  | fibrinogen complex                  | 2     | 1.3 | 8.20E-03| 2.10E-01  | 5.80E-02  | 6.70E+00| 1.80E-05    |
| GOTERM_MF_FAT  | serine hydrolase activity           | 8     | 5.2 | 4.30E-07| 3.30E-05  | 3.30E-05  | 4.60E-04| 2.50E-08    |
| GOTERM_MF_FAT  | serine-type peptidase activity      | 8     | 5.2 | 4.30E-07| 3.30E-05  | 3.30E-05  | 4.60E-04| 2.50E-08    |
| GOTERM_MF_FAT  | serine-type endopeptidase activity  | 7     | 4.5 | 1.90E-06| 1.50E-04  | 7.40E-05  | 2.00E-03| 1.00E-07    |
| GOTERM_MF_FAT  | peptidase activity, acting on L-amino acid peptides | 11 | 7.1 | 8.10E-06 | 6.30E-04  | 2.10E-04  | 8.60E-03 | 1.30E-06    |
| GOTERM_MF_FAT  | peptidase activity                  | 11    | 7.1 | 1.80E-05| 1.40E-03  | 3.40E-04  | 1.90E-02| 3.10E-06    |
| GOTERM_MF_FAT  | endopeptidase activity              | 8     | 5.2 | 1.10E-04| 8.50E-03  | 1.70E-03  | 1.20E-01| 1.50E-05    |
| GOTERM_MF_FAT  | carboxypeptidase activity           | 3     | 1.9 | 5.00E-03| 3.20E-01  | 6.20E-02  | 5.20E+00| 1.70E-04    |
| GOTERM_MF_FAT  | protein binding, bridging           | 2     | 1.3 | 2.40E-02| 8.50E-01  | 2.40E-01  | 2.30E+01| 2.40E-04    |
| GOTERM_MF_FAT  | metalloproteinase activity          | 3     | 1.9 | 3.80E-02| 9.50E-01  | 3.10E-01  | 3.40E+01| 3.90E-03    |

### KIDNEY

| Category       | Term                                | Count | %   | P-Value | Bonferroni | Benjamini | FDR     | Fisher Exact |
|----------------|-------------------------------------|-------|-----|---------|------------|-----------|---------|             |
| GOTERM_BP_ALL  | response to organic substance       | 4     | 3.3 | 3.50E-04| 8.20E-02  | 8.20E-02  | 4.50E-01| 1.20E-05    |
| GOTERM_BP_ALL  | response to estradiol stimulus      | 2     | 1.6 | 1.10E-02| 9.30E-01  | 7.40E-01  | 1.30E+01| 4.20E-05    |
| GOTERM_BP_ALL  | homeostatic process                 | 4     | 3.3 | 1.70E-02| 9.90E-01  | 7.60E-01  | 2.00E+01| 2.30E-03    |
| GOTERM_BP_ALL  | response to estrogen stimulus       | 2     | 1.6 | 1.80E-02| 9.90E-01  | 6.80E-01  | 2.10E+01| 1.40E-04    |
| GOTERM_BP_ALL  | chemical homeostasis                | 3     | 2.4 | 2.20E-02| 1.00E+00  | 6.60E-01  | 2.50E+01| 1.60E-03    |
| Category Term | Count | %   | P-Value | Bonferroni | Benjamini | FDR | Fisher Exact |
|---------------|-------|-----|---------|------------|-----------|-----|--------------|
| GOTERM_BP_ALL | response to hexose stimulus | 2   | 1.6     | 2.20E-02  | 1.00E+00  | 5.90E-01  | 2.50E+01  | 2.10E-04 |
| GOTERM_BP_ALL | response to carbohydrate stimulus | 2   | 1.6     | 2.20E-02  | 1.00E+00  | 5.90E-01  | 2.50E+01  | 2.10E-04 |
| GOTERM_BP_ALL | response to steroid hormone stimulus | 2   | 1.6     | 2.20E-02  | 1.00E+00  | 5.90E-01  | 2.50E+01  | 2.10E-04 |
| GOTERM_BP_ALL | response to glucose stimulus | 2   | 1.6     | 2.20E-02  | 1.00E+00  | 5.90E-01  | 2.50E+01  | 2.10E-04 |
| GOTERM_BP_ALL | response to monosaccharide stimulus | 2   | 1.6     | 2.20E-02  | 1.00E+00  | 5.90E-01  | 2.50E+01  | 2.10E-04 |
| GOTERM_BP_ALL | regulation of transcription, DNA-dependent | 10  | 8.1     | 2.60E-02  | 1.00E+00  | 6.00E-01  | 2.90E+01  | 1.10E-02 |
| GOTERM_BP_ALL | regulation of RNA metabolic process | 10  | 8.1     | 2.70E-02  | 1.00E+00  | 5.60E-01  | 3.00E+01  | 1.20E-02 |
| GOTERM_BP_ALL | regulation of macromolecule biosynthetic process | 11  | 8.9     | 3.80E-02  | 1.00E+00  | 6.50E-01  | 3.90E+01  | 1.90E-02 |
| GOTERM_BP_ALL | regulation of biosynthetic process | 11  | 8.9     | 3.90E-02  | 1.00E+00  | 6.20E-01  | 4.00E+01  | 1.90E-02 |
| GOTERM_BP_ALL | regulation of cellular biosynthetic process | 11  | 8.9     | 3.90E-02  | 1.00E+00  | 6.20E-01  | 4.00E+01  | 1.90E-02 |
| GOTERM_BP_ALL | response to chemical stimulus | 4   | 3.3     | 3.90E-02  | 1.00E+00  | 5.80E-01  | 4.00E+01  | 7.10E-03 |
| GOTERM_BP_ALL | response to hormone stimulus | 2   | 1.6     | 4.00E-02  | 1.00E+00  | 5.60E-01  | 4.10E+01  | 7.50E-04 |
| GOTERM_BP_ALL | glucose metabolic process | 3   | 2.4     | 4.20E-02  | 1.00E+00  | 5.50E-01  | 4.30E+01  | 4.50E-03 |
| GOTERM_BP_ALL | carboxylic acid metabolic process | 5   | 4.1     | 4.20E-02  | 1.00E+00  | 5.30E-01  | 4.30E+01  | 1.10E-02 |
| GOTERM_BP_ALL | oxoacid metabolic process | 5   | 4.1     | 4.20E-02  | 1.00E+00  | 5.30E-01  | 4.30E+01  | 1.10E-02 |
| GOTERM_BP_ALL | organic acid metabolic process | 5   | 4.1     | 4.40E-02  | 1.00E+00  | 5.20E-01  | 4.40E+01  | 1.20E-02 |
| GOTERM_BP_ALL | cellular ketone metabolic process | 5   | 4.1     | 4.50E-02  | 1.00E+00  | 5.10E-01  | 4.50E+01  | 1.20E-02 |
| GOTERM_BP_ALL | regulation of cellular metabolic process | 11  | 8.9     | 4.60E-02  | 1.00E+00  | 5.00E-01  | 4.60E+01  | 2.40E-02 |
| GOTERM_BP_ALL | response to endogenous stimulus | 2   | 1.6     | 4.70E-02  | 1.00E+00  | 4.80E-01  | 4.60E+01  | 1.10E-03 |
| GOTERM_MF_FAT | sequence-specific DNA binding | 10  | 8.1     | 3.50E-04  | 3.10E-02  | 3.10E-02  | 3.80E-01  | 8.20E-05 |
| GOTERM_MF_FAT | transcription factor activity | 10  | 8.1     | 7.10E-03  | 4.70E-01  | 2.80E-01  | 7.50E+00  | 2.50E-03 |
| GOTERM_MF_FAT | hexokinase activity | 2   | 1.6     | 1.90E-02  | 8.20E-01  | 4.30E-01  | 1.90E-01  | 1.50E-04 |
| GOTERM_MF_FAT | transcription regulator activity | 10  | 8.1     | 3.60E-02  | 9.80E-01  | 5.60E-01  | 3.30E+01  | 1.60E-02 |

**LIVER**

| Category Term | Count | %   | P-Value | Bonferroni | Benjamini | FDR | Fisher Exact |
|---------------|-------|-----|---------|------------|-----------|-----|--------------|
| GOTERM_BP_FAT | response to organic substance | 4   | 3.3     | 4.80E-04  | 7.70E-02  | 7.70E-02  | 5.80E-01  | 1.80E-05 |
| GOTERM_BP_FAT | response to estradiol stimulus | 2   | 1.6     | 1.20E-02  | 8.70E-01  | 6.40E-01  | 1.40E+01  | 5.20E-05 |
| GOTERM_BP_FAT | response to estrogen stimulus | 2   | 1.6     | 2.00E-02  | 9.70E-01  | 6.80E-01  | 2.20E+01  | 1.70E-04 |
| GOTERM_BP_FAT | homeostatic process | 4   | 3.3     | 2.30E-02  | 9.80E-01  | 6.20E-01  | 2.50E+01  | 3.50E-03 |
| GOTERM_BP_FAT | response to hexose stimulus | 2   | 1.6     | 2.40E-02  | 9.80E-01  | 5.60E-01  | 2.60E+01  | 2.60E-04 |
| GO TERM_BP_FAT                                                                 |   |   |   |   |
|-----------------------------------------------------------------------------|---|--|--|--|
| response to steroid hormone stimulus                                       | 2 | 1.6 | 2.40E-02 | 9.80E-01 | 5.60E-01 | 2.60E+01 | 2.60E-04 |
| response to glucose stimulus                                               | 2 | 1.6 | 2.40E-02 | 9.80E-01 | 5.60E-01 | 2.60E+01 | 2.60E-04 |
| response to monosaccharide stimulus                                        | 2 | 1.6 | 2.40E-02 | 9.80E-01 | 5.60E-01 | 2.60E+01 | 2.60E-04 |
| response to carbohydrate stimulus                                          | 2 | 1.6 | 2.40E-02 | 9.80E-01 | 5.60E-01 | 2.60E+01 | 2.60E-04 |
| chemical homeostasis                                                        | 3 | 2.4 | 2.60E-02 | 9.90E-01 | 5.30E-01 | 2.80E+01 | 2.20E-03 |
| response to hormone stimulus                                               | 2 | 1.6 | 4.40E-02 | 1.00E+00 | 6.60E-01 | 4.20E+01 | 9.40E-04 |
| regulation of transcription, DNA-dependent                                 | 10| 8.1 | 4.80E-02 | 1.00E+00 | 6.40E-01 | 4.50E+01 | 2.30E-02 |
| regulation of RNA metabolic process                                        | 10| 8.1 | 4.90E-02 | 1.00E+00 | 6.10E-01 | 4.60E+01 | 2.40E-02 |
| glucose metabolic process                                                  | 3 | 2.4 | 5.10E-02 | 1.00E+00 | 5.80E-01 | 4.70E+01 | 6.10E-03 |
| response to endogenous stimulus                                            | 2 | 1.6 | 5.20E-02 | 1.00E+00 | 5.60E-01 | 4.80E+01 | 1.30E-03 |
| carboxylic acid biosynthetic process                                       | 3 | 2.4 | 7.20E-02 | 1.00E+00 | 6.50E-01 | 6.00E+01 | 1.00E-02 |
| organic acid biosynthetic process                                          | 3 | 2.4 | 7.30E-02 | 1.00E+00 | 6.20E-01 | 6.00E+01 | 1.10E-02 |
| hexose metabolic process                                                   | 3 | 2.4 | 7.90E-02 | 1.00E+00 | 6.30E-01 | 6.30E+01 | 1.20E-02 |
| monosaccharide metabolic process                                           | 3 | 2.4 | 9.50E-02 | 1.00E+00 | 6.70E-01 | 7.00E+01 | 1.60E-02 |
| sequence-specific DNA binding                                              | 10| 8.1 | 3.50E-04 | 3.10E-02 | 3.10E-02 | 3.80E-01 | 8.20E-05 |
| transcription factor activity                                              | 10| 8.1 | 7.10E-03 | 4.70E-01 | 2.80E-01 | 7.50E+00 | 2.50E-03 |
| hexokinase activity                                                        | 2 | 1.6 | 1.90E-02 | 8.20E-01 | 4.30E-01 | 1.90E+01 | 1.50E-04 |
| transcription regulator activity                                           | 10| 8.1 | 3.60E-02 | 9.60E-01 | 5.60E-01 | 3.30E+01 | 1.60E-02 |
| carbohydrate kinase activity                                               | 2 | 1.6 | 7.30E-02 | 1.00E+00 | 7.50E-01 | 5.60E+01 | 2.70E-03 |
| oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor | 2 | 1.6 | 9.40E-02 | 1.00E+00 | 7.70E-01 | 6.60E+01 | 4.60E-03 |
| NADH dehydrogenase (quinone) activity                                       | 2 | 1.6 | 9.40E-02 | 1.00E+00 | 7.70E-01 | 6.60E+01 | 4.60E-03 |
Table S8- List of differentially expressed genes generated using EdgeR including FDR values <0.1 and fold changes (FC) for each tissue. Significantly up-regulated genes in the Hayle fish compared to the Teign fish are highlighted in red and significantly down-regulated genes are highlighted in green. Where no expression was calculated for a transcript in one sample, direction of change is indicated by ‘up’ or ‘down’.

| GeneID          | Symbol/Accession | Description                                      | Database          | GILL FDR | GILL FC | GUT FDR | GUT FC | KIDNEY FDR | KIDNEY FC | LIVER FDR | LIVER FC |
|-----------------|------------------|--------------------------------------------------|-------------------|----------|---------|---------|--------|------------|-----------|-----------|----------|
| ENSGACG00000003077 | abhd12b (2 of 2) | abhydrolase domain containing 12B                | Ensembl_stickleback | -        | -1.4    | -1.5    | 4.41E-02| 6.4        | -1.4      | -1.1      |
| ENSGACG00000016406 | ab1 (1 of 2)    | abl-interactor 1                                 | Ensembl_stickleback | -        | 0.0     | 4.41E-02| down   | -1.4       | down      | down      |
| ENSGACG00000020048 | ascII           | achaete-scute complex homolog 1 (Drosophila)     | Ensembl_stickleback | -        | -1.7    | 1.77E-03| down   | down       | down      | down      |
| ENSGACG00000007368 | arpc5           | actin related protein 2/3 complex, subunit 5, 16kDa | Ensembl_stickleback | -        | 1.1     | -1.8    | 8.67E-02| -6.9       | -down     | down      |
| ENSGACG00000012675 | actr10          | actin-related protein 10 homolog (S. cerevisiae) | Ensembl_stickleback | -        | up      | down   | 5.65E-02| down       | down      | down      |
| ENSGACG00000014650 | acot11 (1 of 2) | acyl-CoA thioesterase 11                         | Ensembl_stickleback | -        | -1.7    | up      | 3.02E-02| -1.4       | up         | -1.4      |
| ENSGACG00000006135 | adam10          | ADAM metalloproteinase domain 10                 | Ensembl_stickleback | -        | 4.0     | -1.5    | 2.72E-02| -7.7       | -1.0       | -2.2      |
| ENSGACG00000015076 | adams1t         | ADAM metalloproteinase with thrombospondin type 1 motif, 1 | Ensembl_stickleback | -        | -1.5    | -5.2    | 4.76E-02| 9.9        | 2.2        |
| ENSORLG00000006708 | ak1              | adenylate kinase 1                               | Ensembl_medaka     | -        | 1.8     | -8.3    | 3.11E-02| -24.3      | up         | -24.3     |
| ENSDARG00000042382 | arf4 (2 of 3)   | ADP-ribosylation factor 4                        | Ensembl_zebrafish  | 4.69E-02 | down    | down   | -1.6    | up         | -1.6       | up        |
| S453305     | AF141606.1      | AF141606 Salmo salar clone 12(B)                | nt                | down     | - up    | - 2.9  | 7.14E-03| -11.4      | - 2.8      | -1.1      |
| 14581944    | AF256852.1      | AF256852 Salmo salar clone BHMS395              | nt                | down     | up      | - 2.9  | 7.14E-03| -11.4      | - 2.8      | -1.1      |
| 13625997    | AAK35224.1      | AF367368_B yolk ferritin                        | nr                | up       | - 0.0  | - 0.0  | - 0.0   | - 0.0      | - 0.0      | - 0.0     |
| ENSORLG00000017577 | agps           | alkyglycerone phosphate synthase                 | Ensembl_medaka     | -        | -2.2    | 1.27E-03| down   | -2.4       | up         | -2.4      |
| ENSGACG00000013328 | alyref          | Aly/REF export factor                           | Ensembl_stickleback | -        | 1.4     | - 1.7  | 1.59E-02| 10.5       | -10.5      | -10.5     |
| AM402664    | emb|AM402664.1      | AM402664 Salmo salar liver Parr Salmo salar cDNA clone liv_al_L3E5, mRNA sequence. | EST_others | 1.0     | 3.54E-02| -6.9    | - 0.0   | - 1.4      | AM402664   | AM402664  |
| ENSGACG0000000493 | npepl1          | aminopeptidase-like 1                           | Ensembl_stickleback | -        | 1.7     | 6.65E-02| down   | -2.8       | -2.8       | -2.8      |
| ENSDARG00000013856 | amy2a           | amylase, alpha 2A; pancreatic                    | Ensembl_zebrafish  | -        | 0.0     | 2.58E-06| -24.0   | -24.0      | -2.8       | -2.8      |
| ENSGACG00000013115 | apolp2          | amyloid beta (A4) precursor-like protein 2       | Ensembl_stickleback | -        | down    | down   | 6.99E-02| down       | down       | down      |
| ENSGACG00000018367 | anxa6           | annexin A6                                      | Ensembl_stickleback | -        | 0.0     | 2.51E-04| down   | 1.57E-03   | down       | down      |
| ENSDARG00000070480 | agr2            | anterior gradient homolog 2 (Xenopus laevis)     | Ensembl_zebrafish  | -        | 3.3     | -1.1   | 9.43E-02| 5.5        | -2.8       | -2.8      |
| ENSDARG00000053279 | apln            | apelin                                          | Ensembl_zebrafish  | -        | -2.5    | 0.0    | 8.78E-02| 17.3       | -1.1       | -1.1      |
| Gene ID            | Gene Name                  | Organism                          | accession       | FPKM  | RPKM   | log2 fold change | P-value |
|-------------------|----------------------------|-----------------------------------|----------------|-------|--------|-----------------|---------|
| ENSORLG00000012653| apob (6 of 6)              | apolipoprotein B (including ApoB) antigen in medaka | Ensembl_medaka | -1.3  | -12.3  | -5.7            | -1.7    |
| ENSGACG00000012729| apoo (2 of 2)              | apolipoprotein O in stickleback   | Ensembl_stickleback | 1.1   | -1.4   | 3.22E-03        | -8.7    |
| ENSORLG00000017624| apq1                       | aquaporin 1 (Colton blood group)  | Ensembl_medaka | -1.8  | - down  | 8.79E-02        | -5.0    |
| ENSDARG00000007086| apq10a                     | aquaporin 10a in stickleback      | Ensembl_stickleback | up    | 3.50E-05| -24.9           | -2.2    |
| ENSGACG00000012346| arg2                       | arginase, type II in stickleback  | Ensembl_stickleback | 7.49E-12| down   | 6.21E-08        | 3.52E-10 |
| 388815820         | JQ764761.1                 | Arion lusitanicus hypothetical protein mRNA, complete cds | nt             | 0.0   | up     | 4.98E-05        | -         |
| 188529830         | EU541926.1                 | Arion rufus isolate FR1.01 16S ribosomal RNA gene, partial sequence; mitochondrial | nt             | up    | 3.77E-12| 307.9           | 5.87E-02 |
| ENSGACG00000002986| armc1 (1 of 2)             | armadillo repeat containing 1 in stickleback | Ensembl_stickleback | -     | 4.8    | 3.02E-02        | -1.9    |
| ENSGACG00000019091| asnal1                     | asnA arsenite transporter, ATP-binding, homolog 1 (bacterial) | Ensembl_stickleback | -145.0| up     | 4.67E-03        | -3.8    |
| ENSGACG00000007981| aspg                       | asparaginase homolog (S. cerevisiae) in stickleback | Ensembl_stickleback | -     | -3.0   | 6.99E-02        | -1.2    |
| ENSGACG00000007419| aq12                       | ATP-binding cassette, sub-family C (CFTR/MRP), member 2 | Ensembl_stickleback | 0.0   | down   | - down          | 5.91E-02 |
| 66471773          | AJ971743.1                 | Baetis harrisoni partial mitochondrial 16S rRNA gene for 16S ribosomal RNA, strain BMNH 704090 | nt             | down  | 5.76E-04| -13.8           | -1.4    |
| ENSGACG00000015604| bcl7a                      | B-cell CLL/lymphoma 7A in stickleback | Ensembl_stickleback | 3.75E-02| up     | 2.1             | -1.1    |
| ENSGACG00000042833| bcl21l1 (1 of 2)           | BCL2-like 1 in stickleback        | Ensembl_stickleback | -     | down   | 1.22E-03        | -1.2    |
| ENSGACG00000016888| bmper                      | BMP binding endothelial regulator in stickleback | Ensembl_stickleback | -     | -2.1   | - down          | 1.57E-03 |
| ENSGACG00000012929| bre                        | brain and reproductive organ-expressed (TNFRSF1A modulator) in stickleback | Ensembl_stickleback | 0.0   | 0.0    | 5.65E-02        | up      |
| ENSDARG00000045568| bcat1                      | branched chain aminotransferase 1, lysosomal in zebrafish | Ensembl_stickleback | 1.6   | up     | 1.5             | 1.46E-04 |
| ENSORLG0000015803| brox                       | BRO1 domain and CAAX motif containing in stickleback | Ensembl_stickleback | 3.35E-03| up     | -1.2            | -2.9    |
| ENSGACG00000041588| bzz1a                      | bromodomain adjacent to zinc finger domain, 1A in medaka | Ensembl_medaka | 1.2   | -1.2   | 2.4             | 3.37E-15 |
| ENSGACG00000057344| bzz2b (4 of 4)             | bromodomain adjacent to zinc finger domain, 2B in stickleback | Ensembl_stickleback | down  | 0.0    | 6.04E-02        | -13.7   |
| ENSGACG00000010106| brrd4                      | bromodomain containing 4 in stickleback | Ensembl_stickleback | -     | -3.4   | 1.09E-03        | -24.1   |
| 213514654         | NP_001134905.1             | Butyrophilin subfamily 2 member A2 in stickleback | Refseq_proteins | 1.5   | -1.4   | 9.82E-02        | 5.2     |
| ENSGACG00000057534| celhr3                     | cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila) in stickleback | Ensembl_stickleback | -2.2  | 9.39E-03| down            | 6.99E-02 |
| ENSGACG00000012602| capc1 (2 of 2)             | calcium binding protein 1 in stickleback | Ensembl_stickleback | 7.32E-02| down  | 1.7             | -1.5    |
| ENSDARG00000019990| capa1                      | calcium binding protein 1a in zebrafish | Ensembl_zebrafish | 2.4   | -1.1   | 8.79E-02        | up      |
| ENSORLG00000010644| cald1 (1 of 2)             | caldesmon 1 in medaka              | Ensembl_medaka | -4.2  | 1.77E-03| -14.4           | -2.9    |
| ENSGACG00000012384| cama1 (1 of 2)             | calmodulin binding transcription activator 1 in stickleback | Ensembl_stickleback | 1.0   | -2.0   | -2.4            | 2.28E-03 |

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| Gene ID          | Description                                      | Ensembl          | Direction | Adj P-Value | Log2 Fold Change |
|------------------|--------------------------------------------------|------------------|-----------|-------------|-----------------|
| ENSGACG00000016957 | calml4                                           | Ensembl_stickleback | down     | 1.5          | 5.64E-02        |
| ENSGACG00000013281 | capn5 (2 of 2)                                   | Ensembl_stickleback | down     | -0.0         | 1.48E-02        |
| ENSDARG00000093937 | cnn1                                             | Ensembl_zebrafish | down     | -5.3         | 5.31E-02        |
| ENSGACG00000014122 | casq1 (2 of 2)                                   | Ensembl_stickleback | down     | -1.3         | 1.42E-03        |
| ENSDARG00000054456 | clip3                                            | Ensembl_zebrafish | down     | 2.1          | 7.77E-02        |
| ENSDARG00000056499 | ca6                                              | Ensembl_zebrafish | -         | -1.3         | 4.66E-03        |
| ENSORLGV00000014439 | cel (2 of 3)                                     | Ensembl_medaka    | down     | -33.0        | 0.0             |
| ENSDARG00000029822 | cel2                                             | Ensembl_zebrafish | -         | -1.7         | 6.6             |
| ENSDARG00000021339 | cpa5                                             | Ensembl_zebrafish | down     | -35.6        | 0.0             |
| ENSGACG00000017379 | clic2                                            | Ensembl_stickleback | down     | -1.0         | 1.96E-02        |
| ENSDARG00000002365 | cers5                                            | Ensembl_zebrafish | down     | -1.2         | 9.95E-02        |
| ENSGACG000000045442 | cbp1                                             | Ensembl_zebrafish | up       | 1.19E-02      | 6.5             |
| ENSGACG00000007280 | clic4                                            | Ensembl_stickleback | down     | -0.0         | 0.0             |
| ENSGACG00000004855 | cbx7 (1 of 2)                                    | Ensembl_stickleback | up       | 1.1         | 13.6            |
| ENSG00000166002  | c11orf75                                         | Ensembl_human     | down     | -1.3         | 1.95E-04        |
| Gene ID               | Description                                      | Species          | log2 Fold Change | p-value   | Expression   |
|----------------------|--------------------------------------------------|------------------|-----------------|-----------|-------------|
| ENSORLG00000001844   | c17orf67                                        | Ensembl_medaka   | -3.6            | 0.4       | down        |
| ENSORLG00000014223   | c4orf33                                         | Ensembl_medaka   | -2.1            | 0.1       | down        |
| ENSONIG00000002851   | c9orf16                                         | Ensembl_nile_tilapia | -2.1           | 0.0       | down        |
| ENSORLG00000004586   | ctrc (2 of 2)                                   | Ensembl_medaka   | -2.1            | 0.0       | down        |
| ENSDARG00000006852   | celsa (2 of 2)                                  | Ensembl_medaka   | -2.1            | 0.0       | down        |
| ENSORLG00000006922   | celsa (2 of 2)                                  | Ensembl_medaka   | -1.2            | 0.1       | up          |
| ENSDARG000000090428  | ctrb1                                           | Ensembl_medaka   | -1.2            | 0.0       | down        |
| ENSGACG000000013999  | f5                                              | Ensembl_medaka   | -0.9            | 0.2       | down        |
| ENSACG00000014046    | cc2d2a (1 of 2)                                 | Ensembl_medaka   | 2.1             | 0.0       | up          |
| ENSDARG00000028524   | col5a3b                                         | Ensembl_medaka   | -0.5            | 0.5       | up          |
| ENSGACG00000011303   | coro7                                           | Ensembl_medaka   | -1.4            | 0.1       | down        |
| ENSORLG00000001844   | c17orf67                                        | Ensembl_medaka   | -3.6            | 0.4       | down        |
| ENSORLG00000014223   | c4orf33                                         | Ensembl_medaka   | -2.1            | 0.1       | down        |
| ENSONIG00000002851   | c9orf16                                         | Ensembl_nile_tilapia | -2.1           | 0.0       | down        |
| ENSORLG00000004586   | ctrc (2 of 2)                                   | Ensembl_medaka   | -2.1            | 0.0       | down        |
| ENSDARG00000006852   | celsa (2 of 2)                                  | Ensembl_medaka   | -2.1            | 0.0       | down        |
| ENSORLG00000006922   | celsa (2 of 2)                                  | Ensembl_medaka   | -1.2            | 0.1       | up          |
| ENSDARG000000090428  | ctrb1                                           | Ensembl_medaka   | -1.2            | 0.0       | down        |
| ENSGACG000000013999  | f5                                              | Ensembl_medaka   | -0.9            | 0.2       | down        |
| ENSACG00000014046    | cc2d2a (1 of 2)                                 | Ensembl_medaka   | 2.1             | 0.0       | up          |
| ENSDARG00000028524   | col5a3b                                         | Ensembl_medaka   | -0.5            | 0.5       | up          |
| ENSGACG00000011303   | coro7                                           | Ensembl_medaka   | -1.4            | 0.1       | down        |
| CR371595              | emb|CR371595.2                                      | CR371595 AGENAE Rainbow trout normalized testis library (tcbl) Oncorhynchus mykiss cDNA clone tcbl0031.o.10 5', mRNA sequence. | EST_others | up | up |
| CR37403               | emb|CR37403.2                                       | CR37403 AGENAE Rainbow trout normalized testis library (tcbl) Oncorhynchus mykiss cDNA clone tcbl0023.m.23 5', mRNA sequence. | EST_others | up | up |
| ENSONIG00000002925    | crebsf                                          | Ensembl_nile_tilapia | 9.89E-02       | 0.1       | up          |
| 113671701             | NP_001038787.1                                  | Crebsf homolog 3a precursor | Refseq_proteins | 1.94E-02 | up |
| ENSGACG00000006821    | ctdsl2 (1 of 2)                                 | Ensembl_stickleback | -1.4            | 0.1       | down        |
| CU069447              | emb|CU069447.1                                      | CU069447 AGENAE Rainbow trout multi-tissues library (tcce) Oncorhynchus mykiss cDNA clone tcay0022.o.06 3', mRNA sequence. | EST_others | 4.78E-02 | down |
| ENSGACG00000008425    | cuedc2                                          | Ensembl_stickleback | 1.11E-07        | 0.0       | down        |
| ENSONIG00000003295    | cdk18                                           | Ensembl_nile_tilapia | -2.1            | 0.0       | down        |
| 375196821             | JN739111.1                                      | Cyclin-dependent kinase 18 | nt | -1.8 | down |
| ENSGACG00000009382    | cth                                             | Ensembl_stickleback | -5.9            | 0.1       | down        |
| Gene Accession         | Gene Name     | Description                                                                 | Species       | ENSEMBL         | Gene Expression | Fold Change | p-Value  |
|------------------------|---------------|------------------------------------------------------------------------------|---------------|----------------|-----------------|-------------|----------|
| ENSONIG000000001633    | cox4i2        | Cytochrome oxidase subunit IV isoform 2 (lung)                              | Ensembl Nile tilapia | 9.61E-03       | down            | -2.1        | 1.8      |
| ENSONIG00000001074     | cyp46a1       | Cytochrome P450, family 46, subfamily A, polypeptide 1                       | Ensembl Nile tilapia | 4.68E-03       | up              | 2.8         | 5.78E-03 |
| ENSGACG0000017414      | cyp8b1        | Cytochrome P450, family 8, subfamily B, polypeptide 1                       | Ensembl Stickleback | -3.1           | -0.0            | up          | 8.31E-05 |
| ENSDARG00000053068     | cyp8b1        | Cytochrome P450, family 8, subfamily B, polypeptide 1                       | Ensembl Zebras | 0.0            | 1.87E-02        | -1.1        | -1.2     |
| ENSGACG0000011632      | cyth3 (1 of 2)| Cytohesin 3                                                                  | Ensembl Stickleback | -4.0           | -4.4            | 6.86E-02    | -3.1     |
| ENSGACG0000008861      | dao           | D-amino-acid oxidase                                                         | Ensembl Stickleback | 0.0            | 9.01E-02        | down        | down     |
| 41055872               | NM_200993.1   | Danio rerio zgc:55733 (zgc:55733), mRNA Refseq Genes                        | Ensembl Genes  | -3.2           | -1.4            | -1.5        | 2.11E-07 |
| ENSGACG0000016060      | ddx21         | DEAD (Asp-Glu-Ala-Asp) box helicase 21                                      | Ensembl Stickleback | -16.6          | -3.8            | -1.9        | 1.37E-03 |
| ENSGACG0000010201      | dkk2 (2 of 2)| Death-associated protein kinase 2                                            | Ensembl Stickleback | 3.13E-08       | down            | -0.0        | down     |
| ENSGACG0000001844      | doxx          | Death-domain associated protein                                             | Ensembl Stickleback | 2.42E-03       | down            | -2.1        | -1.8     |
| ENSGACG00000018923     | dock4         | Dedicator of cytokinesis 4                                                   | Ensembl Stickleback | 1.4            | 1.3             | 1.1         | 6.43E-04 |
| ENSGACG0000002377      | dhrs7c (2 of 2)| Dehydrogenase/reductase (SDR family) member 7C                              | Ensembl Stickleback | -3.8           | 1.4             | 1.3         | 1.4      |
| ENSGACG00000005878     | dnak1        | Deoxyribonuclease 1                                                          | Ensembl Stickleback | 0.00           | 1.26E-07        | down        | down     |
| ENSGACG0000015594      | ddal1 (2 of 2)| DET1 and DDB1 associated 1                                                    | Ensembl Stickleback | -8.0           | -1.8            | 1.28E-02    | down     |
| ENSGACG0000018166      | dpyl2 (1 of 2)| Dihydropyrimidinase-like 2                                                  | Ensembl Stickleback | -6.8           | 6.40E-02        | 4.39E-02    | 30.3     |
| ENSGACG0000006240      | dip2a         | DIP2 disco-interacting protein 2 homolog A (Drosophila)                     | Ensembl Stickleback | -5.3           | -3.2            | 1.22E-03    | 5.14E-04 |
| ENSGACG0000000671      | dip2b (2 of 2)| DIP2 disco-interacting protein 2 homolog B (Drosophila)                    | Ensembl Stickleback | -2.2           | -1.6            | -3.1        | 2.80E-03 |
| 19171735               | AF382036.1    | Discocytote sagittata 28S large subunit ribosomal RNA, partial sequence     | nt            | 8.88E-02       | 27.2            | up          | 1.4      |
| ENSDARG00000062177     | dcbld2       | Discoidin, CUB and LCCL domain containing 2                                | Ensembl Zebras | 4.69E-02       | up              | 4.49E-02    | up       |
| ENSORLG00000011807     | dcbld2       | Discoidin, CUB and LCCL domain containing 2                                | Ensembl Medaka | 6.54E-03       | down            | -1.2        | 3.65E-02 |
| ENSDARG000000164110    | dncj3         | Dnas (Hsp40) homolog, subfamily C member 3                                 | Ensembl Zebras | 2.7            | 2.6             | 1.5         | 1.13E-02 |
| ENSGACG00000003355     | dusp22 (1 of 2)| Dual specificity phosphatase 22                                            | Ensembl Stickleback | 0.00           | down            | 2.28E-03    | down     |
| ENSGACG0000003355      | dynb2 (1 of 2)| Dynnein, light chain, Ctxt-type 3                                          | Ensembl Stickleback | 9.28E-02       | down            | -1.6        | up       |
| ENSORLG0000002091      | elf2          | E74-like factor 2 (ets domain transcription factor)                         | Ensembl Medaka | 5.65E-03       | down            | -2.7        | -3.1     |
| ENSGACG0000003978      | egfl6         | EGF-like-domain, multiple 6                                                | Ensembl Stickleback | 2.87E-03       | down            | 4.39E-02    | -28.0    |
| ENSGACG00000015896     | egfl8         | EGF-like-domain, multiple 8                                                | Ensembl Stickleback | -2.8           | 5.65E-02        | down        | -0.0     |
| ENSDARG000000056744 | ela2 | elastase 2 | Ensembl_zebrafish | - | 0.00 | 3.21E-07 | -30.7 | - | 0.0 | - | down |
| ENSDARG000000007276 | ela3l | elastase 3 like | Ensembl_zebrafish | - | 0.00 | 1.10E-07 | -46.4 | - | 0.0 | - | down |
| ENSDARG000000045639 | elav4 | ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D) | Ensembl_zebrafish | - | up | - | 0.0 | - | up | 9.95E-02 | up |
| ENSGACG00000014563 | eaf2 | ELL associated factor 2 | Ensembl_stickleback | - | 0.00 | 9.01E-02 | down | - | 0.0 | - | down |
| ENSDARG00000004979 | elovl5 | ELOVL family member 5, elongation of long chain fatty acids (yeast) | Ensembl_zebrafish | - | 1.5 | - | 1.4 | - | -1.3 | 3.47E-03 | 8.4 |
| ENSORLG00000020058 | endou | endonuclease, polyU-specific | Ensembl_medaka | - | 0.00 | 1.52E-06 | down | - | 0.0 | - | down |
| ENSGACG00000005596 | erlec1 | endoplasmic reticulum lectin 1 | Ensembl_stickleback | - | -1.1 | - | 3.7 | 3.18E-04 | up | - | 1.3 |
| 269860691 XM_002650019.1 | erfc2 | epithelial cell transforming sequence 2 oncogene | Ensembl_nile_tilapia | - | 0.00 | - | up | 3.02E-02 | down | - | 1.6 |
| 225715605 BT079225.1 | esr1 | estrogen receptor 1 | Ensembl_zebrafish | - | 0.00 | - | up | 2.9 | 1.19E-10 | 105.2 |
| ENSGACG000000015608 | eef1a1 | eukaryotic translation elongation factor 1 alpha 1 | Ensembl_human | - | 8.70E-06 | up | - | 0.0 | - | down |
| ENSGACG00000008569 | eef2s1 | eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa | Ensembl_stickleback | - | 0.00 | 1.32E-10 | -54.3 | - | 2.2 | - | down |
| ENSGACG00000013800 | eif2b3 | eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa | Ensembl_stickleback | - | 2.14E-08 | up | - | down | - | 0.0 |
| ENSGACG0000004504 | eif4h | eukaryotic translation initiation factor 4H | Ensembl_stickleback | - | 4.00 | 1.84E-02 | down | - | -1.7 | - | up |
| ENSGACG00000009227 | esy7l (2 of 2) | extended synaptotagmin-like protein 1 | Ensembl_stickleback | - | -1.9 | - | -4.7 | 6.46E-05 | down | - | 1.2 |
| ENSGACG00000018094 | fam129b | family with sequence similarity 129, member B | Ensembl_stickleback | - | 8.82E-07 | -132.5 | - | up | - | up | - | down |
| ENSDARG000000074317 | fam20c (2 of 2) | family with sequence similarity 20, member C | Ensembl_zebrafish | - | 1.6 | - | 1.5 | - | 0.0 | 1.36E-04 | 40.3 |
| ENSGACG00000003212 | fam20a | family with sequence similarity 204, member A | Ensembl_stickleback | - | 4.90E-02 | 16.0 | - | up | - | 0.0 | - | 0.0 |
| ENSGACG00000019804 | fam3c | family with sequence similarity 3, member C | Ensembl_stickleback | - | 3.75E-02 | down | - | -1.1 | - | 2.1 | - | 1.2 |
| ENSDARG000000010437 | fam46c | family with sequence similarity 46, member C | Ensembl_zebrafish | - | -4.2 | - | 1.2 | - | -1.9 | 2.05E-02 | 11.1 |
| Gene Symbol | Description | Reference: Species | Status: Gene Expression | Log2 Fold Change | P-value |
|-------------|-------------|-------------------|-------------------------|-----------------|----------|
| fam65b      | family with sequence similarity 65, member B | Ensembl_stickleback | down                  | -2.0            | 2.47E-02 |
| fanco       | Fanconi anemia, complementation group C | Ensembl_stickleback | down                  | 5.86E-02        | 2.85E-09 |
| fabp10a     | fatty acid binding protein 10a, liver basic | Ensembl_zebrafish   | down                  | -1.7            | 5.44E-02 |
| fancc       | Fanconi anemia, complementation group C | Ensembl_stickleback | up                     | -6.6            | 5.24E-02 |
| fabp10a     | fatty acid binding protein 10a, liver basic | Ensembl_zebrafish   | down                  | 4.7             | 3.01E-02 |
| fgg         | fibrinogen, B beta polypeptide | Ensembl_zebrafish   | down                  | -1.3            | 1.70E-02 |
| fscb        | fibrous sheath CABY binding protein | Ensembl_medaka      | up                     | -2.0            | 1.66E-02 |
| fimo        | formin homology 2 domain containing 3 | Ensembl_zebrafish   | down                  | 1.3             | 3.03E-02 |
| forkhead box D1 | Refseq_proteins | -  | down                  | 2.45E-03        | 1.65E-04 |
| foxo4       | forkhead box 04 | Ensembl_stickleback | down                  | -1.0            | 1.02E-04 |
| fhod3 (1 of 2) | formin homology 2 domain containing 3 | Ensembl_stickleback | down                  | 0.00            | 3.67E-05 |
| fmn1 (2 of 2) | formin-like 1 | Ensembl_stickleback | down                  | -1.1            | 3.17E-02 |
| fut9 (14 of 16) | formin homology 2 domain containing 3 | Ensembl_zebrafish   | down                  | -1.2            | 8.81E-02 |
| fumurate hydratase | Ensembl_zebrafish | -  | down                  | -1.5            | 9.01E-02 |
| fhod3 (1 of 2) | formin homology 2 domain containing 3 | Ensembl_stickleback | down                  | -1.1            | 3.17E-02 |
| formin-like 1 | Ensembl_zebrafish | -  | down                  | -1.3            | 3.17E-02 |
| formin homology 2 domain containing 3 | Ensembl_zebrafish | -  | down                  | -1.3            | 3.17E-02 |
| formin homology 2 domain containing 3 | Ensembl_zebrafish | -  | down                  | -1.3            | 3.17E-02 |
| formin homology 2 domain containing 3 | Ensembl_zebrafish | -  | down                  | -1.3            | 3.17E-02 |
| formin homology 2 domain containing 3 | Ensembl_zebrafish | -  | down                  | -1.3            | 3.17E-02 |
| formin homology 2 domain containing 3 | Ensembl_zebrafish | -  | down                  | -1.3            | 3.17E-02 |
| formin homology 2 domain containing 3 | Ensembl_zebrafish | -  | down                  | -1.3            | 3.17E-02 |

**Note:** The table lists gene symbols, descriptions, reference species, gene expression status, log2 fold change, and p-value for various genes.
| Gene Symbol | Description | Species | Ensembl ID | Regulation | Fold Change | P-value |
|-------------|-------------|---------|------------|------------|-------------|----------|
| gnm | glycine N-methyltransferase | Ensembl_stickleback | ENSGACG00000005698 | down | -3.3 | -5.3 | -1.2 | 5.17E-05 |
| gatm | glycine amidotransferase (L-arginine:glycine amidotransferase) | Ensembl_zebrafish | ENSDARG000000036239 | down | -0.00 | -1.1 | 3.24E-03 | down |
| grhl3 | grainyhead-like 3 (Drosophila) | Ensembl_stickleback | ENSGACG00000009501 | up | up | 2.75E-04 | up |
| gremlin1 | gremlin 1 | Ensembl_stickleback | ENSGACG00000006103 | down | 1.84E-02 | up | 5.17E-05 |
| hspb1 | heat shock 27kDa protein 1 | Ensembl_stickleback | ENSGACG00000020233 | down | -1.2 | 5.59E-02 | down |
| gatm | glycine amidotransferase (L-arginine:glycine amidotransferase) | Ensembl_zebrafish | ENSDARG000000092362 | up | 0.00 | 1.1 | 3.24E-03 | up |
| grhl3 | grainyhead-like 3 (Drosophila) | Ensembl_stickleback | ENSGACG00000009501 | up | up | 2.75E-04 | up |
| gremlin1 | gremlin 1 | Ensembl_stickleback | ENSGACG00000006103 | down | 1.84E-02 | up | 5.17E-05 |
| grhl3 | grainyhead-like 3 (Drosophila) | Ensembl_stickleback | ENSGACG00000009501 | up | up | 2.75E-04 | up |
| gremlin1 | gremlin 1 | Ensembl_stickleback | ENSGACG00000006103 | down | 1.84E-02 | up | 5.17E-05 |

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| Gene ID               | Name                  | Species                  | Expression | Log2 Fold Change | p-value     | Effect  | Direction |
|----------------------|-----------------------|--------------------------|------------|-----------------|-------------|---------|-----------|
| ENSGACG00000009872   | kat7 (1 of 2)         | K(lysine) acetyltransferase 7 | Ensembl_stickleback | -1.4  | 4.39E-02 | up       | 1.6       |
| ENSORLG00000011216   | kans13                | KAT8 regulatory NSL complex subunit 3 | Ensembl_medaka | down | 3.10E-02 | up       | -1.1      |
| ENSDARG00000015815   | kdr                   | kinase insert domain receptor like | Ensembl_zebrafish | -1.4  | 1.50E-04 | up       | -1.4      |
| ENSGACG00000011649   | face1 (1 of 2)        | lactation elevated 1     | Ensembl_stickleback | -0.0  | 3.11E-02 | up       | -0.0      |
| ENSONIG00000014788   | lrig2                 | leucine-rich repeats and immunoglobulin-like domains 2 | Ensembl_nile_tilapia | -1.4  | 1.34E-04 | up       | -2.4      |
| ENSGACG00000005614   | lmf1                  | lipase maturation factor 1 | Ensembl_stickleback | -1.6  | 6.99E-02 | up       | -1.3      |
| ENSGACG00000019500   | ldlr (2 of 2)         | low density lipoprotein receptor | Ensembl_stickleback | -1.4  | 6.99E-02 | up       | -1.1      |
| ENSGACG00000011854   | kdm2b (2 of 2)        | lysine (K)-specific demethylase 2B | Ensembl_zebrafish | -2.4  | 1.50E-04 | up       | -2.4      |
| ENSDARG00000013542   | lpgat1                | lysophosphatidylglycerol acyltransferase 1 | Ensembl_zebrafish | -1.5  | 1.34E-04 | up       | -1.1      |
| ENSGACG00000018078   | man1b1 (1 of 2)       | mannosidase, alpha, class 1B, member 1 | Ensembl_stickleback | -1.5  | 6.99E-02 | up       | -1.1      |
| ENSGACG00000013607   | man1c1                | mannosidase, alpha, class 1C, member 1 | Ensembl_stickleback | -1.1  | 1.50E-04 | up       | -2.2      |
| ENSGACG00000015955   | mthfsd                | methenyltetrahydrofolate synthetase domain containing | Ensembl_stickleback | 2.9   | 7.69E-02 | up       | -2.6      |
| ENSDARG000000090444   | mthfd2                | methyleneptetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase | Ensembl_zebrafish | 2.1   | 1.19E-02 | up       | 2.8       |
| ENSGACG00000053087   | mthfr                 | methyleneptetrahydrofolate reductase (NAD(P)H) | Ensembl_zebrafish | 1.2   | 2.69E-02 | up       | 28.0      |
| ENSGACG00000016984   | msmo1                 | methylsterol monoxygenase 1 | Ensembl_stickleback | 3.54E-02 | -0.00 | up       | -         |
| ENSGACG00000005096   | metti5                | methyltransferase like 5 | Ensembl_stickleback | -1.1  | 8.04E-02 | up       | -         |
| ENSGACG00000006537   | mcph1                 | microcephalin 1          | Ensembl_stickleback | -1.5  | 1.50E-04 | up       | -         |
| ENSONIG00000009665   | mcph1                 | microcephalin 1          | Ensembl_nile_tilapia | 9.01E-02 | 0.00  | up       | -         |
| ENSGACG0000000210   | mfap4 (8 of 9)        | microfibrillar-associated protein 4 | Ensembl_zebrafish | 1.49E-02 | -3.0  | up       | -2.6      |
| ENSGACG00000010541   | mrp1l2                | mitochondrial ribosomal protein L12 | Ensembl_stickleback | 1.4  | 6.99E-02 | down     | -2.2      |
| ENSGACG0000002919   | mrp3l0                | mitochondrial ribosomal protein L30 | Ensembl_stickleback | -3.0  | 1.07E-03 | down     | -2.2      |
| ENSGACG00000013019   | map8ip3               | mitogen-activated protein kinase 8 interacting protein 3 | Ensembl_stickleback | 2.5   | -2.2    | up       | -2.2      |
| 159490               | M28397.1              | MOTARYBB Tobacco hornworm (M.sexta) | Ensembl_stickleback | 2.00E-05 | 0.00  | up       | 0.0       |
| gene_symbol | gene_name | description | organism | fold_change | p_value | direction | fold_change | p_value | direction | fold_change | p_value | direction |
|-------------|-----------|-------------|----------|-------------|---------|----------|-------------|---------|----------|-------------|---------|----------|
| mre11a      | MRE11 meiotic recombination 11 homolog A (S. cerevisiae) | Ensembl_stickleback | 7.32E-02 | up | - | 2.3 | 6.84E-03 | up | - | 1.1 |
| mtnd4p12    | MT-ND4 pseudogene 12 | Ensembl_human | - | down | 7.76E-04 | down | 1.03E-04 | down | 2.27E-04 | down |
| mtnd5p12    | MT-ND5 pseudogene 12 | Ensembl_human | - | down | - | down | - | down | 9.95E-02 | down |
| megfl8      | multiple EGF-like-domains 8 | Ensembl_stickleback | - | up | - | 1.0 | 9.02E-05 | up | - | 2.0 | 1.6 |
| mras        | muscle RAS oncogene homolog | Ensembl_stickleback | - | down | - | 3.9 | 3.92E-03 | down | - | 1.6 |
| myo18b (1 of 2) | myosin X VIII B | Ensembl_stickleback | - | 0.0 | - | 0.0 | 3.24E-03 | down | - | 0.0 |
| ndufb8      | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa | Ensembl_stickleback | - | down | - | 0.0 | 2.21E-03 | down | - | 1.6 |
| nduof2      | NADH dehydrogenase (ubiquinone) complex I, assembly factor 2 | Ensembl_stickleback | - | 0.0 | - | 0.0 | 3.65E-02 | down | - | 0.0 |
| nd1         | NADH dehydrogenase subunit 1 | Ensembl_stickleback | 2.42E-03 | down | 1.43E-06 | down | 8.60E-08 | down | 1.55E-09 | down |
| nd4         | NADH dehydrogenase subunit 4 | Ensembl_stickleback | - | down | - | down | 8.79E-02 | down | - | down |
| nd5         | NADH dehydrogenase subunit 5 | Ensembl_stickleback | 6.09E-02 | -24.5 | 8.40E-02 | -6.8 | 1.77E-03 | -55.2 | 5.64E-06 | down |
| nckap5      | NCK-associated protein 5 | Ensembl_stickleback | - | 1.3 | - | 1.9 | 3.04E-02 | -6.8 | - | down |
| ndfp1 (2 of 2) | Nedd4 family interacting protein 1 | Ensembl_nile_tilapia | - | -1.5 | 5.59E-02 | down | 5.83E-05 | down | 1.19E-02 | down |
| napa        | N-ethylmaleimide-sensitive factor attachment protein, alpha | Ensembl_stickleback | 4.19E-04 | down | 5.07E-03 | -40.2 | 8.79E-02 | down | - | 0.0 |
| nsf (1 of 2) | N-ethylmaleimide-sensitive factor | Ensembl_stickleback | 1.24E-02 | -10.5 | - | 1.3 | - | -1.1 | - | -3.4 |
| nbeal1      | neurobeachin-like 1 | Ensembl_stickleback | 3.75E-08 | -199.3 | - | 3.1 | - | 1.5 | - | -1.1 |
| ncf1        | neutrophil cytosolic factor 1 | Ensembl_stickleback | - | 1.9 | 3.04E-02 | -6.8 | - | down |
| nid1 (1 of 2) | nidogen 1 | Ensembl_stickleback | - | 0.0 | 1.13E-04 | down | - | up | - | 1.6 |
| ninj1       | ninjurin 1 | Ensembl_stickleback | 3.75E-08 | -199.3 | - | 3.1 | - | 1.5 | - | -1.1 |
| nosip       | nitric oxide synthase interacting protein | Ensembl_stickleback | 3.75E-02 | down | - | 2.1 | - | 2.8 | - | 2.3 |
| nkx6.2      | NK6 transcription factor related, locus 2 | Ensembl_stickleback | - | 0.0 | 1.45E-02 | - | 9.0 | - | up | - | 2.2 |
| nfatc3      | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 | Ensembl_stickleback | 1.34E-08 | 97.1 | - | 1.0 | - | 2.2 | - | 0.0 |
| nr1h4       | nuclear receptor subfamily 1, group H, member 4 | Ensembl_stickleback | - | 0.0 | 1.8 | 6.04E-02 | - | 19.5 | - | -1.1 |
| nucb1       | nucleobindin 1 | Ensembl_stickleback | - | 1.3 | - | 1.5 | 3.65E-02 | down | - | 2.3 |
| Gene ID          | Description                                      | Species       | Strand | Start | End   | Start_1 | End_1 | Strain | Gene Name | Start_2 | End_2 | Strain_2 | Start_3 | End_3 | Strain_3 |
|-----------------|--------------------------------------------------|---------------|--------|-------|-------|---------|-------|--------|-----------|---------|-------|----------|---------|-------|----------|
| ENSGACG00000015626 | nucb2 (1 of 2) nucleobindin 2                     | Ensembl_stickleback | -      | 1.6   | -1.4  | 6.60E-02 | -6.9   | up     |           |         |       |          |         |       |          |
| ENSORLG00000011426 | NOLC1 (1 of 2) nucleolar and coiled-body phosphoprotein 1 | Ensembl_medaka  | 4.69E-02 | up    | -4.2  | -       | -5.5   | down   |           |         |       |          |         |       |          |
| ENSGACG00000019459 | nap1I nucleosome assembly protein 1-like 1        | Ensembl_stickleback | -      | 4.3   | -     | 3.02E-02 | -5.5   | down   |           |         |       |          |         |       |          |
| ENSDARG00000016256 | nud3a nudix (nucleoside diphosphate linked moiety X)-type motif 3a | Ensembl_zebrafish | -      | 1.0   | 2.24E-04 | 3.27E-02 | -7.4   | down   |           |         |       |          |         |       |          |
| 1296952         | X92804.1 O.mykiss vtg1 gene                       | nt            | -      | 0.00  | -     | 9.87E-04 | up     |         |           |         |       |          |         |       |          |
| ENSGACG00000016390 | odz3 (2 of 2)                                   | nt            | -      | 0.00  | -     | 5.91E-02 | up     | -16.2  |           |         |       |          |         |       |          |
| ESS55559        | gb|ESS55559.1 Oncorhynchus gorbuscha microsatellite locus Ogo2, (ga)24 | EST_others    | -      | 3.75E-02 | up    | 3.3    | down   | -1.1   |           |         |       |          |         |       |          |
| 2258079         | AF009794.1 Oncorhynchus masou formosanus complement factor H1 protein (CFH) mRNA, complete cds | nt            | -      | 3.90E-03 | down  | 0.0    | -       | 0.0    |           |         |       |          |         |       |          |
| 185133427       | NM_001124346.1 Oncorhynchus mykiss apolipoprotein E (apoE), mRNA | Refseq_genes  | -      | 1.5   | -1.8  | 5.0    | up     | 3.3    |           |         |       |          |         |       |          |
| 225705221       | BT074033.1 Oncorhynchus mykiss clone omyk-evo-501-128 Leucine-rich repeat-containing protein 42 putative mRNA, complete cds | nt            | -      | 2.29E-02 | up    | 1.2    | up      | up     |           |         |       |          |         |       |          |
| 225705363       | BT074104.1 Oncorhynchus mykiss clone omyk-evo-501-224 Retinoic acid receptor responder protein 3 putative mRNA, complete cds | nt            | -      | 3.75E-02 | up    | up     | up      | up     |           |         |       |          |         |       |          |
| 225704491       | BT073668.1 Oncorhynchus mykiss clone omyk-evo-509-076 Cytochrome c oxidase subunit Vila-related protein, mitochondrial precursor putative mRNA, complete cds | nt            | -      | 1.7   | 3.1   | 6.04E-02 | 8.11   | -       | 4.6     |         |       |          |         |       |          |
| 225705745       | BT074295.1 Oncorhynchus mykiss clone omyk-evo-514-224 Tetrameric peptide repeat protein 1 putative mRNA, complete cds | nt            | -      | 1.6   | 4.41E-02 | up    | 1.4    | 3.3    |         |         |       |          |         |       |          |
| 185135625       | NM_001124385.1 Oncorhynchus mykiss complement component 4 (c4), mRNA | Refseq_genes  | -      | 4.41E-02 | down  | up     | -       | 2.0    |         |         |       |          |         |       |          |
| 350537414       | NM_001246346.1 Oncorhynchus mykiss complement factor D (adipsin) (cfd), mRNA | Refseq_genes  | -      | 1.0   | 2.1   | 6.04E-02 | -5.0   | -       | 2.0     |         |       |          |         |       |          |
| 185134284       | NM_001124556.1 Oncorhynchus mykiss FBPL4 (LOC100133630), mRNA | Refseq_genes  | -      | 8.3   | -     | 9.49E-03 | -7.2   | -       |         |         |       |          |         |       |          |
| 261245070       | NM_001160506.1 Oncorhynchus mykiss fish virus induced TRIM protein (trim), mRNA | Refseq_genes  | -      | 1.3   | -1.5  | 7.58E-02 | -4.9   | -       | 1.2     |         |       |          |         |       |          |
| 185132277       | NM_001124400.1 Oncorhynchus mykiss fucosyltransferase 9 (ft9), mRNA | Refseq_genes  | 2.0   | -1.5  | 6.85E-02 | 6.6    | -       | 0.0     |         |         |       |          |         |       |          |
| 185132952       | NM_001124249.1 Oncorhynchus mykiss glucokinase (gk), mRNA | Refseq_genes  | 2.4   | -     | 1.4   | 1.28E-04 | 67.1   | -       |         |         |       |          |         |       |          |
| 259089083       | NM_001165108.1 Oncorhynchus mykiss heme binding protein 2 (hebp2), mRNA | Refseq_genes  | 1.5   | 1.3   | -     | 4.52E-03 | 10.2   | -       |         |         |       |          |         |       |          |
| 350537622       | NM_001246355.1 Oncorhynchus mykiss IL-13 receptor-alpha-2-b precursor (il13ra2b), mRNA | Refseq_genes  | 2.3   | 0.0   | 2.27E-04 | -0.9    | -1.2   |         |         |         |       |          |         |       |          |
| Accession | Gene ID | Description | RefSeq Genes | Log2 Fold Change | p-value |
|-----------|---------|-------------|--------------|-----------------|---------|
| NM_001124308.1 | Oncorhynchus mykiss interleukin 13 receptor alpha-2 (LOC100133596), mRNA | Refseq Genes | -2.5 | -1.7 | 9.34E-06 |
| NM_001124324 | Oncorhynchus mykiss keratin 13 (k13), mRNA | Refseq Genes | -1.4 | -6.9 | 6.99E-02 |
| NM_0011243579 | Oncorhynchus mykiss LECT2 neutrophil chemotactic factor (lect2), mRNA | Refseq Genes | down | down | 1.95E-02 |
| NM_001124309.1 | Oncorhynchus mykiss lipopolysaccharide-induced TNF factor (litaf), mRNA | Refseq Genes | down | down | 2.3 |
| NM_001124376.1 | Oncorhynchus mykiss keratin 13 (k13), mRNA | Refseq Genes | up | 1.4 |
| NM_001165121.1 | Oncorhynchus mykiss mannann-binding lectin H2 (LOC100301642), mRNA | Refseq Genes | down | 1.95E-02 |
| NM_001160480.1 | Oncorhynchus mykiss mannan-binding lectin H2 (LOC100301642), mRNA | Refseq Genes | down | 1.95E-02 |
| NM_001165118.1 | Oncorhynchus mykiss SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae) (sumo2), mRNA | Refseq Genes | down | down | 1.95E-02 |
| NM_001124290.1 | Oncorhynchus mykiss partial mRNA for Lamin B2 protein | Refseq Genes | down | down | 1.95E-02 |
| NM_001124285.1 | Oncorhynchus mykiss VIG-2 protein (vig-2), mRNA | Refseq Genes | -1.6 | -6.2 | 6.04E-02 |
| NM_001124274.1 | Oncorhynchus mykiss vitelline envelope protein gamma (LOC1001335907), mRNA | Refseq Genes | down | down | 0.0 |
| NM_001124600.1 | Oncorhynchus mykiss zona pellucida glycoprotein 2.3 (zp2.3), mRNA | Refseq Genes | 0.00 | 0.0 | 0.0 |
| NM_001124396 | Oncorhynchus tshawytscha clone Ots.u211.76.64 genomic sequence | Refseq Genes | down | down | 5.70E-06 |
| AF527060.1 | Oncorhynchus tshawytscha virus-inducible stress protein (VISP) mRNA, complete cds | Refseq Genes | -1.3 | -2.1 | 6.27E-02 |
| NM_001105103.1 | Oryzias latipes Mhc class I A (orla-uaa), mRNA | Refseq Genes | 8.93E-05 | -7.2 | 2.66E-02 |
| NM_001124308.1 | Oncorhynchus mykiss interleukin 13 receptor alpha-2 (LOC100133596), mRNA | Refseq Genes | -2.5 | -1.7 | 9.34E-06 |
| NM_001124324 | Oncorhynchus mykiss keratin 13 (k13), mRNA | Refseq Genes | -1.4 | -6.9 | 6.99E-02 |
| NM_0011243579 | Oncorhynchus mykiss LECT2 neutrophil chemotactic factor (lect2), mRNA | Refseq Genes | down | down | 1.95E-02 |
| NM_001124309.1 | Oncorhynchus mykiss lipopolysaccharide-induced TNF factor (litaf), mRNA | Refseq Genes | down | down | 2.3 |
| NM_001124376.1 | Oncorhynchus mykiss keratin 13 (k13), mRNA | Refseq Genes | up | 1.4 |
| NM_001165121.1 | Oncorhynchus mykiss mannann-binding lectin H2 (LOC100301642), mRNA | Refseq Genes | down | 1.95E-02 |
| NM_001160480.1 | Oncorhynchus mykiss mannan-binding lectin H2 (LOC100301642), mRNA | Refseq Genes | down | 1.95E-02 |
| NM_001165118.1 | Oncorhynchus mykiss SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae) (sumo2), mRNA | Refseq Genes | down | down | 1.95E-02 |
| NM_001124290.1 | Oncorhynchus mykiss partial mRNA for Lamin B2 protein | Refseq Genes | down | down | 1.95E-02 |
| NM_001124285.1 | Oncorhynchus mykiss VIG-2 protein (vig-2), mRNA | Refseq Genes | -1.6 | -6.2 | 6.04E-02 |
| NM_001124274.1 | Oncorhynchus mykiss vitelline envelope protein gamma (LOC1001335907), mRNA | Refseq Genes | down | down | 0.0 |
| NM_001124600.1 | Oncorhynchus mykiss zona pellucida glycoprotein 2.3 (zp2.3), mRNA | Refseq Genes | 0.00 | 0.0 | 0.0 |
| NM_001124396 | Oncorhynchus tshawytscha clone Ots.u211.76.64 genomic sequence | Refseq Genes | down | down | 5.70E-06 |
| AF527060.1 | Oncorhynchus tshawytscha virus-inducible stress protein (VISP) mRNA, complete cds | Refseq Genes | -1.3 | -2.1 | 6.27E-02 |
| NM_001105103.1 | Oryzias latipes Mhc class I A (orla-uaa), mRNA | Refseq Genes | 8.93E-05 | -7.2 | 2.66E-02 |
| NM_001124308.1 | Oncorhynchus mykiss interleukin 13 receptor alpha-2 (LOC100133596), mRNA | Refseq Genes | -2.5 | -1.7 | 9.34E-06 |
| NM_001124324 | Oncorhynchus mykiss keratin 13 (k13), mRNA | Refseq Genes | -1.4 | -6.9 | 6.99E-02 |
| NM_0011243579 | Oncorhynchus mykiss LECT2 neutrophil chemotactic factor (lect2), mRNA | Refseq Genes | down | down | 1.95E-02 |
| NM_001124309.1 | Oncorhynchus mykiss lipopolysaccharide-induced TNF factor (litaf), mRNA | Refseq Genes | down | down | 2.3 |
| NM_001124376.1 | Oncorhynchus mykiss keratin 13 (k13), mRNA | Refseq Genes | up | 1.4 |
| NM_001165121.1 | Oncorhynchus mykiss mannann-binding lectin H2 (LOC100301642), mRNA | Refseq Genes | down | 1.95E-02 |
| NM_001160480.1 | Oncorhynchus mykiss mannan-binding lectin H2 (LOC100301642), mRNA | Refseq Genes | down | 1.95E-02 |
| NM_001165118.1 | Oncorhynchus mykiss SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae) (sumo2), mRNA | Refseq Genes | down | down | 1.95E-02 |
| NM_001124290.1 | Oncorhynchus mykiss partial mRNA for Lamin B2 protein | Refseq Genes | down | down | 1.95E-02 |
| NM_001124285.1 | Oncorhynchus mykiss VIG-2 protein (vig-2), mRNA | Refseq Genes | -1.6 | -6.2 | 6.04E-02 |
| NM_001124274.1 | Oncorhynchus mykiss vitelline envelope protein gamma (LOC1001335907), mRNA | Refseq Genes | down | down | 0.0 |
| NM_001124600.1 | Oncorhynchus mykiss zona pellucida glycoprotein 2.3 (zp2.3), mRNA | Refseq Genes | 0.00 | 0.0 | 0.0 |
| NM_001124396 | Oncorhynchus tshawytscha clone Ots.u211.76.64 genomic sequence | Refseq Genes | down | down | 5.70E-06 |
| AF527060.1 | Oncorhynchus tshawytscha virus-inducible stress protein (VISP) mRNA, complete cds | Refseq Genes | -1.3 | -2.1 | 6.27E-02 |
| NM_001105103.1 | Oryzias latipes Mhc class I A (orla-uaa), mRNA | Refseq Genes | 8.93E-05 | -7.2 | 2.66E-02 |
| GenBank Accession | Ensembl ID | Symbol | Description | Type | Tag | Down | Up | FDR | Log2 fold change |
|-------------------|------------|--------|-------------|------|-----|------|-----|-----|-----------------|
| S29               |            |        |             |      |     |      |     |     |                 |

**S29**
| Accession       | Description                                      | Refseq Type     | Value 1          | Value 2         | Value 3         | Value 4          | Value 5         |
|----------------|--------------------------------------------------|-----------------|------------------|-----------------|-----------------|------------------|-----------------|
| XM_003221811.1 | PREDICTED: Anolis carolinensis synaptopodin-2-like (LOC100567593), mRNA | Refseq_genes    | down             | 7.30E-02        | -7.0            | -                | 0.0             | 2.8             |
| XP_001922687.3 | PREDICTED: antihemorrhagic factor chLBP          | Refseq_proteins | -                | 1.1             | 5.49E-02        | -15.5           | -2.7            | -2.3            |
| XP_003975453.1 | PREDICTED: apolipoprotein D-like                 | Refseq_proteins | -                | 0.00            | 1.43E-06        | -39.3           | -                | 0.0             | 10.4            |
| XP_003963988.1 | PREDICTED: cadherin-5-like                      | Refseq_proteins | -                | -1.0            | -                | -                | -19.9           | 7.67E-02        | 12.2            | -1.8            |
| XP_004083297.1 | PREDICTED: cathepsin E-A-like                   | Refseq_proteins | up               | 0.0             | 1.59E-02        | -34.4           | 3.55E-02        | -7.4            |
| XP_004074040.1 | PREDICTED: cell division cycle-associated 7-like protein-like | Refseq_proteins | down             | 1.1             | 5.49E-02        | -34.4           | 3.55E-02        | -7.4            |
| XP_004074040.1 | PREDICTED: cytochrome P450 2F2-like             | Refseq_proteins | down             | 5.59E-02        | -1.0            | -                | 4.84E-11        | -               |
| XP_004074040.1 | PREDICTED: dimethylaniline monooxygenase        | Refseq_proteins | up               | 1.8             | -                | -1.5            | -               |
| XP_004074040.1 | PREDICTED: endonuclease domain-containing 1 protein-like | Refseq_proteins | up               | -1.1            | 8.77E-02        | -14.4           | 0.0             | 0.0             |
| XP_004074040.1 | PREDICTED: fatty acid-binding protein, adipocyte-like | Refseq_proteins | up               | 2.08E-03        | -                | 0.0             | 0.0             | 0.0             |
| XP_004074040.1 | PREDICTED: fatty acyl-CoA hydrolase precursor, medium chain isoform 1 | Refseq_proteins | up               | -1.7            | -                | -9.3            | 2.2             | 3.74E-02        |
| XP_004074040.1 | PREDICTED: GTPase SLIP-GC-like, partial         | Refseq_proteins | down             | -1.1            | -                | -10.0           | 1.96E-04        | -               |
| XP_004074040.1 | PREDICTED: heat shock 70 kDa protein 12A-like   | Refseq_proteins | down             | 3.56E-06        | -                | 0.0             | 0.0             | 11.4            |
| XP_004074040.1 | PREDICTED: hypothetical protein LOC100004199    | Refseq_proteins | down             | 2.5             | 2.02E-04        | -13.5           | 9.69E-02        | 5.6             |
| XP_004074040.1 | PREDICTED: hypothetical protein LOC100149918    | Refseq_proteins | down             | 2.5             | 2.02E-04        | -13.5           | 9.69E-02        | 5.6             |
| XP_004074040.1 | PREDICTED: hypothetical protein LOC100561123    | Refseq_proteins | down             | 2.5             | 2.02E-04        | -13.5           | 9.69E-02        | 5.6             |
| XP_004074040.1 | PREDICTED: hypothetical protein LOC100690208    | Refseq_proteins | down             | 2.5             | 2.02E-04        | -13.5           | 9.69E-02        | 5.6             |
| XP_004074040.1 | PREDICTED: hypothetical protein LOC100696199    | Refseq_proteins | down             | 2.5             | 2.02E-04        | -13.5           | 9.69E-02        | 5.6             |
| XP_004074040.1 | PREDICTED: hypothetical protein LOC100707007    | Refseq_proteins | down             | 2.5             | 2.02E-04        | -13.5           | 9.69E-02        | 5.6             |
| XP_004074040.1 | PREDICTED: hypothetical protein LOC100709472    | Refseq_proteins | down             | 2.5             | 2.02E-04        | -13.5           | 9.69E-02        | 5.6             |
| Gene Accession | Gene Name | Function | Description | Refseq Protein | Expression | p-value | Fold Change | Log2 Fold Change |
|---------------|-----------|----------|-------------|----------------|------------|--------|-------------|-----------------|
| XP_003460252.1 | PREDICTED: hypothetical protein LOC100709671 | Refseq proteins | - | down | down | 4.49E-02 | down |
| XP_003452206.1 | PREDICTED: hypothetical protein LOC1007010425 | Refseq proteins | - | 0.00 | down | 0.0 | 4.20E-02 |
| XP_0076427.1 | PREDICTED: hypothetical protein LOC567961 | Refseq proteins | - | 4.4 | 2.87E-03 | up | - |
| XP_001335256.1 | PREDICTED: hypothetical protein LOC795145 | Refseq proteins | - | -2.5 | down | -2.8 | 2.94E-02 |
| XP_003200076.1 | PREDICTED: integrin alpha-E-like | Refseq proteins | - | -1.8 | - | -1.5 | 6.95E-03 |
| XP_691524.5 | PREDICTED: interferon-induced guanylate-binding protein 1 | Refseq proteins | - | -1.1 | 1.5 | 7.71E-05 | -88.2 |
| XM_003453747.1 | PREDICTED: leucine-rich repeats and immunoglobulin-like domains protein 2 | Refseq proteins | - | down | 7.27E-02 | down | 3.39E-04 |
| XR_134778.1 | PREDICTED: Oreochromis niloticus fibroblast growth factor receptor 2-like (LOC100699731), miscRNA | Refseq genes | - | -1.7 | 1.2 | 1.5 | 1.00E-02 |
| XM_003437837.1 | PREDICTED: Oreochromis niloticus fibroblast growth factor receptor 2-like (LOC100699731), mRNA | Refseq genes | - | down | 0.0 | 3.02E-02 | down |
| XM_003440906.1 | PREDICTED: Oreochromis niloticus hypothetical protein LOC100703724 (LOC100703724), mRNA | Refseq genes | 1.36E-02 | down | -2.0 | -2.6 | - |
| XM_003459573.1 | PREDICTED: Oreochromis niloticus hypothetical protein LOC100710022 (LOC100710022), mRNA | Refseq genes | 3.15E-02 | down | 9.39E-03 | down | 1.97E-05 |
| XM_003450884.1 | PREDICTED: interferon-induced protein 44 | Refseq genes | 3.15E-02 | up | down | 4.86E-03 | 7.8 |
| XM_003449682.1 | PREDICTED: Oreochromis niloticus transmembrane protein 192-like (LOC100691376), mRNA | Refseq genes | 3.15E-02 | up | up | 4.67E-03 | up |
| XP_003446516.1 | PREDICTED: protachykinin-like | Refseq proteins | 3.15E-02 | up | up | -1.8 | -1.3 |
| XP_003449271.1 | PREDICTED: protection of telomeres protein 1-like | Refseq proteins | - | down | 7.32E-02 | down | -4.3 |
| XP_003456974.1 | PREDICTED: protein GP1R08-like | Refseq proteins | 7.32E-02 | down | -4.3 | 0.0 | 9.95E-02 |
| XP_004072298.1 | PREDICTED: putative defense protein 3-like | Refseq proteins | - | 0.00 | down | 1.21E-02 | 13.4 |
| XP_002941477.1 | PREDICTED: retinal homeobox protein Rx-like | Refseq proteins | - | 0.00 | 7.90E-02 | -11.71 | 0.0 |
| XP_003445773.1 | PREDICTED: RNA-binding protein 26-like | Refseq proteins | 3.2 | 1.0 | 8.79E-02 | down | - |
| XP_003197704.1 | PREDICTED: synaptopodin-2 | Refseq proteins | - | 0.00 | 7.34E-02 | -6.81 | - |
| XP_003440648.1 | PREDICTED: synemin-like | Refseq proteins | - | 4.8 | 4.41E-02 | up | 2.2 |
| XM_003975798.1 | PREDICTED: Takifugu rubripes alpha-2-HS-glycoprotein-like (LOC101076681), mRNA | Refseq genes | 0.00 | 0.0 | up | 2.29E-18 | down |
| Ensembl_ID | RefSeq_ID | Description | Peptide ID | Gene Description | Expression | Fold Change | p-Value | Log2 Fold Change | Status |
|------------|-----------|-------------|------------|------------------|------------|-------------|--------|-----------------|--------|
| ENSDARG00000035350 | XM_003975286.1 | PREDICTED: Takifugu rubripes glycosylphosphatidylinositol anchor attachment protein-like (Takifugu rubripes), mRNA | Refseq_genes | -1.2 | down | 1.61E-02 | -3.5 | -1.1 |
| ENSDARG0000003973185.1 | XM_003973185.1 | PREDICTED: Takifugu rubripes poly(U)-specific endoribonuclease-like (Takifugu rubripes), mRNA | Refseq_genes | 5.95E-04 | down | 9.95E-04 | 8.51 | -1.3 |
| ENSDARG0000003974543.1 | XM_003974543.1 | PREDICTED: Takifugu rubripes UDP-glucuronosyltransferase 2A2-like (Takifugu rubripes), mRNA | Refseq_genes | 9.79E-02 | down | 8.31E-04 | -110.8 | -2.7 |
| ENSDARG0000003976977 | XM_003976977 | PREDICTED: trypsinogen-like protein 3-like (Takifugu rubripes), partial Refseq_proteins | Refseq_proteins | 3.12E-04 | up | 1.36E-02 | 1.3 |
| ENSDARG0000003441640.1 | XP_003441640.1 | PREDICTED: tsukushin-like Refseq_proteins | Refseq_proteins | 9.62E-02 | down | 3.65E-03 | -17.3 |
| ENSDARG0000004080813.1 | XP_004080813.1 | PREDICTED: UDP-glucuronosyltransferase 2B31-like Refseq_proteins | Refseq_proteins | 9.62E-02 | down | 9.62E-02 | -20.6 |
| ENSDARG0000003966124.1 | XP_003966124.1 | PREDICTED: urokinase plasminogen activator surface receptor-like (Takifugu rubripes), mRNA | Refseq_proteins | 9.62E-02 | down | 3.65E-03 | -17.3 |
| ENSDARG0000003978065.1 | XP_003978065.1 | PREDICTED: WAS/WASL-interacting protein family member 2-like Refseq_proteins | Refseq_proteins | 2.85E-02 | down | 1.36E-02 | -1.5 |
| ENSDARG000000035350 | ins | preproinsulin | Ensembl_zebrafish | 3.65E-03 | down | 1.36E-02 | -17.3 |
| ENSDARG00000009139 | pfn2 (1 of 2) | profilin 2 | Ensembl_stickleback | 4.49E-02 | down | -1.5 | -2.1 |
| ENSDARG00000007715 | prl (1 of 2) | prolactin receptor | Ensembl_nile_tilapia | 8.9 | down | -1.5 | -2.1 |
| ENSDARG00000009922 | psoap1 | prosaposin-like 1 (gene/pseudogene) | Ensembl_nile_tilapia | 8.9 | down | -1.5 | -2.1 |
| ENSDARG00000017213 | prss35 | protease, serine, 35 | Ensembl_zebrafish | 1.9 | down | 2.07E-03 | 8.31E-04 |
| ENSDARG00000000107 | psmb9 (5 of 5) | proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2) | Ensembl_stickleback | 1.9 | down | 3.51E-04 | 8.31E-04 |
| ENSDARG00000019857 | pacsin2 | protein kinase C and casein kinase substrate in neurons 2 | Ensembl_stickleback | 1.9 | down | 3.51E-04 | 8.31E-04 |
| ENSDARG00000015712 | prkch | protein kinase C, eta | Ensembl_medaka | 4.49E-02 | down | -1.5 | -2.1 |
| ENSDARG00000007985 | pkn3 | protein kinase N3 | Ensembl_zebrafish | 6.5 | up | 1.9 | 1.04E-02 |
| ENSDARG000000089608 | ppp1cbl | protein-phosphatase 1, catalytic subunit, beta isomorph, like | Ensembl_zebrafish | 2.7 | up | 1.9 | 1.04E-02 |
| ENSDARG00000005491 | ppp1r21 | protein-phosphatase 1, regulatory subunit 21 | Ensembl_stickleback | 2.7 | up | 1.9 | 1.04E-02 |
| ENSDARG00000007843 | ptprc | protein tyrosine phosphatase, receptor C | Ensembl_stickleback | 2.7 | up | 1.9 | 1.04E-02 |
| ENSDARG00000012481 | ralgapa1 | Ral GTPase activating protein, alpha subunit 1 (catalytic) | Ensembl_stickleback | 2.7 | up | 1.9 | 1.04E-02 |
| ENSDARG00000005989 | rgl2 | Ral GTPase activating protein, alpha subunit 1 (catalytic) | Ensembl_zebrafish | 2.7 | up | 1.9 | 1.04E-02 |
| ENSDARG00000005989 | rgl2 | Ral GTPase activating protein, alpha subunit 1 (catalytic) | Ensembl_zebrafish | 2.7 | up | 1.9 | 1.04E-02 |
| ENSDARG00000005989 | rgl2 | Ral GTPase activating protein, alpha subunit 1 (catalytic) | Ensembl_zebrafish | 2.7 | up | 1.9 | 1.04E-02 |
| ENSDARG0000001138713.1 | XP_001138713.1 | RalGDS1 required for cell differentiation1 homolog (S. pombe) | Refseq_proteins | 3.65E-03 | down | 1.36E-02 | -17.3 |
| ENSDARG000000021869 | rcan2 | regulator of calcineurin 2 | Ensembl_zebrafish | 1.36E-02 | down | 1.36E-02 | -17.3 |

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| Gene ID          | Description                                      | Species               | Value          | Effect | p-Value | Direction | Log2FoldChange | p-Value (log2) |
|-----------------|--------------------------------------------------|-----------------------|----------------|--------|---------|-----------|---------------|---------------|
| ENSDARG000000090039 | reck reversion-inducing- cysteine-rich protein with kazal motifs | Ensembl_zebrafish      | -1.4           | up     | 6.99E-02| 0.0       | 1.3           |               |
| ENSGAGC00000013298  | arhdia (1 of 2) Rho GDP dissociation inhibitor (GDI) alpha | Ensembl_stickleback   | 3.85E-03       | down   | -83.1  | 1.0       | -1.0          |               |
| ENSGAGC00000019358  | arhgef15 Rho guanine nucleotide exchange factor (GEF) 15 | Ensembl_stickleback   | 3.85E-03       | down   | -1.2   | -2.3      |               |               |
| 222137251         | FJ002822.1 Rhacophila balcanica voucher RbalL1 16S ribosomal RNA gene, partial sequence; mitochondrial | nt                | -0.00          | 1.52E-06| 123.1  | 0.0       | -0.0          | 0.0           |
| ENSONIG00000002839  | rpp21 ribonuclease P/MRP 21kDa subunit | Ensembl_nile_tilapia  | -1.3           | down   | -1.2   | -1.2      | 1.2           | 2.30E-02      |
| ENSGACG00000012811  | rps6ka3 ribosomal protein 56 kinase, 90kDa, polyepitope 3 | Ensembl_stickleback   | 9.69E-02       | down   | -2.2   | -1.1      | 1.1           | 8.95E-02      |
| ENSORLG00000011879  | rrbp1 ribosome binding protein 1 homolog 180kDa (dog) | Ensembl_medaka         | -1.1           | down   | -1.2   | -1.6      | 1.2           | 8.95E-02      |
| ENSONIG00000010011  | rrbp1 ribosome binding protein 1 homolog 180kDa (dog) | Ensembl_nile_tilapia  | 0.00           | up     | -1.2   | -1.6      | 1.2           | 8.95E-02      |
| ENSMUSG00000026955  | 2010317E24Rik RIKEN cDNA 2010317E24 gene | Ensembl_male           | -1.3           | down   | -1.2   | -1.2      | 1.2           | 2.30E-02      |
| ENSGACG00000016138  | rnf165 (1 of 2) RNA binding motif, single stranded interacting protein 1 | Ensembl_stickleback   | -0.00          | down   | -3.02E-05| 3.02E-05 | down         | 1.87E-02      |
| ENSGACG00000005671  | rbms1 (1 of 2) RNA binding motif, single stranded interacting protein 1 | Ensembl_stickleback   | -0.00          | down   | -3.02E-05| 3.02E-05 | down         | 1.87E-02      |
| ENSDARG00000008590  | rbms2 (1 of 2) RNA binding motif, single stranded interacting protein 1 | Ensembl_zebrafish      | -1.0           | down   | -6.1   | -1.8      | -1.8          |               |
| ENSONIG00000008341  | rbfox2 (1 of 2) RNA binding protein, fox-1 homolog (C. elegans) 2 | Ensembl_nile_tilapia  | 0.00           | up     | -1.2   | 1.6       | -1.2          | 1.87E-02      |
| ENSGACG000000020220  | rvub2 RuvB-like 2 (E. coli) | Ensembl_stickleback   | -0.00          | down   | -15.9  | 0.0       | -15.9         | 0.0           |
| 213513492         | NM_001140687.1 Salmo salar 40S ribosomal protein S15a (rs15a), mRNA | Refseq_genes          | -1.3           | 5.59E-02| up     | -1.8      | 5.59E-02      |               |
| 213513418         | NM_001139890.1 Salmo salar 60 kDa lysophospholipase (lpp60), mRNA | Refseq_genes          | -2.5           | down   | 4.41E-02| up         | 4.41E-02      |               |
| 259155117         | NM_001165329.1 Salmo salar adenosine monophosphate deaminase 3 (ampd3), mRNA | Refseq_genes          | -1.1           | -5.2    | 8.79E-02| 5.3        | -5.2          |               |
| 291190403         | NM_001173641.1 Salmo salar Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylgulosaminiytransferase A (mgt4a), mRNA | Refseq_genes          | -2.6           | 1.9     | 8.78E-02| -25.6      | -25.6         |               |
| 213513162         | NM_001141362.1 Salmo salar Apolipoprotein C-I (apoc1), mRNA | Refseq_genes          | -1.0           | 5.68E-03| up     | -1.0      | 5.68E-03      |               |
| 291190593         | NM_001173935.1 Salmo salar aquaporin 8 (aqp8), mRNA | Refseq_genes          | -0.00          | 1.9     | 6.99E-02| up         | 6.99E-02      |               |
| 259155215         | NM_001165377.1 Salmo salar Beta-adducin (addb), mRNA | Refseq_genes          | -1.9           | -2.1    | 6.99E-02| -6.3       | 6.99E-02      |               |
| 213511949         | NM_001140737.1 Salmo salar Bridging integrator 2 (bin2), mRNA | Refseq_genes          | -0.00          | 1.6     | 2.18E-02| 7.2        | 2.18E-02      |               |
| 185134143         | NM_001123580.1 Salmo salar C type lectin receptor B (LOC100136447), mRNA | Refseq_genes          | -0.00          | 0.0     | 9.06E-15| down       | 9.06E-15      | 0.0           |
| 213512283         | NM_001140113.1 Salmo salar Cadherin-17 (cad17), mRNA | Refseq_genes          | -0.00          | 1.19E-08| up     | 3.24E-07   | 3.24E-07      |               |
| 213514195         | NM_001140522.1 Salmo salar Cathepsin B (catb), mRNA | Refseq_genes          | -0.00          | 0.0     | 3.02E-02| 0.0        | 3.02E-02      |               |
| Accession   | Description                                                                 | RefSeq Genes | log2 Fold Change | p-value  | log2 Fold Change | q-value | log2 Fold Change | q-value |
|-------------|------------------------------------------------------------------------------|--------------|------------------|----------|------------------|---------|------------------|---------|
| NM_001140779.1 | Salmo salar Cathepsin M (catm), mRNA                                         | Refseq_genes | -2.5             | 1.5      | 1.34E-03         | 10.6    | -1.0             |
| NM_001146421.1 | Salmo salar CK046 protein (ck046), mRNA                                    | Refseq_genes | down             | down     | 6.99E-02         | down    | down             |
| NM_001173776.1 | Salmo salar Clarin-3 (clrn3), mRNA                                        | Refseq_genes | -0.00            | 9.39E-03 | down             | 0.0     | 0.0              |
| AF273013.1    | Salmo salar clone 01-04L Immunoglobulin light chain precursor (IgL) mRNA, complete cds | nt           | 3.43E-12         | down     | 0.0              | 0.0     | 0.0              |
| BT049635.1    | Salmo salar clone ssal-eve-504-024 39S ribosomal protein LA1, mitochondrial precursor putative mRNA, complete cds | nt           | -1.1             | 9.01E-02 | down             | -4.1    | -1.5             |
| BT047766.1    | Salmo salar clone ssal-eve-517-354 Gamma-interferon-inducible lysosomal thiol reductase precursor putative mRNA, complete cds | nt           | down             | 4.50E-08 | down             | 2.85E-09 | down             | 7.68E-02 | down   |
| BT057267.1    | Salmo salar clone ssal-eve-531-071 Non-histone chromosomal protein H6 putative mRNA, complete cds | nt           | -4.9             | 1.27E-03 | down             | 2.73E-11 | -195.2           | -4.1    |
| BT047990.1    | Salmo salar clone ssal-eve-544-022 Translationally-controlled tumor protein putative mRNA, complete cds | nt           | -2.2             | -4.0     | 1.96E-02         | -6.4    | -3.9             |
| BT057018.1    | Salmo salar clone ssal-eve-547-356 Non-histone chromosomal protein H6 putative mRNA, complete cds | nt           | 0.00             | 1.13E-09 | down             | 2.26E-03 | down             |
| BT050272.1    | Salmo salar clone ssal-eve-560-145 Deoxyribonuclease gamma precursor putative mRNA, complete cds | nt           | 7.51E-06         | down     | 0.0              | 0.0     | 0.0              |
| BT056711.1    | Salmo salar clone ssal-eve-566-360 High mobility group protein B2 putative mRNA, complete cds | nt           | down             | down     | 5.65E-02         | down    | down             |
| BT056528.1    | Salmo salar clone ssal-eve-579-363 P4A1 family protein 3 putative mRNA, complete cds | nt           | 0.00             | 2.87E-03 | down             | 4.67E-03 | down             |
| BT050045.1    | Salmo salar clone ssal-eve-502-345 Glyceraldehyde-3-phosphate dehydrogenase putative mRNA, complete cds | nt           | down             | 6.22E-03 | down             | down    | 2.26E-03         | down    |
| BT056923.1    | Salmo salar clone ssal-eve-504-128 SRA stem-loop-interacting RNA-binding protein, mitochondrial precursor putative mRNA, complete cds | nt           | 3.75E-02         | up       | up               | up      | 0.0              |
| BT057457.1    | Salmo salar clone ssal-eve-522-007 Vitamin D3 hydroxylase-associated protein putative mRNA, complete cds | nt           | -2.0             | 1.9      | 1.62E-03         | -14.2   | -0.0             |
| BT046649.1    | Salmo salar clone ssal-eve-527-292 Mitochondrial 28S ribosomal protein S36 putative mRNA, complete cds | nt           | 1.9              | 9.01E-02 | down             | -1.8    | 3.1              |
| BT057411.1    | Salmo salar clone ssal-eve-550-301 Eukaryotic translation initiation factor 3 subunit C putative mRNA, complete cds | nt           | down             | down     | 1.18E-04         | down    | down             |
| Accession    | Description                                                                 | nt  | -2.8 | -4.4 | 8.30E-03 | -21.0 | -1.3 |
|--------------|------------------------------------------------------------------------------|-----|------|-------|----------|-------|------|
| 303663498    | Salmo salar clone ssal-evf-563-255 C8orf40 homolog putative mRNA, complete cds| nt  | down | -4.9  | 6.99E-02 | down  | 0.0  |
| 209734397    | Salmo salar clone ssal-plnb-004-066 Gastrotrpin putative mRNA, complete cds  | nt  | down | 3.07E-10 | -273.9 | up    | up   |
| 304376917    | Salmo salar clone ssal-plnb-506-126 Lipocalin precursor putative mRNA, complete cds | nt  | -1.4 | 2.87E-03 | 5.66E-03 | down  | -3.2 |
| 209730649    | Salmo salar clone ssal-plnb-027-103 Lectin precursor putative mRNA, complete cds | nt  | 0.00 | -1.2  | 1.18E-02 |       |      |
| 209738155    | Salmo salar clone ssal-rfb-563-255 C8orf40 homolog putative mRNA, complete cds | nt  | 8.88E-02 | 27.2  | 0.0     | 0.0   | 0.0  |
| 209735875    | Salmo salar clone ssal-rfb-617-026 Nattecin precursor putative mRNA, complete cds | nt  | 0.00 | 9.10E-07 | -39.41 | 0.0   | 0.0  |
| 209730271    | Salmo salar clone ssal-rfb-641-117 Tetraspanin-8 putative mRNA, complete cds  | nt  | 3.14E-04 | up    | -0.0     | -5.4  | 5.91E-02 | up |
| 224587002    | Salmo salar clone ssal-rfb-002-348 Collagen alpha-3VI chain precursor putative mRNA, pseudogene cds | nt  | 8.00E-03 | down  | -1.5 | 8.30E-03 | down  | 0.0  |
| 209148888    | Salmo salar clone ssal-rfb-501-044 BCL2 adenovirus E1B 19 kDa protein-interacting protein 3 putative mRNA, complete cds | nt  | 0.00 | 4.41E-02 | up    | down  | 0.0  |
| 224587036    | Salmo salar clone ssal-rfb-502-231 unknown large open reading frame mRNA, novel cds | nt  | -1.1 | -1.7  | 4.44E-02 | -5.7  | -1.3 |
| 224587090    | Salmo salar clone ssal-rfb-504-369, novel cds | nt  | down | -0.0   | 6.38E-08 | down  | 0.0  |
| 223647599    | Salmo salar clone ssal-rfb-507-102 Actin-related protein 2-A putative mRNA, complete cds | nt  | 3.75E-02 | down  | up   | -2.9  | 0.0  |
| 209154129    | Salmo salar clone ssal-rfb-510-148 Ubiquitin-conjugating enzyme E2 D2 putative mRNA, complete cds | nt  | down | -5.4  | 3.65E-02 | down  | down |
| 223647861    | Salmo salar clone ssal-rfb-517-215 Stromal cell-derived factor 1 precursor putative mRNA, complete cds | nt  | -1.9 | down  | 8.02E-14 | -312.0 | 4.7  |
| 223647865    | Salmo salar clone ssal-rfb-517-265 Actin-related protein 2-A putative mRNA, complete cds | nt  | -1.3 | -1.3  | 3.02E-02 | -11.7 | down |
| 224587384    | Salmo salar clone ssal-rfb-517-384 unknown large open reading frame mRNA, novel cds | nt  | -1.6 | 6.21E-08 | -121.6 | 9.52E-03 | -8.0  | down |
| 224587388    | Salmo salar clone ssal-rfb-518-093 Proto-oncogene vav putative mRNA, pseudogene cds | nt  | 0.00 | 0.0   | 1.91E-06 | down  | -1.2 |
| 224587400    | Salmo salar clone ssal-rfb-518-306 Myosin-9 putative mRNA, pseudogene cds | nt  | down | down  | 8.79E-02 | down  | 0.0  |
| Accession  | Description                                                                 | Log2 Fold Change | p-value     | Gene ID                                      | Log2 Fold Change | p-value     |
|------------|------------------------------------------------------------------------------|------------------|-------------|----------------------------------------------|------------------|-------------|
| 224587424  | Salmo salar clone ssal-rgf-519-255 Ubiquitin-conjugating enzyme E2 L3 putative mRNA, partial cds | - 1.2            | 3.7         | 8.09E-06                                     | up               | 8.31E-04    |
| 209154931  | Salmo salar clone ssal-rgf-521-193 B-cell receptor-associated protein 31 putative mRNA, complete cds | - 0.00           | 1.19E-02    | down                                        | - 0.0            | up          |
| 224587488  | Salmo salar clone ssal-rgf-521-227 unknown large open reading frame mRNA, novel cds | 7.32E-02         | -6.3        | 1.4                                          | - 1.1            |            |
| 223649215  | Salmo salar clone ssal-rgf-521-267 Tripartite motif-containing protein 25 putative mRNA, complete cds | - 2.0            | - 2.2       | 4.73E-02                                     | - 7.3            | - 5.9       |
| 224587510  | Salmo salar clone ssal-rgf-522-242 Biotin--protein ligase putative mRNA, pseudogene cds | 3.75E-02         | - 1.8       | - 1.7                                        | - 0.0            |            |
| 209155099  | Salmo salar clone ssal-rgf-523-374 max putative mRNA, complete cds            | - 4.1            | 3.7         | 3.02E-02                                     | down             |            |
| 209155209  | Salmo salar clone ssal-rgf-525-166 Histone chaperone asf1-B putative mRNA, complete cds | - 4.1            | 3.7         | 3.02E-02                                     | down             |            |
| 224613399  | Salmo salar clone ssal-rgf-525-359 Transketolase-like protein 2 putative mRNA, partial cds | - 1.1            | 1.1         | 5.65E-02                                     | up               | 1.1         |
| 224613403  | Salmo salar clone ssal-rgf-526-138 Fructose-1,6-bisphosphatase 1 putative mRNA, partial cds | - down           | down        | 9.71E-10                                     | down             |            |
| 224587622  | Salmo salar clone ssal-rgf-527-126 unknown large open reading frame mRNA, novel cds | - down           | down        | 3.24E-03                                     | down             |            |
| 224587648  | Salmo salar clone ssal-rgf-528-100 Poly polymerase 14 putative mRNA, pseudogene cds | 1.58E-03         | - 5.3       | 4.41E-02                                     | - 7.8            | - 2.2       |
| 223640117  | Salmo salar clone ssal-rgf-532-019 Actin, cytoplasmic 1 putative mRNA, complete cds | - 2.5            | - 19.7      | 7.77E-04                                     | - 31.8           |            |
| 223648461  | Salmo salar clone ssal-rgf-538-059 F-box/LRR-repeat protein 5 putative mRNA, complete cds | - 0.00           | 7.67E-02    | down                                        | - 14.6           |            |
| 209156037  | Salmo salar clone ssal-rgf-538-237 Serine/threonine-protein kinase MST4 putative mRNA, complete cds | - 0.00           | 4.16E-06    | down                                        | - down           |            |
| 224587895  | Salmo salar clone ssal-rgf-539-307 Ras GTPase-activating-like protein IQGAP1 putative mRNA, partial cds | - 1.4            | - 2.0       | 5.91E-03                                     | - 9.9            | 0.0         |
| 224587922  | Salmo salar clone ssal-rgf-541-083 unknown large open reading frame mRNA, novel cds | - 1.2            | 1.4         | 8.79E-02                                     | up               | 0.0         |
| 223672306  | Salmo salar clone ssal-rgf-541-084 Ig kappa chain V-IV region B17 precursor putative mRNA, complete cds | - down           | up          | 8.79E-02                                     | - 5.4            | 0.0         |
| 223672718  | Salmo salar clone ssal-rgf-507-311 Ig kappa chain V region K29-213 putative mRNA, complete cds | - down           | down        | 1.50E-04                                     | down             | - 1.1       |
| 291190370  | Salmo salar Clusterin (clus), mRNA Refseq_genes                              | - down           | down        | 4.05E-05                                     | down             |            |
| 21351351   | Salmo salar COMM domain-containing protein 9 (comd9), mRNA Refseq_genes      | - down           | down        | 1.07E-03                                     | down             |            |
| Genbank | Accession | Description | Refseq | Genes | Change | Value1 | Value2 | Value3 | Value4 |
|---------|-----------|-------------|--------|-------|--------|--------|--------|--------|--------|
| 291190431 | NM_001173900.1 | Salmo salar complement component 1, q subcomponent, B chain (c1qb), mRNA | Refseq | genes |  | -5.1 | -4.1 | 6.97E-02 | 4.9 |
| 226442587 | NM_001146430.1 | Salmo salar Complement component C8 gamma chain (co8g), mRNA | Refseq | genes |  | -1.1 | 2.5 | 4.44E-02 | 8.0 |
| 226443114 | NM_001146569.1 | Salmo salar CU070 protein (cu070), mRNA | Refseq | genes |  | 3.4 | -1.7 | 6.04E-02 | -18.4 |
| 213512792 | NM_001140055.1 | Salmo salar Dual specificity protein kinase CLK4 (clk4), mRNA | Refseq | genes | down | 8.39E-02 | -6.7 | -1.1 | -1.9 |
| 185133694 | NM_001123697.1 | Salmo salar eggshell protein (LOC100136930), mRNA | Refseq | genes |  | 0.00 | 0.0 | 0.0 | 7.25E-10 |
| 213512966 | NM_001139774.1 | Salmo salar Epidermis-type lipoxigenase 3 (loxe3), mRNA | Refseq | genes | 1.24E-02 | 8.6 | -1.4 | up | 0.0 |
| 194396635 | EU643669.1 | Salmo salar Haplotypic type NADH dehydrogenase subunit 5 (NADH-5) gene, partial cds; mitochondrial | nt | - | down | 9.01E-02 | down | 3.65E-02 | down | 7.28E-04 | down |
| 213512932 | NM_001140489.1 | Salmo salar Haplotypic NADH dehydrogenase subunit 5 (NADH-5) gene, partial cds; mitochondrial | nt | - | down | -2.0 | -14.6 | 6.72E-02 | -5.2 |
| 158702273 | EU025707.1 | Salmo salar immediate early response 2 (ier2), mRNA | Refseq | genes |  | -1.0 | -1.1 | -1.5 | 6.25E-04 | -11.5 |
| 213513791 | NM_001140121.1 | Salmo salar immediate early response 2 (ier2), mRNA | Refseq | genes |  | -1.0 | 1.1 | 6.49E-05 | up | -1.4 |
| 259155205 | NM_001165372.1 | Salmo salar Inosine-5-monophosphate dehydrogenase 1 (imdh1), mRNA | Refseq | genes | up | 3.54E-02 | down | -1.8 | up |
| 356640272 | NM_001252361.1 | Salmo salar intermediate family regulatory factor 1 (irf1), mRNA | Refseq | genes | down | -1.6 | 9.04E-04 | -472.8 | down |
| 213514485 | NM_001140576.1 | Salmo salar Leukocyte surface antigen CDS3 (cds3), mRNA | Refseq | genes | - | -2.3 | 8.30E-03 | down | -0.0 |
| 218931109 | NM_001140986.1 | Salmo salar Mannose-specific lectin (asal), mRNA | Refseq | genes | 2.16E-05 | -29.8 | -2.7 | down | down |
| 213512998 | NM_001140457.1 | Salmo salar matrix metalloproteinase 9 (mmp9), mRNA | Refseq | genes | - | 1.2 | down | 4.41E-02 | -12.1 |
| 185132565 | NM_001123669.1 | Salmo salar mitochondrion, complete genome | nt | - | down | 9.37E-03 | 8.2 | 6.22E-03 | 7.7 | 2.7 | 4.46E-02 | 5.6 |
| 25573079 | AF504023.1 | Salmo salar mitochondrion, complete genome | nt | 2.19E-08 | down | 7.25E-07 | -142.8 | 7.44E-06 | down |
| 36548533 | JN897012.1 | Salmo salar mitochondrion, complete genome | nt | - | down | 1.84E-02 | down | down | down |
| 378554505 | JQ390056.1 | Salmo salar mitochondrion, complete genome | nt | 5.37E-03 | -11.4 | 2.37E-05 | -22.9 | 7.44E-06 | -23.7 |
| 3775976 | u12143.1 | Salmo salar mitochondrion, complete genome | nt | 1.51E-06 | down | 1.38E-08 | down | 3.07E-11 | down | 4.47E-12 | down |
| 259155233 | NM_001165386.1 | Salmo salar mitochondrial coactivator 4 (mtcoa), mRNA | Refseq | genes | - | -1.9 | down | 7.89E-04 | down | down |
| 259155169 | NM_001165355.1 | Salmo salar mitochondrial coactivator 4 (mtcoa), mRNA | Refseq | genes | - | -1.2 | 1.2 | -1.2 | 3.97E-02 | 7.0 |
| Gene ID      | Accession       | Description                                                   | Refseq Genes | log2 Fold Change | p-value       | Admixture   | Mixture          |
|-------------|-----------------|---------------------------------------------------------------|--------------|-----------------|---------------|-------------|-----------------|
| 226443008   | NM_001146539.1  | Salmo salar Nucleoplasmin-like protein NO29 (no29), mRNA     | Refseq Genes | -0.00           | 1.04E-02      | down        | 0.0             |
| 329130751   | HM133629.1      | Salmo salar olfactory receptor family C subfamily 2 member 1 gene, complete cds | nt           | -0.00           | 4.61E-02      | down        | -8.4            |
| 329130737   | HM133622.1      | Salmo salar olfactory receptor family C subfamily 4 member 11 gene, complete cds | nt           | -7.6            | 6.47E-04      | down        | 1.1             |
| 238154523   | NM_001140090.1  | Salmo salar olfactory receptor family C subfamily 2 member 1 gene, complete cds | Refseq Genes | 0.00            | 6.99E-02      | down        | 0.0             |
| 21351391    | NM_001140288.1  | Salmo salar Polypyrimidine tract-binding protein 1 (ptbp1), mRNA | Refseq Genes | -4.3            | 8.25E-07      | down        | 0.0             |
| 226443419   | NM_001146429.1  | Salmo salar Proheparin-binding EGF-like growth factor (hbegf), mRNA | Refseq Genes | 1.4             | 1.31E-03      | up          | 0.0             |
| 213513082   | NM_001141336.1  | Salmo salar Pyrroline-5-carboxylate reductase 2 (p5cr2), mRNA | Refseq Genes | -3.0            | 1.21E-03      | up          | 0.0             |
| 226443273   | NM_001146626.1  | Salmo salar Ran-binding protein 10 (rpb10), mRNA              | Refseq Genes | 1.2             | 9.95E-02      | down        | 0.0             |
| 213512635   | NM_001140741.1  | Salmo salar Rhamnose-binding lectin (sal), mRNA               | Refseq Genes | -2.0            | 1.98E-02      | down        | 0.0             |
| 213514719   | NM_001141345.1  | Salmo salar S100-A16 (s10ag), mRNA                           | Refseq Genes | -3.0            | 7.29E-07      | down        | 0.0             |
| 213515517   | NM_001140898.1  | Salmo salar Sclerostin domain-containing protein 1 (sosd1), mRNA | Refseq Genes | -13.5           | 4.39E-02      | down        | -1.1            |
| 213512394   | NM_001141358.1  | Salmo salar SOD462 (y4629), mRNA                             | Refseq Genes | 9.61E-03        | 6.42E-03      | up          | 0.0             |
| 291190832   | NM_001173937.1  | Salmo salar Selenide, water dikinase 1 (sps1), mRNA          | Refseq Genes | 0.00            | 2.24E-04      | down        | 0.0             |
| 185133666   | NM_001123692.1  | Salmo salar serum albumin 2 (LOC100136922), mRNA              | Refseq Genes | 1.0             | 3.02E-02      | up          | -1.5            |
| 185133997   | NM_001123569.1  | Salmo salar serum lectin isoform 1 precursor (LOC100136435), mRNA | Refseq Genes | 1.0             | 6.71E-03      | up          | 0.0             |
| 213514919   | NM_001141637.1  | Salmo salar Sporozoite surface protein 2 (ssp2), mRNA         | Refseq Genes | -4.2            | 2.27E-02      | up          | 0.0             |
| 213513389   | NM_001140261.1  | Salmo salar Transcobalamin-2 (tco2), mRNA                     | Refseq Genes | 0.00            | 1.79E-03      | down        | 0.0             |
| 291190285   | NM_001173882.1  | Salmo salar Tropomodulin-3 (tmod3), mRNA                      | Refseq Genes | 0.00            | 6.84E-03      | down        | 0.0             |
| 185135858   | NM_001123711.1  | Salmo salar trypsin IA (trp-ia), mRNA                         | Refseq Genes | 0.00            | 0.00         | -1.4         | up              |
| 213514129   | NM_001139633.1  | Salmo salar upstream transcription factor 1 (usf1), mRNA      | Refseq Genes | 0.00            | 0.00         | -1.4         | up              |
| 185133517   | NM_001123588.1  | Salmo salar zonadhesin-like (LOC100136455), mRNA              | Refseq Genes | 1.0             | 0.90E-02      | up          | 0.0             |
| 7769634     | AF228581.1      | Salmo trutta IgM-B heavy chain constant region mRNA, partial cds | Refseq Genes | 0.00            | 2.07E-03      | down        | 0.0             |
| 164510790   | AM262766.1      | Salmo trutta partial mRNA for MHC class I heavy chain, Satr-UBA*2801 allele (uba gene) | nt           | 6.67E-04        | 0.00         | down        | 0.0             |
| Gene Symbol | Description | Species | Expression Change | Log2 Fold Change | p-Value |
|-------------|-------------|---------|------------------|-----------------|---------|
| s39         | Salvelinus namaycush transposon Tsn1-3 transposase (Tsn1) pseudogene, complete sequence | nt       | -1.6             | 7.27E-02        | 0.0019  |
| sar1b       | SAR1 homolog B (S. cerevisiae) | Ensembl_stickleback | -4.8             | 0.0019          | -1.0   |
| sec24b      | SEC24 family, member B (S. cerevisiae) | Ensembl_stickleback | -1.1             | 0.0019          | -1.0   |
| sec61a1 (2 of 2) | Sec61 alpha 1 subunit (S. cerevisiae) | Ensembl_stickleback | 1.5              | 0.0019          | -1.0   |
| serpina1    | serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 | Ensembl_zebrafish | 2.4              | 15.7            | 0.0019 |
| serpin1     | serine (or cysteine) proteinase inhibitor, clade D (heparin cofactor), member 1 | Ensembl_zebrafish | 2.3              | 12.2            | 0.0019 |
| serinc2 (1 of 2) | serine incorporator 2 | Ensembl_stickleback | 1.5              | 0.0019          | -1.0   |
| srsf5       | serine/arginine-rich splicing factor 5 | Ensembl_stickleback | -1.9             | 30.0            | 0.0019 |
| srlg         | serine/arginine-rich splicing factor 5 | Ensembl_stickleback | 2.2              | 4.1             | 0.0019 |
| srbf1       | SET binding factor 1 | Ensembl_nile_tilapia | -1.3             | 12.4            | 0.0019 |
| sdr42e1     | short chain dehydrogenase/reductase family 4E2, member 1 | Ensembl_stickleback | 2.42E-03         | 1.3             | 0.0019 |
| srich112-207c6.2 | srich112-207c6.2 | Ensembl_zebrafish | -3.8             | 0.0019          | -1.0   |
| srich7-103b2.3 | srich7-103b2.3 | Ensembl_zebrafish | 0.00             | 0.0019          | -1.0   |
| srich3-18b11.1 | srich3-18b11.1 | Ensembl_zebrafish | -3.6             | 1.0             | 0.0019 |
| srich-119f1.1 | srich-119f1.1 | Ensembl_zebrafish | -0.00            | 0.0019          | -1.0   |
| srich-179j5.2 | srich-179j5.2 | Ensembl_zebrafish | 0.00             | 0.0019          | -1.0   |
| srich-17f3.15 | srich-17f3.15 | Ensembl_zebrafish | -1.5             | 1.5             | 0.0019 |
| srich-176d12.1 | srich-176d12.1 | Ensembl_zebrafish | -1.5             | 1.5             | 0.0019 |
| srich-176d12.1 | srich-176d12.1 | Ensembl_zebrafish | 1.5              | 4.52E-02        | 0.0019 |
| neu1        | sialidase 1 (lysosomal sialidase) | Ensembl_stickleback | -32.8            | 0.0019          | -1.0   |
| srs72       | signal recognition particle 72kDa | Ensembl_stickleback | 1.6              | 36.5E-02        | 0.0019 |
| srbp        | signal recognition particle receptor, B subunit | Ensembl_medaka | 1.0              | 9.01E-02        | 0.0019 |
| srs9a (1 of 2) | SIN3 transcription regulator homolog A (yeast) | Ensembl_nile_tilapia | 0.00             | 4.67E-03        | 0.0019 |
| srix1       | SIX homeobox 1 | Ensembl_stickleback | 3.6              | 8.79E-02        | 0.0019 |
| srix4       | six-cysteine containing astacin protease 4 | Ensembl_zebrafish | 0.00             | 2.12E-06        | 0.0019 |
| sbg         | SBG Atlantic Salmon liver SSH Salmo salar cDNA clone SL3-0294, mRNA sequence. EST_others | Ensembl_stickleback | 0.00             | 5.51E-02        | 0.0019 |

ENSGACG00000001474
ENSDARG000000069983
ENSGACG00000016757
ENSGACG00000008080
ENSDARG000000090286
ENSDARG00000021208
ENSGACG00000007719
ENSGACG00000007834
ENSORLG00000016512
ENSGACG0000010973
ENSORLG00000016512
ENSGACG000000014791
ENSDARG000000095304
ENSGACG00000073742
ENSGACG00000093374
ENSDARG00000058719
ENSDARG00000060325
ENSDARG00000094929
ENSDARG00000068515
ENSGACG00000002914
ENSGACG00000016749
ENSLQG000000066430
ENSONIG000000012851
ENSGACG00000008432
ENSDARG00000052578
BQ036199
ENSGACG00000016411
| Gene ID               | Gene Symbol | Description                                                                 | Species      | log2FoldChange | Adj. p-value |
|----------------------|-------------|------------------------------------------------------------------------------|--------------|----------------|--------------|
| ENSDARG000000071430  | smyc1       | slow myosin heavy chain 1                                                    | Ensembl_zebrafish | 2.44E-03       | -1.5         |
| ENSGACG00000015581  | sumo1       | SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)                       | Ensembl_stickleback | -11            | -14.4        |
| DW592332             |             | ssmus1-016AE03.g1_00016.0 DIAS_SMUS Salmo salar cDNA 5', mRNA sequence.     | EST_others    | 4.1            | 3.65E-02     |
| ENSIONIG00000004201  | slc12a9     | solute carrier family 12 (potassium/chloride transporters), member 9         | Ensembl_nile_tilapia | 1.6            | 3.67E-05     |
| ENSDARG00000013855  | slc12a3     | solute carrier family 12 (sodium/chloride transporters), member 3            | Ensembl_zebrafish | 1.3            | 7.2E-02       |
| ENSGACG00000007935  | slc16a4     | solute carrier family 16, member 4 (monocarboxylic acid transporter 5)       | Ensembl_stickleback | 0.00           | 1.42E-03     |
| ENSGACG00000010985  | slc2a2      | solute carrier family 2 (facilitated glucose transporter), member 2         | Ensembl_stickleback | up             |
| ENSGACG00000019384  | slc2a4      | solute carrier family 2 (facilitated glucose transporter), member 4         | Ensembl_stickleback | down           |
| ENSGACG00000013596  | slc2a6      | solute carrier family 24 (sodium/lithium/calcium exchanger), member 6       | Ensembl_nile_tilapia | 1.9            | 1.68E-03     |
| ENSGACG00000015473  | slc25a36    | solute carrier family 25 (pyrimidine nucleotide carrier), member 36         | Ensembl_stickleback | up             |
| ENSGACG00000005439  | slc35a2b    | solute carrier family 35, member E2B                                        | Ensembl_stickleback | -11            | 1.96E-03     |
| ENSGACG00000016873  | slc39a2     | solute carrier family 39 (zinc transporter), member 2                       | Ensembl_stickleback | -1.6           | 8.3E-03      |
| ENSGACG00000007949  | slc48a1     | solute carrier family 48 (heme transporter), member 1                        | Ensembl_stickleback | -1.8           | 1.08E-03     |
| ENSGACG00000004673  | snx5        | sorting nexin 5                                                             | Ensembl_stickleback | up             |
| ENSGACG00000006733  | spc24       | SPC24, NDC80 kinetochore complex component, homolog 5 (S. cerevisiae)       | Ensembl_stickleback | 0.00           | 4.5E-02      |
| ENSGACG00000020699  | spag7       | sperm associated antigen 7                                                   | Ensembl_stickleback | -1.1           | 8.6E-02      |
| ENSGACG00000013537  | s1pr1       | sphingosine-1-phosphate receptor 1                                           | Ensembl_stickleback | 2.1            | 1.85E-07     |
| ENSGACG00000008317  | skap2       | src kinase associated phosphoprotein 2                                       | Ensembl_stickleback | 3.75E-02       | 1.9          |
| ENSGACG00000011185  | sax9(2 of 2) | SRY (sex determining region Y)-box 9                                        | Ensembl_stickleback | 0.00           | 4.1          |
| ENSGACG00000016008  | st6galnac6  | ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1, 3'-N-acetylgalactosamine alpha-) | Ensembl_stickleback | -1.4           | 5.07E-02     |
| ENSORLG00000018292  | stab2       | stabilin 2                                                                  | Ensembl_medaka | -1.1           | 9.95E-02     |
| ENSORLG00000003328  | stc1(2 of 2) | stanniocalcin 1                                                              | Ensembl_medaka | down           |
| ENSDARG000000058476  | stc1l       | stanniocalcin 1, like                                                        | Ensembl_zebrafish | down           |
| ENSDARG00000033662  | stcd        | stearoyl-CoA desaturase (delta-9-desaturase)                                  | Ensembl_zebrafish | 1.2            | 1.0          |
| ENSDARG00000024026  | stfd2       | stromal cell-derived factor 2                                                | Ensembl_zebrafish | 1.2            | 1.8          |
| ENSGACG00000020581  | sod1        | superoxide dismutase 1, soluble                                             | Ensembl_stickleback | 1.15E-02       | 6.61E-04     |

S40
| Gene Symbol | Gene Name | Description | Species | Direction | Ratio | p-value | Regulation | Species | Direction | Ratio | p-value | Regulation |
|-------------|-----------|-------------|---------|----------|-------|---------|------------|---------|----------|-------|---------|------------|
| ENSGACG00000013091 | st14 (1 of 3) | suppression of tumorigenicity 14 (colon carcinoma) | Ensembl_stickleback | | 6.09E-02 | 29.6 | -1.3 | 1.96E-02 | 30.7 | - | 0.0 |
| ENSGACG00000006093 | st7l | suppression of tumorigenicity 7 like | Ensembl_stickleback | | - | 0.0 | 2.62E-05 | -33.1 | - | 0.0 | up |
| ENSGACG00000016739 | sapcd2 | suppressor APC domain containing 2 | Ensembl_stickleback | | - | 1.9 | 4.41E-02 | 25.0 | - | 1.3 | down |
| ENSGACG00000007257 | sufu | suppressor of fused homolog (Drosophila) | Ensembl_stickleback | | down | down | 3.65E-02 | down | | up |
| ENSGACG00000013526 | suv420h2 | suppressor of variegation 4-20 homolog 2 (Drosophila) | Ensembl_stickleback | | up | down | 6.99E-02 | down | | up |
| ENSGACG00000012650 | smarcc1 (1 of 2) | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 | Ensembl_stickleback | | - | 0.0 | 2.29E-02 | up | | 0.0 | down |
| ENSGACG00000003136 | syt11 | synaptotagmin XI | Ensembl_stickleback | | - | 1.0 | 8.90E-08 | down | -2.8 | -1.3 | up |
| 288548571 | GU569096.1 | Taenia pisiformis mitochondrion, complete genome | nt | | - | 0.0 | 6.59E-03 | 8.6 | - | 0.0 | up |
| ENSDARG00000054255 | tctex1d2 | Tctex1 domain containing 2 | Ensembl_zebrafish | | - | 1.3 | 1.3 | 2.28E-03 | up | - | 1.9 |
| ENSONIG00000012488 | tctex1d2 | Tctex1 domain containing 2 | Ensembl_nile_tilapia | | 0.0 | 0.0 | 6.99E-02 | down | | 0.0 | up |
| 56326278 | CR650765.2 | Tetraodon nigroviridis full-length cDNA | nt | | - | 1.2 | 9.01E-02 | up | - | 1.4 | 2.0 |
| ENSGACG00000005236 | tspan2 (2 of 2) | tetraspanin 2 | Ensembl_stickleback | | up | 5.20E-03 | up | | - | down | -1.7 |
| ENSDARG0000008407 | tspan7b | tetraspanin 7b | Ensembl_zebrafish | | -3.0 | -2.5 | 5.07E-02 | -14.4 | up | - | 0.0 |
| ENSONIG00000003747 | ttc14 | tetratricopeptide repeat domain 14 | Ensembl_nile_tilapia | | 6.54E-03 | up | down | 6.84E-03 | up | - | 1.0 |
| 290793107 | GU217573.1 | Thunnus thynnus vitellogenin C mRNA, complete cds | nt | | - | 0.0 | 0.0 | up | 1.57E-20 | up | |
| ENSGACG00000016986 | trip4 | thyroid hormone receptor interactor 4 | Ensembl_stickleback | | 1.61E-02 | up | up | - | -1.0 | - | up |
| ENSDARG0000002909 | tip3 | tight junction protein 3 | Ensembl_zebrafish | | - | 1.2 | 1.1 | 1.59E-02 | 11.6 | 2.14E-02 | 12.3 |
| ENSGACG0000003028 | timp2 (2 of 2) | TIMP metalloproteinase inhibitor 2 | Ensembl_stickleback | | 0.0 | 0.0 | 2.75E-04 | down | | 0.0 | up |
| ENSORLG00000012522 | tsta3 | tissue specific transplantation antigen P35B | Ensembl_medaka | | 2.00E-02 | down | 3.88E-05 | down | | - | 0.0 | up |
| ENSDARG00000063420 | tox4 (2 of 2) | TOX high mobility group box family member 4 | Ensembl_zebrafish | | -15.1 | 6.40E-02 | 23.5 | - | 4.7 | down | |
| ENSGACG00000017200 | told1 | transaldolase 1 | Ensembl_stickleback | | down | 2.29E-02 | down | | -1.6 | 0.0 | up |
| ENSONIG00000009845 | tf | transferrin | Ensembl_nile_tilapia | | down | 9.01E-02 | up | 8.78E-08 | down | | 1.1 |
| ENSGACG00000019195 | tmc7 | transmembrane channel-like 7 | Ensembl_stickleback | | 5.86E-02 | up | - | 1.3 | down | | 0.0 |
| ENSGACG00000015584 | tmed2 | transmembrane emp24 domain trafficking protein 2 | Ensembl_stickleback | | - | 0.0 | 0.0 | 8.79E-02 | down | | 0.0 |
| ENSGACG00000016336 | tmed9 | transmembrane emp24 protein transport domain containing 9 | Ensembl_stickleback | | 1.8 | 6.04E-03 | -22.0 | up | 4.7 | down | |
| ENSGACG00000004023 | tmem106c | transmembrane protein 106C | Ensembl_stickleback | | 1.71E-02 | up | -15.3 | - | 0.0 | down | |
| ENSGACG00000009084 | tmem136 (2 of 2) | transmembrane protein 136 | Ensembl_stickleback | | 2.50E-02 | down | - | 8.79E-02 | up | | 0.0 |
| Gene ID                | Description                                      | Species                      | Up/Down   | Log2 Fold Change | p-value       |
|-----------------------|--------------------------------------------------|------------------------------|-----------|-----------------|--------------|
| ENSGACG00000013071    | tmem161a transmembrane protein 161A              | Ensembl_stickleback          | up        | 5.69E-02        | -5.41        |
| ENSGACG00000016548    | tmem38b transmembrane protein 38B                | Ensembl_stickleback          | 4.11E-07  | 43.7            | -1.1         |
| ENSGACG00000003118    | tmem42 transmembrane protein 42                  | Ensembl_stickleback          | -4.4      | 0.0             | 2.01E-17     |
| ENSGACG00000004640    | tmem64 transmembrane protein 64                  | Ensembl_stickleback          | -1.8      | -4.3            | -5.3         |
| ENSGACG00000015841    | tnpo1 transportin 1                              | Ensembl_stickleback          | down      | down            | 3.24E-03     |
| ENSGACG00000007382    | trim36 tripartite motif containing 36            | Ensembl_stickleback          | -7.5      | -4.0            | 8.81E-02     |
| ENSDARG00000028027    | trim63 tripartite motif containing 63            | Ensembl_zebrafish            | -1.7      | 1.0             | 2.69E-02     |
| ENSGACG00000004198    | tnc2 (1 of 2)                                    | Ensembl_stickleback          | -6.2      | 1.17E-03        | -12.4        |
| ENSDARG00000042993    | try trypsin                                      | Ensembl_zebrafish            | -1.2      | 1.73E-07        | -12.4        |
| ENSNIG0000003233      | tdrd3 tudor domain containing 3                 | Ensembl_nile_tilapia         | -1.5      | 1.6             | 5.65E-02     |
| ENSGACG00000009537    | tpcn1 two pore segment channel 1                 | Ensembl_stickleback          | -1.4      | -4.7            | 2.2          |
| ENSDARG00000036833    | cyt1l type I cytokeratin, enveloping layer, like | Ensembl_zebrafish            | 1.1       | 9.41            | -2.6         |
| ENSGACG0000005854     | uchi5 ubiquitin carboxyl-terminal hydrolase L5   | Ensembl_stickleback          | down      | 0.0             | 4.49E-02     |
| ENSDARG00000087495    | usp2 (2 of 3)                                    | Ensembl_zebrafish            | 2.4       | 2.2             | 3.36E-02     |
| ENSGACG0000011028     | usp36 ubiquitin specific peptide 36              | Ensembl_stickleback          | 1.08E-02  | -34.3           | 2.07E-03     |
| ENSDARG0000007714     | ube2q1 ubiquitin-conjugating enzyme E2Q (putative) 1 | Ensembl_zebrafish           | -3.7      | 3.54E-02        | up           |
| ENSDARG0000011537     | ugt2a5 UDP glucuronosyltransferase 2 family, polypeptide A5 | Ensembl_zebrafish | down      | down            | 1.91E-07     |
| ENSDARG0000039501     | ugt2a6 UDP glucuronosyltransferase 2 family, polypeptide A6 | Ensembl_zebrafish | 0.00      | down            | 4.36E-09     |
| ENSORLG0000007327     | galtl4 UDP-N-acetyl-alpha-D-galactosamine-polypeptide N-acetylglactosaminyltransferase-like 4 | Ensembl_medaka | down      | 0.0             | 1.96E-02     |
| ENSGACG0000009985     | unc45b unc-45 homolog B (C. elegans)             | Ensembl_stickleback          | 1.8       | up              | 6.59E-02     |
| ENSDARG00000078382    | CABZ01075938.1 Uncharacterized d protein        | Ensembl_zebrafish            | -1.6      | 6.21E-08        | up           |
| ENSDARG00000087843    | CABZ01092722.1 Uncharacterized protein           | Ensembl_zebrafish            | -1.1      | 3.0             | up           |
| ENSDARG00000088309    | ct573337.1 Uncharacterized protein               | Ensembl_zebrafish            | 3.75E-02  | 8.5             | -5.5         |
| 116517246             | NP_001070844.1 uncharacterized protein LOC59260 precursor | Refseq_proteins          | -1.2      | -1.0            | 2.26E-02     |
| 158534007             | NP_001103579.1 uncharacterized protein LOC56171 precursor | Refseq_proteins          | 0.00      | down            | 0.0          |
| ENSGACG00000017435    | upf3b UPF3 regulator of nonsense transcripts homolog B (yeast) | Ensembl_stickleback          | 2.50E-02  | down            | 0.0          |
| ENSGACG00000014740    | upf18 UTP18 small subunit (SSU) processome component homolog (yeast) | Ensembl_stickleback          | - up      | 0.0             | 1.28E-02     |
| Gene Symbol | Ensembl Name | Description | Species | Accession | Start | End | Log2 Fold Change | p-Value |
|-------------|--------------|-------------|---------|-----------|-------|-----|-----------------|---------|
| crk        | ENSGACG00000005430 | v-crk sarcoma virus CT10 oncogene homolog (avian) | Ensembl_stickleback | 4.69E-02 | down | -1.6 | 1.4 | down |
| vis2       | ENSGACG00000005867 | visual system homeobox 2 | Ensembl_stickleback | 7.32E-02 | down | -1.0 | 1.8 | -1.2 |
| vmo1       | ENSRLG00000016336 | vitellogenin membrane outer layer 1 homolog (chicken) | Ensembl_medaka | - | 0.00 | 9.89E-05 | -17.4 | up | -2.2 |
| vtg2       | ENSDARG00000095809 | vitellogenin 2 | Ensembl_zebrafish | - | -1.2 | 2.7 | -1.5 | 9.15E-33 | 20268.3 |
| vtg7       | ENSDARG00000092419 | vitellogenin 7 | Ensembl_zebrafish | - | -1.5 | -1.6 | -1.4 | 2.57E-15 | 317.5 |
| wdr61      | ENSGACG00000007380 | WD repeat domain 61 | Ensembl_stickleback | 1.36E-02 | down | 3.54E-02 | down | 0.0 | down |
| wls        | ENSRLG00000005299 | wontless homolog (Drosophila) | Ensembl_medaka | - | 2.8 | -1.2 | 9.04E-04 | down | down |
| yipf5      | ENSGACG00000207240 | Yip1 domain family, member 5 | Ensembl_stickleback | 7.95E-05 | down | 23.6 | up | -1.0 | down |
|            |              | Zebrafish DNA sequence from clone CH73-348N11 in linkage group 3, complete sequence | nt | - | 1.3 | 1.76E-04 | up | 5.1 | 1.2 |
|            |              | Zebrafish DNA sequence from clone CH73-360N3 in linkage group 3, complete sequence | nt | - | 1.6 | 2.85E-02 | -63.5 | -2.6 | -1.4 |
| zfbx3      | ENSGACG0000015779 | zinc finger homeobox 3 | Ensembl_stickleback | - | 1.0 | 4.30E-03 | down | 4.65E-02 | -7.9 | 3.74E-02 | down |
| zfbx4      | ENSGACG000002418 | zinc finger homeobox 4 | Ensembl_stickleback | - | -3.9 | -6.0 | -1.7 | 6.34E-11 | -403.4 |
| znf423     | ENSGACG000002626 | zinc finger protein 423 | Ensembl_stickleback | - | -16.1 | 1.49E-02 | down | 1.98E-03 | -53.9 | down |
| znf710     | ENSGACG0000016481 | zinc finger protein 710 | Ensembl_stickleback | - | up | up | 3.02E-02 | up | 3.2 |
| znf750     | ENSGACG0000010661 | zinc finger protein 750 | Ensembl_stickleback | - | -1.1 | 9.89E-05 | down | 1.28E-02 | down | down |
| zcchc11    | ENSGACG0000005282 | zinc finger, CCHC domain containing 11 | Ensembl_stickleback | - | 1.3 | -1.4 | 2.2 | 5.72E-03 | -9.7 |
| zranb2     | ENSGACG0000009457 | zinc finger, RAN-binding domain containing 2 | Ensembl_stickleback | - | 1.0 | down | -2.1 | 5.91E-02 | up |
| zwilch     | ENSGACG0000005043 | Zwilch, kinetochore associated, homolog (Drosophila) | Ensembl_stickleback | - | down | down | 1.28E-02 | down | down |
|            | CX256055      | gb|CX256055.1 | 1308952 NCCCWA 02RT Oncorhynchus mykiss cDNA clone 02RT111K06 3', mRNA sequence. | EST_others | 0.00 | 1.29E-03 | -23.7 | -0.0 | 1.4 |
|            | CX261231      | gb|CX261231.1 | 1314740 NCCCWA 02RT Oncorhynchus mykiss cDNA clone 02RT125C20 5', mRNA sequence. | EST_others | 0.00 | 0.0 | 0.0 | 7.12E-03 | 11.2 |
|            | CX262650      | gb|CX262650.1 | 1316309 NCCCWA 02RT Oncorhynchus mykiss cDNA clone 02RT128O12 5', mRNA sequence. | EST_others | 1.36E-02 | up | 1.0 | 1.59E-02 | up | 0.0 |
|            | CX035424      | gb|CX035424.1 | 1348057 NCCCWA 10RT#3 Oncorhynchus mykiss cDNA clone 10RT#3_133F07 5', mRNA sequence. | EST_others | up | 1.0 | 3.02E-02 | down | 0.0 |
|            | CX036514      | gb|CX036514.1 | 1349239 NCCCWA 10RT#3 Oncorhynchus mykiss cDNA clone 10RT#3_137A19 5', mRNA sequence. | EST_others | 1.4 | 2.85E-02 | up | 1.4 | up |
|            | CX039308      | gb|CX039308.1 | 1352460 NCCCWA 10RT#3 Oncorhynchus mykiss cDNA clone 10RT#3_137A19 5', mRNA sequence. | EST_others | 1.3 | 4.12E-02 | -11.4 | -2.0 | 1.4 |
| Ensembl_stickleback       | 5'-nucleotidase domain containing 2 | mRNA sequence | EST_others | down | up |
|--------------------------|------------------------------------|---------------|------------|------|----|
| CA350320 gb|CA350320.1                          | 621050 NCCCW 1RT Oncorhynchus mykiss cDNA clone 1RT147P01_B_H01 5', mRNA sequence. | EST_others | - | 0.00 | - | 1.3 | 4.49E-02 | down | - | up |
| CA367945 gb|CA367945.1                          | 643065 NCCCW 1RT Oncorhynchus mykiss cDNA clone 1RT148K13_A_F07 5', mRNA sequence. | EST_others | 1.4 | - | 0.0 | 1.59E-02 | up | - | 0.0 |
| CA376054 gb|CA376054.1                          | 645297 NCCCW 1RT Oncorhynchus mykiss cDNA clone 1RT34F22_D_C11 5', mRNA sequence. | EST_others | -3.6 | 9.01E-02 | - | 3.0 | - | down |
| CA383249 gb|CA383249.1                          | 663393 NCCCW 1RT Oncorhynchus mykiss cDNA clone 1RT13C10_C_806 5', mRNA sequence. | EST_others | -1.1 | - | 1.5 | - | up | 6.86E-02 | 23.1 |
| BX079066 emb|BX079066.3                          | BX079066 AGENAE Rainbow trout normalized multi-tissues library (tcad) Oncorhynchus mykiss cDNA clone tcad0007.e.09 5prim, mRNA sequence. | EST_others | 0.00 | - | 2.3 | 3.65E-02 | -31.7 | - | 0.0 |
| BX081886 emb|BX081886.2                          | BX081886 AGENAE Rainbow trout normalized multi-tissues library (tcac) Oncorhynchus mykiss cDNA clone tcac0002.f.09 5prim, mRNA sequence. | EST_others | -1.4 | 2.87E-03 | down | - | -1.3 | - | 1.9 |
| BX085529 emb|BX085529.3                          | BX085529 tcav Oncorhynchus mykiss cDNA clone tcav0001.i.12 5prim, mRNA sequence. | EST_others | -1.5 | - | 1.5 | 4.39E-02 | - | 6.4 | - | 1.0 |
| BX860267 emb|BX860267.3                          | BX860267 tcba Oncorhynchus mykiss cDNA clone tcba0008.c.09 5prim, mRNA sequence. | EST_others | 0.00 | 6.34E-04 | -22.7 | - | -1.4 | - | 0.0 |
| BX862653 emb|BX862653.3                          | BX862653 tcba Oncorhynchus mykiss cDNA clone tcba0011.k.06 5prim, mRNA sequence. | EST_others | 0.00 | - | 0.0 | 7.19E-06 | down | 4.78E-02 | down |
| BX862659 emb|BX862659.3                          | BX862659 tcba Oncorhynchus mykiss cDNA clone tcba0011.k.13 5prim, mRNA sequence. | EST_others | 2.4 | - | 1.7 | - | 1.7 | 4.71E-06 | up |
| BX863438 emb|BX863438.3                          | BX863438 tcba Oncorhynchus mykiss cDNA clone tcba0014.c.06 5prim, mRNA sequence. | EST_others | -1.5 | - | 0.0 | 1.22E-03 | down | - | 4.71E-06 | up |
| BX866879 emb|BX866879.3                          | BX866879 tcba Oncorhynchus mykiss cDNA clone tcba0026.f.12 5prim, mRNA sequence. | EST_others | -1.7 | - | up | - | 1.19E-02 | up |
| BX871489 emb|BX871489.2                          | BX871489 tcdb Oncorhynchus mykiss cDNA clone tcdb0008.d.18 5prim, mRNA sequence. | EST_others | -1.1 | 5.82E-03 | -10.2 | - | - | - | down |
| ENSGACG00000000665 ENSGACG00000000655 | ENSGACT000000000858 | Ensembl_stickleback | - | down | down | 3.11E-02 | -32.4 | 3.24E-02 | -29.2 |
| ENSGACG0000000001046 ENSGACG0000000001046 | ENSGACT000000001352 | Ensembl_stickleback | - | 0.00 | 5.20E-03 | up | - | up | - | 0.0 |
| ENSGACG0000000001102 ENSGACG0000000001103 | ENSGACT000000001428 | Ensembl_stickleback | 8.33E-04 | -53.3 | - | 1.1 | - | 1.3 | 2.3 |
| ENSGACG0000000002397 ENSGACG0000000002397 | ENSGACT000000003154 | Ensembl_stickleback | - | 0.00 | - | 1.1 | - | 1.4 | 9.95E-02 | up |
| ENSGACG000000003684 ENSGACG000000003684 | ENSGACT000000004857 | Ensembl_stickleback | 2.50E-02 | down | - | 1.1 | - | 1.4 | 9.95E-02 | up |
| Gene Accession | Ensembl_ID | Ensembl Species | P.Value | Fold_Change | Status       | q.Value | Log2Fold_Change | Status       | q.Value |
|----------------|------------|-----------------|---------|-------------|--------------|---------|----------------|--------------|---------|
| ENSGACG00000003787 | ENSGACT00000004984 | Ensembl_stickleback | 4.56E-06 | up          | 0.0          | 1.0     | -              | up           | -       |
| ENSGACG00000004988 | ENSGACT00000006645 | Ensembl_stickleback | 1.95E-02 | down        | 0.0          | -       | -              | down         | -       |
| ENSGACG00000005457 | ENSGACT00000007232 | Ensembl_stickleback | 7.31E-06 | up          | -1.1         | -       | -1.2           | -1.2         | -1.2    |
| ENSGACG00000005610 | ENSGACT00000007471 | Ensembl_stickleback | 2.85E-02 | up          | -1.1         | -       | -36.5          | -36.5        | -36.5   |
| ENSGACG00000006023 | ENSGACT00000007994 | Ensembl_stickleback | 8.30E-03 | down        | 1.7          | -       | -1.8           | -1.8         | -1.8    |
| ENSGACG00000006109 | ENSGACT00000008146 | Ensembl_stickleback | 1.07E-03 | down        | 3.46E-09     | 3.46E-09| -              | 990.0        | -       |
| ENSGACG00000006376 | ENSGACT00000008463 | Ensembl_stickleback | 4.99E-02 | down        | 4.99E-02     | 4.99E-02| -              | 0.0          | -       |
| ENSGACG00000006658 | ENSGACT00000008841 | Ensembl_stickleback | 1.66E-03 | down        | 1.66E-03     | 1.66E-03| -              | 0.0          | -       |
| ENSGACG00000007518 | ENSGACT00000010009 | Ensembl_stickleback | 8.30E-03 | up          | 1.3          | -       | 3.90E-06       | -1.2         | -1.2    |
| ENSGACG00000007857 | ENSGACT00000010455 | Ensembl_stickleback | 3.31E-05 | down        | 3.31E-05     | 3.31E-05| -              | 0.0          | -       |
| ENSGACG00000007990 | ENSGACT00000010603 | Ensembl_stickleback | 9.90E-02 | down        | 9.90E-02     | 9.90E-02| -              | 0.0          | -       |
| ENSGACG00000008104 | ENSGACT00000010748 | Ensembl_stickleback | 1.36E-03 | down        | 1.36E-03     | 1.36E-03| -              | 0.0          | -       |
| ENSGACG00000008362 | ENSGACT00000011076 | Ensembl_stickleback | 1.00E-03 | up          | 1.00E-03     | 1.00E-03| -              | 0.0          | -       |
| ENSGACG00000008527 | ENSGACT00000011292 | Ensembl_stickleback | 4.66E-03 | down        | 4.66E-03     | 4.66E-03| -              | 0.0          | -       |
| ENSGACG00000008544 | ENSGACT00000011317 | Ensembl_stickleback | 1.99E-03 | down        | 1.99E-03     | 1.99E-03| -              | 0.0          | -       |
| ENSGACG00000008811 | ENSGACT00000011669 | Ensembl_stickleback | 3.46E-03 | up          | 3.46E-03     | 3.46E-03| -              | 0.0          | -       |
| ENSGACG00000009769 | ENSGACT00000012954 | Ensembl_stickleback | 990.0    | down        | 990.0        | 990.0   | -              | 0.0          | -       |
| Gene Symbol | Description                  | Ensembl Stickelback | P-value | Direction | Fold Change | Adjusted P-value |
|-------------|------------------------------|---------------------|---------|-----------|-------------|-----------------|
| ENSGACG00000012810 810 | Ensembl_stickleback         | 9.44E-05            | up      | 2.33E-05  | 51.6        | -1.3            |
| ENSGACG00000013819 819 | Ensembl_stickleback         | 2.5                 | up      | 1.0       | 3.90E-03   | up              |
| ENSGACG00000014922 922 | Ensembl_stickleback         | 0.00                | down    | 4.56E-06  | -21.0      | up              |
| ENSGACG00000016744 744 | Ensembl_stickleback         | 0.00                | down    | 9.52E-06  | up          | -2.2            |
| ENSGACG00000020439 439 | Ensembl_stickleback         | 1.08E-02            | up      | -34.4     | 3.45E-10   | down            |
| ENSGACG00000020467 467 | Ensembl_stickleback         | 0.00                | down    | 3.59E-04  | down        | 7.28E-04        |
| ENSGACG00000020921 921 | Ensembl_stickleback         | 2.14E-06            | down    | 7.73E-07  | -65.9       | 3.05E-10        |
| ENSONIG00000000287 27  | Ensembl_nile_tilapia        | -0.00               | -up     | -5.5      | -1.0       | -30.9           |
| ENSONIG00000000450 40  | Ensembl_nile_tilapia        | -1.2                | -2.9    | -1.7      | 2.31E-02   | down            |
| ENSONIG0000000072 19   | Ensembl_nile_tilapia        | -1.4                | 2.12E-06| 55.2      | -2.8       | -1.1            |
| Gene ID               | Accession | Description                                                                 | Log2 Fold Change | p-value     |
|----------------------|-----------|------------------------------------------------------------------------------|------------------|-------------|
| ENSONIG000000011792  |           | Ensembl_nile_tilapia                                                         | -0.00            | 2.37E-03    |
| ENSONIG000000013985  |           | Ensembl_nile_tilapia                                                         | -1.1             | -1.6        |
| ENSONIG000000017323  |           | Ensembl_nile_tilapia                                                         | -1.5             | -4.0        |
| ENSONIG000000019573  |           | Ensembl_nile_tilapia                                                         | -1.3             | -1.4        |
| ENSRLG00000000460    |           | Ensembl_medaka                                                               | 0.00             | 2.1         |
| ENSRLG00000001173    |           | Ensembl_medaka                                                               | 1.1              | 3.7         |
| ENSRLG00000001190    |           | Ensembl_medaka                                                               | 1.3              | 6.31E-02    |
| ENSRLG00000003700    |           | Ensembl_medaka                                                               | -2.5             | -           |
| ENSRLG000000010522   |           | Ensembl_medaka                                                               | 0.00             | 6.16E-05    |
| ENSRLG000000011293   |           | Ensembl_medaka                                                               | 0.00             | 0.0         |
| ENSRLG00000001321    |           | Ensembl_medaka                                                               | 0.00             | 2.1         |
| ENSRLG00000012785    |           | Ensembl_medaka                                                               | -4.9             | -3.7        |
| ENSRLG00000013333    |           | Ensembl_medaka                                                               | 0.00             | 1.17E-02    |
| ENSRLG00000019280    |           | Ensembl_medaka                                                               | 1.36E-03         | 21.0        |
| ENSRLG0000002091     |           | Ensembl_medaka                                                               | 1.61E-02         | -1.5        |
| EV367322             | gb|EV367322.1 | EST ccluev mixed tissue Coregonus clupeaformis cDNA Coregonus clupeaformis clone ccluev 3', mRNA sequence. | EST_others       | down        |
| EV368845             | gb|EV368845.1 | EST ccluev mixed tissue Coregonus clupeaformis cDNA Coregonus clupeaformis clone ccluev 3', mRNA sequence. | EST_others       | up          |
| EV370019             | gb|EV370019.1 | EST ccluev mixed tissue Coregonus clupeaformis cDNA Coregonus clupeaformis clone ccluev 3', mRNA sequence. | EST_others       | down        |
| EV370268             | gb|EV370268.1 | EST ccluev mixed tissue Coregonus clupeaformis cDNA Coregonus clupeaformis clone ccluev 3', mRNA sequence. | EST_others       | up          |
| FK872811             | gb|FK872811.1 | EST crog evp Caligus                                                          | EST_others       | down        |

**Legend:**
- **EST_others:** EST others
- **down:** Downregulated
- **up:** Upregulated
| Accession   | Description                                                                 | Log2 Fold Change | EST Others | Overlap | mRNA Sequence |
|-------------|------------------------------------------------------------------------------|------------------|------------|---------|----------------|
| FK872812    | gb|FK872812.1 EST_crog_evp_904731 crog_evp Caligus rogercresseyi cDNA clone crog_evp_506_315_fwd 5', mRNA sequence. | 8.88E-02        | -22.8     | 0.0     | -1.4           |
| FK882798    | gb|FK882798.1 EST_crog_evp_908098 crog_evp Caligus rogercresseyi cDNA clone crog_evp_520_226_rev 5', mRNA sequence. | 2.6            | 7.27E-02  | down     | -1.4           |
| FK869364    | gb|FK869364.1 EST_crog_evp_915567 crog_evp Caligus rogercresseyi cDNA clone crog_evp_502_015_fwd 5', mRNA sequence. | 0.0            | 7.64E-03  | down     | 2.28E-03       |
| FK879202    | gb|FK879202.1 EST_crog_evp_916574 crog_evp Caligus rogercresseyi cDNA clone crog_evp_515_254_rev 5', mRNA sequence. | 3.75E-02        | down      | down     | 0.0            |
| GW640860    | gb|GW640860.1 EST_Lsaa_evu_1215038 IsaAevu mixed_tissue Lepeophtheirus salmonis (Atlantic Canada) cDNA Lepeophtheirus salmonis cDNA clone Lsaa_evu_506_284 3', mRNA sequence. | -              | 5.9       | -1.1     | 8.30E-03       |
| GE839897    | gb|GE839897.1 EST_omyk_evo_818548 omykevo WBC Oncorhynchus mykiss cDNA Oncorhynchus mykiss cDNA clone omyk_evo_513_148 3', mRNA sequence. | -              | -1.6      | -1.3     | 1.82E-03       |
| GE835715    | gb|GE835715.1 EST_omyk_evo_830394 omykevo WBC Oncorhynchus mykiss cDNA Oncorhynchus mykiss cDNA clone omyk_evo_507_282 5', mRNA sequence. | 4.7            | -2.6      | 4.49E-02 | up             |
| EL553118    | gb|EL553118.1 EST_otshe_evc_1287 otsh_evc mixed_tissue Oncorhynchus tshawytscha cDNA Oncorhynchus tshawytscha cDNA clone otsh_evc_005_046_fwd 3', mRNA sequence. | -              | -1.7      | -2.6     | up             |
| EG807134    | gb|EG807134.1 EST_ssle_evd_17813 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_522_310_fwd 5', mRNA sequence. | -              | 3.1       | 9.89E-05 | up             |
| EG822862    | gb|EG822862.1 EST_ssle_evd_24557 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_006_336_fwd 5', mRNA sequence. | -              | 1.49E-02  | down     | 0.0            |

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| Accession   | Description                                                                 | Others   | Fold Change |
|-------------|------------------------------------------------------------------------------|----------|-------------|
| EG824531    | ssal_evd_531_353_fwd 5', mRNA sequence.                                     | EST_others | 5.86E-02    |
| EG824683    | ssal_evd_534_047_rev 3', mRNA sequence.                                     | EST_others | -2.4        |
| EG806136    | ssal_evd_535_004_rev 3', mRNA sequence.                                     | EST_others | 1.97E-01    |
| EG805357    | ssal_evd_536_188_fwd 5', mRNA sequence.                                     | EST_others | 2.17E-03    |
| EG801892    | ssal_evd_537_355_fwd 1', mRNA sequence.                                     | EST_others | -1.0        |
| EG8020910   | ssal_evd_538_040_fwd 5', mRNA sequence.                                     | EST_others | 3.19E-02    |
| EG803435    | ssal_evd_539_354_fwd 1', mRNA sequence.                                     | EST_others | 4.15E-02    |
| EG838512    | ssal_evd_540_355_fwd 1', mRNA sequence.                                     | EST_others | -1.3        |
| EG855707    | ssal_evd_541_356_fwd 1', mRNA sequence.                                     | EST_others | 1.15E-02    |
| EG879755    | ssal_evd_542_357_fwd 1', mRNA sequence.                                     | EST_others | -2.3        |
| EG879910    | ssal_evd_543_358_fwd 1', mRNA sequence.                                     | EST_others | 3.75E-02    |
| EG858135    | ssal_evd_544_359_fwd 1', mRNA sequence.                                     | EST_others | -4.5        |
| Accession | Description | EST/other | Log2 Fold Change | p-value | Expression | Log2 Fold Change | p-value |
|-----------|-------------|-----------|-----------------|---------|------------|-----------------|---------|
| EG878528  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_529_368_few5 | EST_others | 1.27E-03 | 11.8 | up | 1.8 | 0.0 |
| EG880230  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_532_046_few5 | EST_others | -2.7 | -1.2 | up | -2.9 |
| EG881131  | 3' mRNA sequence of Salmo salar cDNA clone ssal_eve_533_077_few3 | EST_others | down | 6.7 | down | 0.0 |
| EG882237  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_534_046_few5 | EST_others | 21.3 | up | 33.0 | 4.9 |
| EG882682  | 3' mRNA sequence of Salmo salar cDNA clone ssal_eve_535_042_few3 | EST_others | down | down | 8.79E-02 | down |
| EG866124  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_537_252_few5 | EST_others | -1.4 | -1.2 | 5.77E-02 | down |
| EG867991  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_539_349_few5 | EST_others | 1.5 | -1.2 | 2.93E-06 | up |
| EG868203  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_540_067_few5 | EST_others | 4.1 | 2.5 | 2.99E-04 | -24.2 |
| EG869982  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_542_125_few3 | EST_others | 7.42E-04 | down | 0.0 | 0.0 |
| EG870274  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_542_264_few5 | EST_others | 4.3 | down | -1.2 | 1.48E-02 | up |
| EG840326  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_503_137_few5 | EST_others | 5.6 | down | 8.79E-02 | down |
| EG840695  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_503_306_few5 | EST_others | 1.2 | -1.7 | 7.46E-02 | -6.0 |
| EG844851  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_551_105_few5 | EST_others | 5.73E-03 | -11.1 | up | 0.0 | 0.0 |
| EG833455  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_561_291_few3 | EST_others | 0.0 | 4.41E-02 | up | 1.96E-02 | down |
| EG859641  | 5' mRNA sequence of Salmo salar cDNA clone ssal_eve_572_066_few3 | EST_others | -1.7 | -3.1 | 2.33E-02 | -10.8 |
| EG860536  | 5' mRNA sequence of Salmo salar cDNA clone | EST_others | down | down | 2.43E-02 | down |
| Accession | Description                                      | Fold Change | Significance   |
|-----------|-------------------------------------------------|-------------|----------------|
| EG849257 | ssal_eve_573_104_rev 3', mRNA sequence.         | -2.7        | down, 6.99E-02 |
| EG907993 | ssal_eve_6723 scaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_508_052_rev 3', mRNA sequence. | 0.00        | 7.05E-02       |
| EG908200 | ssal_eve_10357 scaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_512_085_rev 3', mRNA sequence. | -2.9        | down, 3.24E-03 |
| EG908809 | ssal_eve_11085 scaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_513_091_rev 3', mRNA sequence. | -2.5        | down, 5.01E-02 |
| EG912415 | ssal_eve_14331 scaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_517_261_rev 3', mRNA sequence. | -2.8        | down, 4.22E-03 |
| EG913326 | ssal_eve_15151 scaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_518_298_fwd 5', mRNA sequence. | -2.4        | down, 7.56E-02 |
| EG914877 | ssal_eve_16547 scaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_520_246_fwd 5', mRNA sequence. | -2.8        | down, 3.11E-02 |
| EG922711 | ssal_eve_1797 scaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_006_217_fwd 5', mRNA sequence. | -2.4        | down, 3.11E-02 |
| EG935627 | ssal_eve_19632 scaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_524_301_fwd 5', mRNA sequence. | -1.5        | 2.85E-02       |
| EG937327 | ssal_eve_21163 scaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_526_319_fwd 5', mRNA sequence. | -1.5        | 2.85E-02       |
| EG937416 | ssal_eve_21243 scaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_526_359_fwd 5', mRNA sequence. | -0.00       | 4.49E-02       |
| EG942312 | ssal_eve_25650 scaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_533_370_fwd 5', mRNA sequence. | -12.9       | down, 2.07E-03 |
| EG899717 | ssal_eve_2676 scaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_501_329_rev 3', mRNA sequence. | -1.4        | 3.54E-02       |
| Accession   | Description                                                                                               | Change | | | | |
|-------------|-----------------------------------------------------------------------------------------------------------|--------|--------|--------|--------|--------|--------|
| EG92672     | EST_ssal_evf_28802 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_538_075_rev 3', mRNA sequence. | down   | 2.43E-02 | down   | -      | down   |
| EG903128    | EST_ssal_evf_2983 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_502_106_rev 3', mRNA sequence. | down   | 2.70E-08 | down   | -      | down   |
| EG928582    | EST_ssal_evf_30881 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_540_380_rev 3', mRNA sequence. | down   | 5.65E-02 | down   | -      | down   |
| EG931057    | EST_ssal_evf_33109 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_544_009_fwd 5', mRNA sequence. | down   | 3.00E-03 | -15.0  | -      | down   |
| EG932783    | EST_ssal_evf_3563 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_550_226_fwd 5', mRNA sequence. | down   | 5.91E-02 | down   | -      | up     |
| EG889573    | EST_ssal_evf_36198 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_558_059_rev 3', mRNA sequence. | down   | 1.6     | -1.1   | -      | down   |
| EG934489    | EST_ssal_evf_37933 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_558_225_rev 3', mRNA sequence. | up     | 4.41E-02 | up     | -      | up     |
| EG901696    | EST_ssal_evf_40428 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_553_372_rev 3', mRNA sequence. | up     | 1.60E-02 | -18.6  | -      | down   |
| EG902053    | EST_ssal_evf_40749 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_554_152_rev 3', mRNA sequence. | down   | 3.65E-02 | down   | -      | 0.0    |
| EG885127    | EST_ssal_evf_43515 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_558_059_rev 3', mRNA sequence. | down   | 4.20E-04 | down   | -      | -0.0   |
| EG908621    | EST_ssal_evf_44490 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_559_176_rev 3', mRNA sequence. | down   | 2.73E-05 | 103.6  | -      | down   |
| EG888583    | EST_ssal_evf_46808 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_562_243_fwd 5', mRNA sequence. | down   | 6.99E-02 | down   | -      | -2.0   |
| EG890543    | EST_ssal_evf_48390 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_562_369_rev 3', mRNA sequence. | down   | 4.20E-04 | down   | -      | 0.0    |
| Accession        | Description                                                                 | Description                                                                 | EST_others | 5' | 3' | 5'-3' | 3'-5' | | | | | |
|------------------|------------------------------------------------------------------------------|------------------------------------------------------------------------------|------------|----|----|-------|-------| | | | | |
| EG893526         | gb|EG893526.1 EST_ssal_evf_51075 ssalev mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_568_136_fwd 5', mRNA sequence. | EST_others | - | 2.0 | - | -1.1 | 3.11E-02 | | | | |
| EG917093         | gb|EG917093.1 EST_ssal_evf_56281 ssalev mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_575_185_rev 3', mRNA sequence. | EST_others | - | down | - | down | 2.77E-03 | | | | |
| EG917122         | gb|EG917122.1 EST_ssal_evf_53007 ssalev mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_575_198_fwd 5', mRNA sequence. | EST_others | - | -3.3 | 1.50E-03 | up | 1.61E-05 | | | | |
| EG918173         | gb|EG918173.1 EST_ssal_evf_57254 ssalev mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_576_303_rev 3', mRNA sequence. | EST_others | - | 2.1 | - | 9.4 | 8.10E-03 | | | | |
| EG918652         | gb|EG918652.1 EST_ssal_evf_57684 ssalev mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_577_153_fwd 5', mRNA sequence. | EST_others | - | down | - | down | 8.78E-02 | | | | |
| EG920601         | gb|EG920601.1 EST_ssal_evf_59439 ssalev mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_579_333_rev 3', mRNA sequence. | EST_others | - | down | - | -2.1 | 8.79E-02 | | | | |
| EG904422         | gb|EG904422.1 EST_ssal_evf_57136 ssalev mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_507_333_fwd 5', mRNA sequence. | EST_others | - | 0.0 | - | 0.0 | 1.59E-02 | | | | |
| EG907324         | gb|EG907324.1 EST_ssal_evf_59748 ssalev mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_511_154_fwd 5', mRNA sequence. | EST_others | - | 0.0 | - | 1.2 | 6.84E-03 | | | | |
| DW532716         | gb|DW532716.1 EST_ssal_plnb_1352 plnb Salmo salar cDNA clone ssal_plnb_011_015_fwd 3', mRNA sequence. | EST_others | - | 0.0 | - | 3.98E-06 | -37.4 | | | | |
| DW533803         | gb|DW533803.1 EST_ssal_plnb_2439 plnb Salmo salar cDNA clone ssal_plnb_018_088_fwd 3', mRNA sequence. | EST_others | - | -1.6 | 5.76E-04 | up | - | up | - | 0.0 |
| DW533681         | gb|DW533681.1 EST_ssal_plnb_2317 plnb Salmo salar cDNA clone ssal_plnb_017_093_rev 5', mRNA sequence. | EST_others | - | 0.0 | - | 6.22E-03 | down | - | 0.0 | | |
| DY692525         | gb|DY692525.1 EST_ssal_plnb_5435 ssalplnb mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_plnb_025_377_fwd 5', mRNA sequence. | EST_others | - | 5.86E-02 | down | 5.59E-02 | down | - | down | - | |
| DY692639         | gb|DY692639.1 EST_ssal_plnb_5549 ssalplnb mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_plnb_027_058_fwd 3', mRNA sequence. | EST_others | - | 0.0 | - | 1.75E-03 | -21.5 | - | up | - | -4.3 |
| EG755292         | gb|EG755292.1 EST_ssal_plnb_6444 ssalplnb mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_plnb_029_080_fwd 3', mRNA sequence. | EST_others | - | 0.0 | - | 5.59E-02 | down | - | 0.0 | - | 0.0 |
| DW557302         | gb|DW557302.1 EST_ssal_rgb2_21721 rgb2 Salmo salar cDNA clone ssal_rgb2_535_127_rev 5', mRNA sequence. | EST_others | 6.83E-05 | up | - | 3.8 | up | - | down | | |
| Gene Description                                                                 | EST_accession | GI | Change | Log2 Fold | P-value |
|---------------------------------------------------------------------------------|---------------|----|--------|-----------|---------|
| EST_ssal_rgb2_22059 rbg2 Salmo salar clone ssal_rgb2_535_331 rev 5', mRNA sequence. | DW557640      | gb| -1.3   | -2.1      | 6.85E-02 |
| EST_ssal_rgb2_29565 rbg2 Salmo salar clone ssal_rgb2_547_373 rev 5', mRNA sequence. | DW55146.1     | gb| 5.86E-02 | down      | 3.59E-04 |
| EST_ssal_rgb2_30190 rbg2 Salmo salar clone ssal_rgb2_548_373 rev 5', mRNA sequence. | DW55771.1     | gb| 0.00   | down      | 7.05E-02 |
| EST_ssal_rgb2_31905 rbg2 Salmo salar clone ssal_rgb2_551_261 rev 5', mRNA sequence. | DW56521.1     | gb| 3.2    | up        | 9.32E-03 |
| EST_ssal_rgb2_33177 rbg2 Salmo salar clone ssal_rgb2_553_284 rev 5', mRNA sequence. | DW56758.1     | gb| 6.54E-03 | down      | 3.65E-03 |
| EST_ssal_rgb2_34503 rbg2 Salmo salar clone ssal_rgb2_555_329 fwd 3', mRNA sequence. | DW570084.1    | gb| 0.00   | 3.65E-03 | -17.2   |
| EST_ssal_rgb2_3888 rbg2 Salmo salar clone ssal_rgb2_557_270 rev 5', mRNA sequence. | DW539469.1    | gb| -4.2   | down      | 6.99E-02 |
| EST_ssal_rgb2_40378 rbg2 Salmo salar clone ssal_rgb2_565_232 fwd 3', mRNA sequence. | DW575959.1    | gb| -6.9   | up        | 4.49E-02 |
| EST_ssal_rgb2_41226 rbg2 Salmo salar clone ssal_rgb2_566_338 rev 5', mRNA sequence. | DW578341      | gb| 2.4    | down      | 7.39E-04 |
| EST_ssal_rgb2_42760 rbg2 Salmo salar clone ssal_rgb2_569_121 rev 5', mRNA sequence. | DW578341.1    | gb| 1.2    | 3.54E-02 | -        |
| EST_ssal_rgb2_45534 rbg2 Salmo salar clone ssal_rgb2_573_258 rev 5', mRNA sequence. | DW58115.1     | gb| 2.1    | 3.5        | 1.96E-03 |
| EST_ssal_rgb2_53276 ssalrgb2 mixed_tissue Salmo salar clone ssal_rgb2_586_071 fwd 3', mRNA sequence. | DY697537.1    | gb| 0.00   | 0.0       | 3.02E-02 |
| EST_ssal_rgb2_5457 rbg2 Salmo salar clone ssal_rgb2_510_041 rev 5', mRNA sequence. | DW541038.1    | gb| - down  | 3.65E-02 | - down |
| EST_ssal_rgb2_57078 ssalrgb2 mixed_tissue Salmo salar clone ssal_rgb2_593_203 rev 5', mRNA sequence. | DY701339.1    | gb| - down  | - 7.24E-05 | - down |
| Accession | Description | Strand | mRNA Sequence | EST Others | Value | p-Value | Change |
|-----------|-------------|--------|---------------|------------|-------|---------|--------|
| DY705472 | gb|DY705472.1 | EST_ssal_rgb2_61211 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_598_195_fwd 3', mRNA sequence. | EST_others | - | 0.00 | 4.56E-06 | -40.6 |
| DW542323 | gb|DW542323.1 | EST_ssal_rgb2_6742 rgb2 Salmo salar cDNA clone ssal_rgb2_512_028_rev 5', mRNA sequence. | EST_others | - | 1.2 | 4.41E-02 | down |
| DY715145 | gb|DY715145.1 | EST_ssal_rgb2_70885 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_614_342_rev 5', mRNA sequence. | EST_others | - | down | - | -2.7 | -1.1 |
| DY715437 | gb|DY715437.1 | EST_ssal_rgb2_71177 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_615_142_fwd 3', mRNA sequence. | EST_others | - | 0.0 | 4.39E-02 | down |
| DY715711 | gb|DY715711.1 | EST_ssal_rgb2_71451 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_615_305_fwd 5', mRNA sequence. | EST_others | - | 3.88E-05 | up | -1.7 | 7.28E-04 |
| DY720448 | gb|DY720448.1 | EST_ssal_rgb2_76187 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_625_087_rev 5', mRNA sequence. | EST_others | - | 0.00 | 2.44E-06 | -48.0 |
| DY720838 | gb|DY720838.1 | EST_ssal_rgb2_76577 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_625_311_fwd 3', mRNA sequence. | EST_others | - | 0.00 | -1.4 | 4.41E-02 | down |
| DY726856 | gb|DY726856.1 | EST_ssal_rgb2_82595 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_635_205_fwd 5', mRNA sequence. | EST_others | 1.81E-04 | up | - | 1.1 | 0.0 |
| DY729177 | gb|DY729177.1 | EST_ssal_rgb2_84916 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_639_034_rev 5', mRNA sequence. | EST_others | 1.34E-03 | down | 9.01E-02 | down | 1.28E-02 | down | -1.6 |
| DY735271 | gb|DY735271.1 | EST_ssal_rgb2_91010 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_649_009_fwd 3', mRNA sequence. | EST_others | - | -1.7 | 1.3 | 2.69E-02 | down | -21.7 | - up |
| DY735321 | gb|DY735321.1 | EST_ssal_rgb2_91060 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_649_040_rev 5', mRNA sequence. | EST_others | - | 0.00 | 0.0 | 0.0 | 5.87E-02 | 24.1 |
| DY735436 | gb|DY735436.1 | EST_ssal_rgb2_91175 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_649_104_fwd 3', mRNA sequence. | EST_others | - | 1.2 | 0.0 | 8.79E-02 | down | - down |
| DY737082 | gb|DY737082.1 | EST_ssal_rgb2_92821 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_651_303_rev 5', mRNA sequence. | EST_others | - | -1.3 | -3.6 | 4.39E-02 | down | -15.2 |
| DW545057 | gb|DW545057.1 | EST_ssal_rgb2_9476 rgb2 Salmo salar cDNA clone ssal_rgb2_516_105_rev 5', mRNA sequence. | EST_others | 4.69E-02 | down | 1.2 | 2.8 | 1.1 | up |
| GE767884 | gb|GE767884.1 | EST_ssal_rgb2_835799 ssalrgb mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_002_311_fwd 3', mRNA sequence. | EST_others | - | -2.1 | 5.59E-02 | down | 5.88E-06 | down |

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| Accession | Description | Expression | Enlargement |
|-----------|-------------|------------|-------------|
| GE775959  | EST_ssal_rgf_839262 ssalrgf mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgf_511_318 5', mRNA sequence. | EST_others | 8.7 | 3.1 | 7.05E-02 | 18.1 | -1.1 |
| GE780214  | EST_ssal_rgf_846100 ssalrgf mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgf_517_244 5', mRNA sequence. | EST_others | -1.3 | -2.4 | 8.79E-02 | down | - down |
| GE795073  | EST_ssal_rgf_858837 ssalrgf mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgf_539_117 3', mRNA sequence. | EST_others | down | down | 6.99E-02 | down | 0.0 |
| GE783177  | EST_ssal_rgf_863208 ssalrgf mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgf_521_264 5', mRNA sequence. | EST_others | 0.00 | down | 8.79E-02 | down | 0.0 |
| GE794330  | EST_ssal_rgf_864206 ssalrgf mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgf_538_110 3', mRNA sequence. | EST_others | 1.3 | -2.0 | -1.0 | 6.26E-06 | 60.2 |
| GE792696  | EST_ssal_rgf_869097 ssalrgf mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgf_536_009 5', mRNA sequence. | EST_others | -1.5 | 2.18E-02 | -6.3 | -1.0 | 1.9 |
| GE793450  | EST_ssal_rgf_872948 ssalrgf mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgf_537_020 3', mRNA sequence. | EST_others | up | 1.4 | 2.43E-02 | up | 0.0 |
| GO04564   | EST_ssal_rgg_1026006 ssalrgg mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgg_505_246 5', mRNA sequence. | EST_others | 1.61E-02 | down | -1.8 | 9.10E-02 | -5.6 | down |
| GO04564   | EST_ssal_rgg_1095730 ssalrgg mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgg_507_082 3', mRNA sequence. | EST_others | -2.2 | -2.6 | 8.30E-03 | -17.0 | -1.2 |
| GO045318  | EST_ssal_rgg_1101007 ssalrgg mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgg_506_367 3', mRNA sequence. | EST_others | 20.1 | up | 4.67E-03 | down | 1.5 |
| GO05151   | EST_ssal_rgh_1035036 ssalrgh mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_502_060 5', mRNA sequence. | EST_others | down | 3.54E-02 | down | -1.6 | -6.8 |
| GO055970  | EST_ssal_rgh_1044020 ssalrgh mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_505_212 5', mRNA sequence. | EST_others | 0.00 | 4.41E-02 | up | up | 8.4 |
| GO063143  | EST_ssal_rgh_1079043 ssalrgh mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_517_291 3', mRNA sequence. | EST_others | down | down | 3.90E-03 | down | down |
| GO064603  | EST_ssal_rgh_1079613 ssalrgh mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_520_093 5', mRNA sequence. | EST_others | 0.00 | 0.0 | 1.22E-03 | down | 0.0 |
| GO061981  | EST_ssal_rgh_1080223 ssalrgh mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_515_319 3', mRNA sequence. | EST_others | -5.2 | 3.54E-02 | -6.5 | 7.44E-06 | -31.5 | -8.6 |
| GO057448  | EST_ssal_rgh_1083386 ssalrgh mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone | EST_others | -1.9 | 3.54E-02 | up | 6.99E-02 | up | 1.3 |
| Accession   | Description                                                                 | EST Others | Log2FoldChange | P-Value | Change | Description                                                                 |
|-------------|------------------------------------------------------------------------------|------------|----------------|---------|--------|----------------------------------------------------------------------------|
| GO057929    | gb|GO057929.1 EST_ssal_rgh_1083694 ssalrg mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_508_334 3', mRNA sequence. | EST_others | -6.8 | -2.1 | 1.28E-06 down |
| GO062248    | gb|GO062248.1 EST_ssal_rgh_1083855 ssalrg mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_516_111 5', mRNA sequence. | EST_others | -1.5 | 1.1 | 1.42E-03 -9.3 |
| GO059796    | gb|GO059796.1 EST_ssal_rgh_1086096 ssalrg mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_512_048 5', mRNA sequence. | EST_others | 0.00 | down | 3.90E-03 down |
| GO064045    | gb|GO064045.1 EST_ssal_rgh_1086921 ssalrg mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_519_105 3', mRNA sequence. | EST_others | -4.2 | -4.1 | 6.65E-06 down |
| GO058122    | gb|GO058122.1 EST_ssal_rgh_1089048 ssalrg mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_511_323 3', mRNA sequence. | EST_others | -3.2 | -7.9 | 2.51E-04 -37.3 |
| EG757222    | gb|EG757222.1 EST_ssal_sjb_5903 salsjb mixed_tissue Salmo salar cDNA Salmo salar cDNA clone salsjb_013_245_fwd 3', mRNA sequence. | EST_others | -1.2 | 1.1 | 4.79E-06 up |
| EG757601    | gb|EG757601.1 EST_ssal_sjb_6246 salsjb mixed_tissue Salmo salar cDNA Salmo salar cDNA clone salsjb_014_052_rev 5', mRNA sequence. | EST_others | -2.5 | 7.27E-02 up |
| BF228600    | gb|BF228600.1 EST00311 Atlantic salmon Lambda Zap Express brain cDNA library Salmo salar cDNA clone BNMG134 5', mRNA sequence. | EST_others | -0.00 | 0.0 | 1.36E-04 down |
| CK873433    | gb|CK873433.1 SGP134561 Atlantic salmon Brain cDNA library Salmo salar cDNA clone H6-0532 5', mRNA sequence. | EST_others | -3.6 | 2.4 | 7.44E-07 down |
| CK873617    | gb|CK873617.1 SGP134767 Atlantic salmon Brain cDNA library Salmo salar cDNA clone H6-0878 5', mRNA sequence. | EST_others | -1.2 | -10.2 | 2.47E-02 -11.1 |
| CK876604    | gb|CK876604.1 SGP137887 Atlantic salmon Eye cDNA library Salmo salar cDNA clone OY4-0782 5', mRNA sequence. | EST_others | -1.2 | -10.2 | 2.47E-02 -11.1 |
| CK893686    | gb|CK893686.1 SGP153778 Atlantic salmon Spleen cDNA library Salmo salar cDNA clone M16-0365 5', mRNA sequence. | EST_others | -1.2 | -10.2 | 2.47E-02 -11.1 |
| CK899155    | gb|CK899155.1 SGP162743 Atlantic salmon Testis cDNA library Salmo salar cDNA clone MG4-1507 5', mRNA sequence. | EST_others | -6.8 | -2.1 | 1.28E-06 down |

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| Accession | Description | Nature | Description | EST_others | Fold_change | P_value | Log2Fold_change | Status |
|-----------|-------------|--------|-------------|------------|-------------|---------|----------------|--------|
| CK885162 | SGP165529 Atlantic salmon intestine cDNA library Salmo salar cDNA clone T4-0448 5', mRNA sequence. | EST_others | - | 0.0 | -1.5 | 2.73E-05 | down | -1.0 |
| CN181335 | SGP169629 Atlantic salmon intestine cDNA library Salmo salar cDNA clone THS-0120 5', mRNA sequence. | EST_others | - | -3.2 | - | 7.85E-02 | - | -1.2 |
| DW471606 | SGP285723 Atlantic salmon Spleen cDNA library Salmo salar cDNA clone Mi5-1529 5', mRNA sequence. | EST_others | - | -3.4 | - | 16.5 | 5.30E-03 | down | -16.4 |
| DW469525 | SGP297862 Atlantic salmon Testis cDNA library Salmo salar cDNA clone MG4-2653 5', mRNA sequence. | EST_others | - | -4.8 | - | 7.05E-02 | down | -17.0 |
| DW472356 | SGP299923 Atlantic salmon Spleen cDNA library Salmo salar cDNA clone Mi5-2368 5', mRNA sequence. | EST_others | 5.86E-02 | down | - | 0.0 | - | 0.0 |
| DW473174 | SGP314039 Atlantic salmon Spleen cDNA library Salmo salar cDNA clone Mi5-3285 5', mRNA sequence. | EST_others | - | up | 7.64E-03 | down | - | -6.3 |
| DW473451 | SGP314316 Atlantic salmon Spleen cDNA library Salmo salar cDNA clone Mi5-3605 5', mRNA sequence. | EST_others | - | 0.0 | 1.0 | 2.27E-04 | down | - | 0.0 |
| GT129117 | ssal_ear_SSH_seismicR_F12p3 Salmo salar ear reverse SSH library designed to be enriched for transcripts down-regulated by seismic sound. Salmo salar cDNA similar to unclassified., mRNA sequence. | EST_others | - | down | - | 0.0 | - | -2.1 |
| CB501817 | ssalga508249 head Salmo salar cDNA, mRNA sequence. | EST_others | 4.69E-02 | down | - | 0.0 | - | 0.0 |
| CA037858 | ssalina007071 liver Salmo salar cDNA, mRNA sequence. | EST_others | - | 0.0 | - | 0.0 | - | 8.31E-04 |
| CK990829 | ssalina08094 liver Salmo salar cDNA, mRNA sequence. | EST_others | - | 0.0 | - | 0.0 | - | 7.86E-02 |
| CK991140 | ssalina014053 liver Salmo salar cDNA, mRNA sequence. | EST_others | - | 0.0 | - | 0.0 | - | 3.69E-05 |
| CA039316 | ssalnh003073 whole Salmo salar cDNA, mRNA sequence. | EST_others | - | 0.0 | 2.04E-04 | - | 65.3 | |
| CA038580 | ssalnh008031 whole Salmo salar cDNA, mRNA sequence. | EST_others | 1.61E-02 | down | - | 0.0 | - | -3.6 |
| CB511060 | ssalnh057328 whole Salmo salar cDNA, mRNA sequence. | EST_others | - | 0.0 | - | 6.99E-02 | down | |
| CA042597 | ssalplnb501369 gut Salmo salar cDNA, mRNA sequence. | EST_others | - | 3.2 | - | 1.9 | 3.65E-02 | - | 7.3 |
| CA042008 | ssalplnb512301 gut Salmo salar cDNA, mRNA sequence. | EST_others | - | -1.6 | 5.49E-02 | 5.4 | - | 2.8 |
| CA054965 | ssalgain0050 mixed_tissue Salmo salar cDNA, mRNA sequence. | EST_others | - | -1.7 | - | 1.3 | 7.56E-02 | 6.4 |

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| Locus   | Name             | mRNA sequence. | EST others | down | down | down | 3.90E-03 | down | down | down |
|---------|------------------|----------------|------------|------|------|------|----------|------|------|------|
| Locus_1 | -                | -              | -          | 2.1  | -    | 1.2  | 0.00     | 0.0  | 0.0  | 0.0  |
| Locus_2 | -                | -              | -          | -    | -    | -    | 0.00     | -5.9 | -    | 0.0  |
| Locus_3 | -                | -              | -          | -    | -    | -    | 0.00     | 0.0  | 0.0  | 0.0  |
| Locus_4 | -                | -              | -          | 0.00 | -    | -    | 0.00     | 0.0  | 0.0  | 0.0  |
| Locus_5 | -                | -              | -          | -    | -    | -    | 0.00     | -    | -    | -    |
| Locus_6 | -                | -              | -          | -    | -    | -    | 0.00     | -    | -    | -    |
| Locus_7 | -                | -              | -          | 1.0  | -    | 1.0  | 1.2     | 1.8E-02| down | down |
| Locus_8 | -                | -              | -          | 2.4  | -    | 5.78E-02| -7.5    | -    | -1.3 | -    |
| Locus_9 | -                | -              | -          | -    | -    | -    | 2.5     | 3.9  | 3.41E-02| -11.7| -    |
| Locus_10| -                | -              | -          | 1.7  | -    | 2.87E-03| down    | -    | -1.1 | -    |
| Locus_11| -                | -              | -          | -    | -    | 6.48E-02| 5.8     | -    | -1.4 | -    |
| Locus_12| -                | -              | -          | 1.2  | -    | 9.01E-02| -8.5    | -    | 1.3  | -    |
| Locus  | Change 1 | Change 2 | Change 3 | Change 4 | p-value 1 | p-value 2 | p-value 3 | p-value 4 |
|--------|----------|----------|----------|----------|-----------|-----------|-----------|-----------|
| locus_21416 | -        | -        | -        | down     | 0.0       | 2.43E-02  | down      | -         | 0.0       |
| locus_110699 | -        | -        | -        | 0.00     | 0.0       | 4.49E-02  | down      | -         | 0.0       |
| locus_21692  | -        | -        | -        | 0.00     | 0.0       | 4.49E-02  | down      | -         | 0.0       |
| locus_93618  | -        | -        | -        | 0.00     | -         | 0.0       | 1.04E-02  | up         | -         | 0.0       |
| locus_42929  | -        | -        | -        | 1.47E-09 | 358.1     | -         | 0.0       | -         | 0.0       |
| locus_63842  | -        | -        | -        | 3.78E-06 | down      | -         | 0.0       | -         | 0.0       |
| locus_42919  | -        | -        | -        | 9.35E-14 | up        | -         | 0.0       | -         | 0.0       |
| locus_43483  | -        | -        | -        | 3.91E-08 | up        | -         | 0.0       | -         | 0.0       |
| locus_43115  | -        | -        | -        | 1.45E-07 | up        | -         | 0.0       | -         | 0.0       |
| locus_45068  | -        | -        | -        | 2.87E-07 | up        | -         | 0.0       | -         | 0.0       |
| locus_43319  | -        | -        | -        | 8.82E-07 | up        | -         | 0.0       | -         | 0.0       |
| locus_47644  | -        | -        | -        | 2.14E-06 | up        | -         | 0.0       | -         | 0.0       |
| locus_45727  | -        | -        | -        | 5.37E-06 | up        | -         | 0.0       | -         | 0.0       |
| locus_43795  | -        | -        | -        | 8.08E-06 | up        | -         | 0.0       | -         | 0.0       |
| locus_80358  | -        | -        | -        | 1.21E-04 | up        | -         | 0.0       | -         | 0.0       |
| locus_46093  | -        | -        | -        | 7.42E-04 | up        | -         | 0.0       | -         | 0.0       |
| locus_80642  | -        | -        | -        | 1.15E-02 | up        | -         | 0.0       | -         | 0.0       |
| locus_81054  | -        | -        | -        | 1.61E-02 | up        | -         | 0.0       | -         | 0.0       |
| locus_80712  | -        | -        | -        | 7.32E-02 | up        | -         | 0.0       | -         | 0.0       |
| locus_56467  | -        | -        | -        | 2.8      | 1.0       | 6.04E-02  | 19.61     | -         | 0.0       |
| locus_52222  | -        | -        | -        | 4.7      | 2.56E-02  | 10.7      | -         | up        | -         | 0.0       |
| locus_90954  | -        | -        | -        | 9.17E-02 | 21.3      | -         | 0.0       | -         | 0.0       |
| locus_21308  | -        | -        | -        | 3.14E-17 | up        | -         | down      | -         | 0.0       |
| locus_52406  | -        | -        | -        | 1.03E-05 | up        | -         | 0.0       | -         | 0.0       |
| locus_43970  | -        | -        | -        | 1.76E-07 | up        | -         | 0.0       | -         | 0.0       |
| locus_21331  | -        | -        | -        | 2.80E-15 | up        | -         | 0.0       | -         | 0.0       |