Supporting Information

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

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This Supporting Information contains:

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 (41dpf), 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 RNeasy 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) 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) 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. 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 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 (*arpc3*). 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	ACGGTCACACAGCCTCAG	83	58.5	96.2 %
Ferroportin	*slc401a*	GGCACATAGAGCACAGGTTC	GACAGGACAGCAGCAAGC	162	58.5	113.4 %
Metallothionein b	*mtb*	ACCAGTTGTGAAAGCAAG	GTCAGTCATAGGGAATGG	155	55.0	109.9 %
Glutathione peroxidise 1b	*gpx1b*	GCCAAGCACATTTCCCAAAG	GAGAGCCATTCAAGCGTTATG	200	55.0	94.3 %
Catalase	*cat*	CGGCTCTCACACCTTCAAG	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).

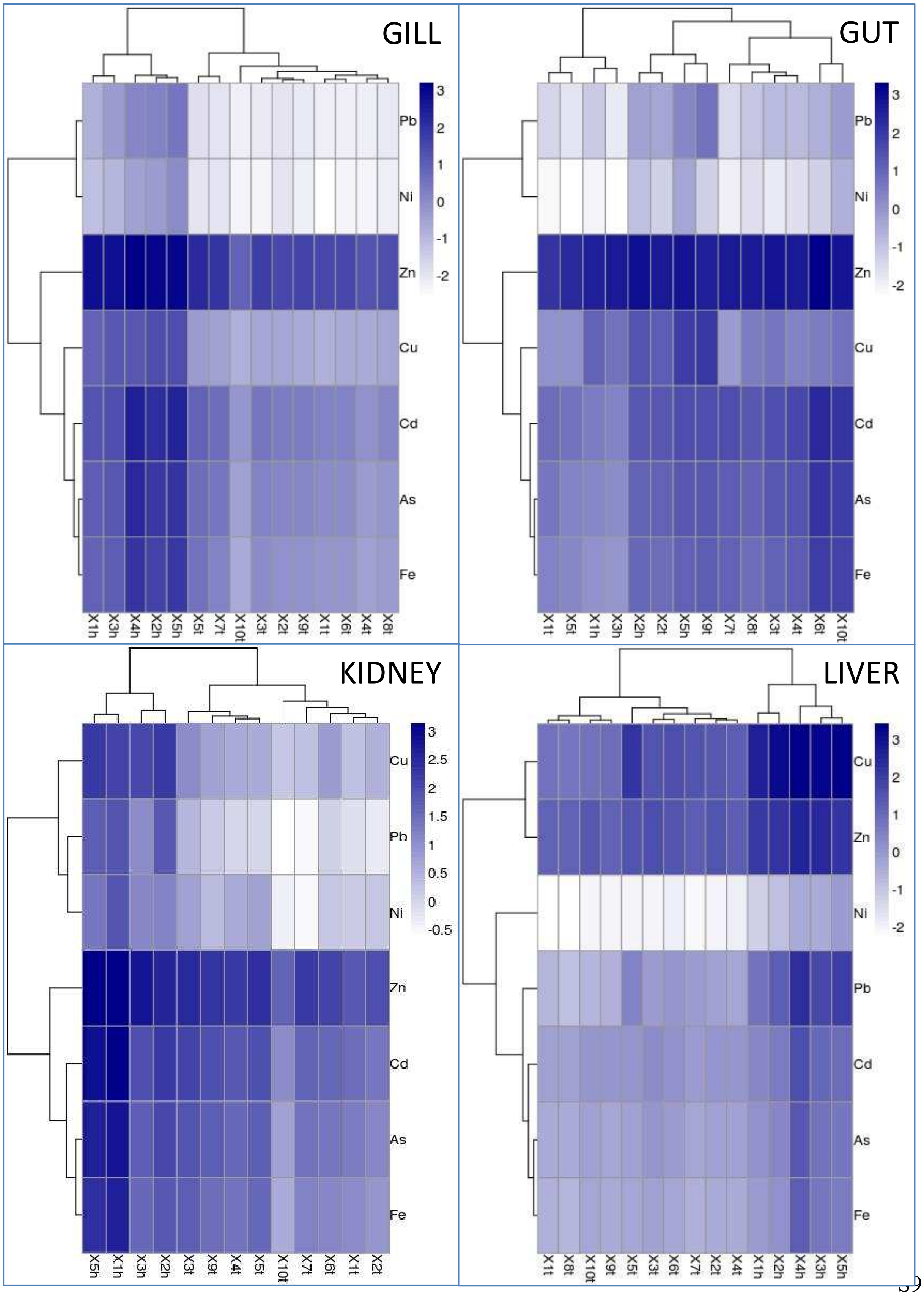

Table S4 - Summary statistics of raw sequencing reads, numbers of reads retained after adaptor removal and quality filtering and retained for input into transcriptome assembly as either paired reads or orphans. 1 and 2 refer to the forward and reverse reads in each paired-end sequence read.

	No. raw reads		**Adaptors removed**		**Quality Filtered**		**No. Paired reads**		**No. orphans**	
Sample	**Read 1**	**Read 2**	**Read 1**	**Read 2**	**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)	No. transcripts							
	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 expressed	**46600**	**50197**	**40558**	**41753**	**49964**	**44775**	**34693**	**33794**
Transcripts not expressed	**50083**	**46486**	**56125**	**54930**	**46719**	**51908**	**61991**	**62889**

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	1.7	4.3	1.2
	0.7	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	1.1	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.

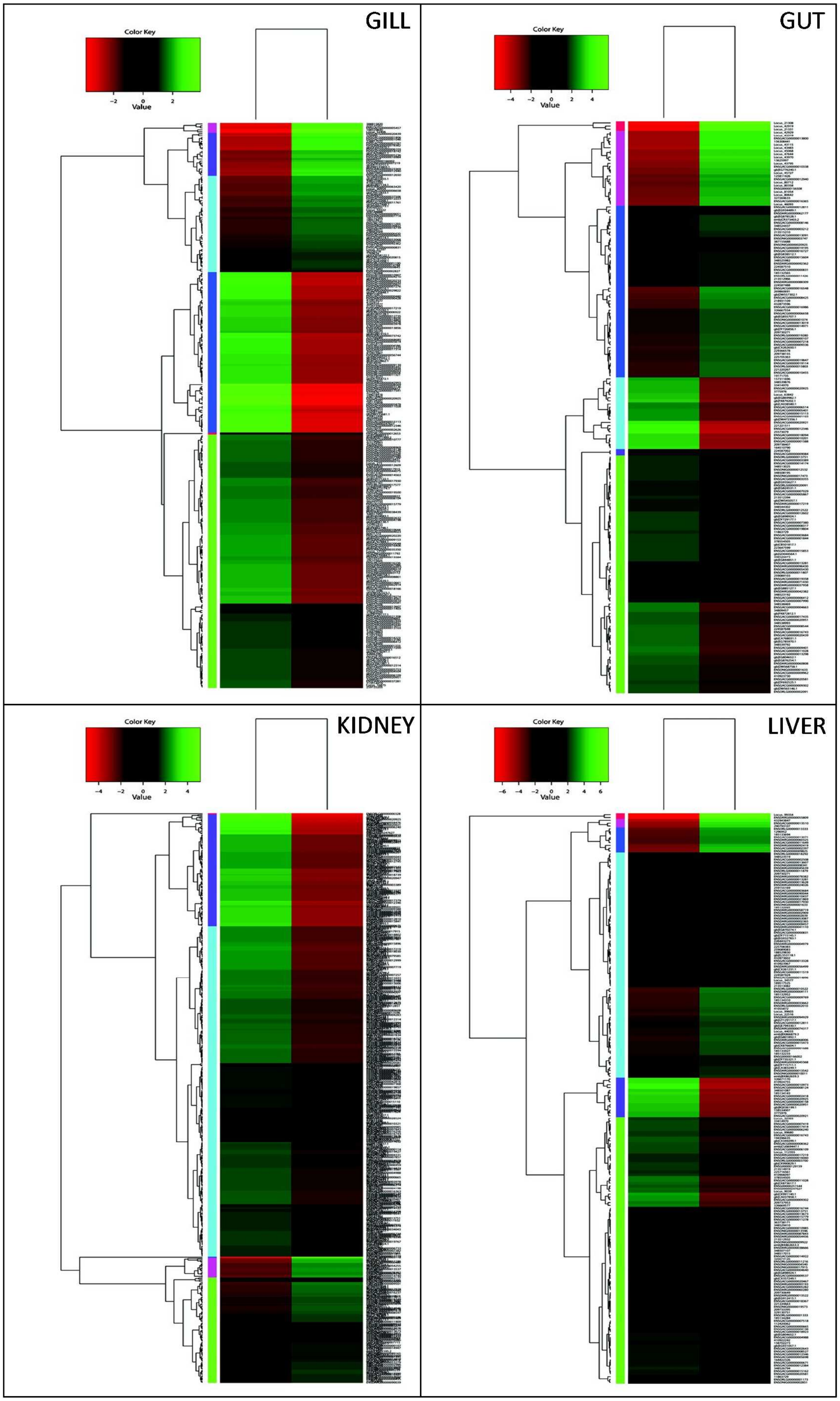

Table S7- Gene Ontology Terms over-represented in the lists of differentially expressed genes between Hayle and Teign fish for each tissue. Values presented are the number and percentage of genes in the tissue-specific gene lists associated with each term and the P-values associated with this over-representation. 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	exopeptidase activity	3	1.9	3.80E-02	9.50E-01	3.10E-01	3.40E+01	3.90E-03
GOTERM_MF_FAT	metallocarboxypeptidase activity	2	1.3	5.20E-02	9.80E-01	3.70E-01	4.30E+01	1.30E-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

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	9.60E-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

GOTERM_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
GOTERM_BP_FAT	response to glucose stimulus	2	1.6	2.40E-02	9.80E-01	5.60E-01	2.60E+01	2.60E-04
GOTERM_BP_FAT	response to monosaccharide stimulus	2	1.6	2.40E-02	9.80E-01	5.60E-01	2.60E+01	2.60E-04
GOTERM_BP_FAT	response to carbohydrate stimulus	2	1.6	2.40E-02	9.80E-01	5.60E-01	2.60E+01	2.60E-04
GOTERM_BP_FAT	chemical homeostasis	3	2.4	2.60E-02	9.90E-01	5.30E-01	2.80E+01	2.20E-03
GOTERM_BP_FAT	response to hormone stimulus	2	1.6	4.40E-02	1.00E+00	6.60E-01	4.20E+01	9.40E-04
GOTERM_BP_FAT	regulation of transcription, DNA-dependent	10	8.1	4.80E-02	1.00E+00	6.40E-01	4.50E+01	2.30E-02
GOTERM_BP_FAT	regulation of RNA metabolic process	10	8.1	4.90E-02	1.00E+00	6.10E-01	4.60E+01	2.40E-02
GOTERM_BP_FAT	glucose metabolic process	3	2.4	5.10E-02	1.00E+00	5.80E-01	4.70E+01	6.10E-03
GOTERM_BP_FAT	response to endogenous stimulus	2	1.6	5.20E-02	1.00E+00	5.60E-01	4.80E+01	1.30E-03
GOTERM_BP_FAT	carboxylic acid biosynthetic process	3	2.4	7.20E-02	1.00E+00	6.50E-01	6.00E+01	1.00E-02
GOTERM_BP_FAT	organic acid biosynthetic process	3	2.4	7.30E-02	1.00E+00	6.20E-01	6.00E+01	1.10E-02
GOTERM_BP_FAT	hexose metabolic process	3	2.4	7.90E-02	1.00E+00	6.30E-01	6.30E+01	1.20E-02
GOTERM_BP_FAT	monosaccharide metabolic process	3	2.4	9.50E-02	1.00E+00	6.70E-01	7.00E+01	1.60E-02
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	9.60E-01	5.60E-01	3.30E+01	1.60E-02
GOTERM_MF_FAT	carbohydrate kinase activity	2	1.6	7.30E-02	1.00E+00	7.50E-01	5.60E+01	2.70E-03
GOTERM_MF_FAT	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
GOTERM_MF_FAT	NADH dehydrogenase (quinone) activity	2	1.6	9.40E-02	1.00E+00	7.70E-01	6.60E+01	4.60E-03
GOTERM_MF_FAT	NADH dehydrogenase (ubiquinone) 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		GUT		KIDNEY		LIVER	
				FDR	FC	FDR	FC	FDR	FC	FDR	FC
ENSGACG00000003077	*abhd12b (2 of 2)*	abhydrolase domain containing 12B	Ensembl_stickleback	-	-1.4	-	1.5	4.41E-02	6.4	-	-1.1
ENSGACG00000016406	*abi1 (1 of 2)*	abl-interactor 1	Ensembl_stickleback	-	0.0	4.41E-02	down	-	-1.4	-	down
ENSGACG00000020048	*ascl1*	achaete-scute complex homolog 1 (Drosophila)	Ensembl_stickleback	-	-1.7	1.77E-03	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
ENSGACG00000012675	*actr10*	actin-related protein 10 homolog (S. cerevisiae)	Ensembl_stickleback	-	up	-	down	5.65E-02	down	-	down
ENSGACG00000014650	*acot11 (1 of 2)*	acyl-CoA thioesterase 11	Ensembl_stickleback	-	-1.7	-	up	3.02E-02	up	-	-1.4
ENSGACG00000006135	*adam10*	ADAM metallopeptidase domain 10	Ensembl_stickleback	-	4.0	-	-1.5	2.72E-02	-7.7	-	1.0
ENSGACG00000015076	*adamts1*	ADAM metallopeptidase 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
ENSDARG00000042382	*arf4 (2 of 3)*	ADP-ribosylation factor 4	Ensembl_zebrafish	4.69E-02	down	-	down	-	-1.6	-	up
5453305	AF141606.1	AF141606 Salmo salar clone 12(B) immunoglobulin heavy chain (IgD) mRNA, partial cds	nt	-	up	-	2.9	7.14E-03	-11.2	-	2.8
14581944	AF256852.1	AF256852 Salmo salar clone BHMS395 microsatellite sequence	nt	-	-1.1	-	-1.2	3.02E-02	18.1	-	-1.1
13625997	AAK35224.1	AF367368_1 yolk ferritin	nr	1.17E-06	up	-	0.0	-	0.0	-	0.0
ENSORLG00000017577	*agps*	alkylglycerone phosphate synthase	Ensembl_medaka	-	-2.2	1.27E-03	down	-	-2.4	-	up
ENSGACG00000013328	*alyref*	Aly/REF export factor	Ensembl_stickleback	-	1.4	-	1.7	-	1.6	1.59E-02	10.5
AM402664	emb|AM402664.1	AM402664 Salmo salar liver Parr Salmo salar cDNA clone liv_ali_L3E5, mRNA sequence.	EST_others	-	1.0	3.54E-02	-6.9	-	0.0	-	-1.4
ENSGACG00000000493	*npepl1*	aminopeptidase-like 1	Ensembl_stickleback	-	1.7	-	2.3	5.65E-02	down	-	0.0
ENSDARG00000013856	*amy2a*	amylase, alpha 2A; pancreatic	Ensembl_zebrafish	-	0.0	2.58E-06	-24.0	-	0.0	-	-2.8
ENSGACG00000013115	*aplp2*	amyloid beta (A4) precursor-like protein 2	Ensembl_stickleback	-	down	-	down	6.99E-02	down	-	down
ENSGACG00000018367	*anxa6*	annexin A6	Ensembl_stickleback	-	0.0	-	0.0	2.51E-04	down	1.57E-03	down
ENSDARG00000070480	*agr2*	anterior gradient homolog 2 (Xenopus laevis)	Ensembl_zebrafish	-	3.3	-	-1.1	9.43E-02	5.5	-	2.8
ENSDARG00000053279	*apln*	apelin	Ensembl_zebrafish	-	-2.5	-	0.0	8.78E-02	17.3	-	1.1

ENSORLG00000012653	*apob (6 of 6)*	apolipoprotein B (including Ag(x) antigen)	Ensembl_medaka	-	-1.3	8.77E-02	-12.3	-	-5.7	-	-1.7
ENSGACG00000012729	*apoo (2 of 2)*	apolipoprotein O	Ensembl_stickleback	-	1.1	-	-1.4	3.22E-03	-8.7	-	1.8
ENSORLG00000017624	*aqp1*	aquaporin 1 (Colton blood group)	Ensembl_medaka	-	-1.8	-	down	8.79E-02	-5.0	-	-1.1
ENSDARG00000007086	*aqp10a*	aquaporin 10a	Ensembl_zebrafish	-	up	3.50E-05	-24.9	-	2.2	-	1.2
ENSGACG00000012346	*arg2*	arginase, type II	Ensembl_stickleback	7.49E-12	down	6.21E-08	down	3.52E-10	-145.8	1.48E-02	down
388815820	JQ764761.1	Arion lusitanicus hypothetical protein mRNA, complete cds	nt	-	0.0	4.98E-05	up	-	0.0	-	0.0
188529830	EU541926.1	Arion rufus isolate FR1.01 16S ribosomal RNA gene, partial sequence; mitochondrial	nt	-	up	3.77E-12	307.9	-	up	5.87E-02	24.0
ENSGACG00000002986	*armc1 (1 of 2)*	armadillo repeat containing 1	Ensembl_stickleback	-	down	-	4.8	3.02E-02	up	-	1.9
ENSGACG00000019091	*asna1*	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	Ensembl_stickleback	-	-145.0	-	1.4	4.67E-03	down	-	3.8
ENSGACG00000007981	*aspg*	asparaginase homolog (S. cerevisiae)	Ensembl_stickleback	-	down	-	-3.0	6.99E-02	down	-	down
ENSGACG00000007419	*abcc2*	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	Ensembl_stickleback	-	0.0	-	down	-	down	5.91E-02	down
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	-	0.0
ENSGACG00000015604	*bcl7a*	B-cell CLL/lymphoma 7A	Ensembl_stickleback	3.75E-02	up	-	-2.1	-	-1.5	-	-1.1
ENSGACG00000004283	*bcl2l1 (1 of 2)*	BCL2-like 1	Ensembl_stickleback	-	up	-	down	1.22E-03	down	-	1.2
ENSGACG00000001688	*bmper*	BMP binding endothelial regulator	Ensembl_stickleback	-	up	-	-2.1	-	down	1.57E-03	up
ENSGACG00000012929	*bre*	brain and reproductive organ-expressed (TNFRSF1A modulator)	Ensembl_stickleback	-	0.0	-	0.0	5.65E-02	up	-	0.0
ENSDARG00000045568	*bcat1*	branched chain aminotransferase 1, cytosolic	Ensembl_zebrafish	-	1.6	-	up	-	1.5	1.46E-04	17.6
ENSORLG00000015803	*brox*	BRO1 domain and CAAX motif containing	Ensembl_medaka	3.35E-03	up	-	-1.2	-	-2.9	-	2.2
ENSGACG00000004158	*baz1a*	bromodomain adjacent to zinc finger domain, 1A	Ensembl_stickleback	-	1.2	-	-1.2	-	2.4	3.37E-15	-318.8
ENSGACG00000005734	*baz2b (4 of 4)*	bromodomain adjacent to zinc finger domain, 2B	Ensembl_stickleback	-	down	-	0.0	6.04E-02	-13.7	-	0.0
ENSGACG00000010106	*brd4*	bromodomain containing 4	Ensembl_stickleback	-	-4.3	-	-3.4	1.09E-03	-24.1	-	-2.8
213514654	NP_001134905.1	Butyrophilin subfamily 2 member A2	Refseq_proteins	-	1.5	-	1.4	9.82E-02	5.2	-	-1.7
ENSGACG00000005753	*celsr3*	cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila)	Ensembl_stickleback	-	-2.2	9.39E-03	down	6.99E-02	up	-	2.5
ENSGACG00000012602	*cabp1 (2 of 2)*	calcium binding protein 1	Ensembl_stickleback	7.32E-02	down	-	1.7	-	-1.5	-	-1.6
ENSDARG00000019990	*cabp1a*	calcium binding protein 1a	Ensembl_zebrafish	-	2.4	-	1.1	8.79E-02	up	-	2.1
ENSORLG00000010644	*cald1 (1 of 2)*	caldesmon 1	Ensembl_medaka	-	-4.2	1.77E-03	-14.4	-	2.9	-	0.0
ENSGACG00000012384	*camta1 (1 of 2)*	calmodulin binding transcription activator 1	Ensembl_stickleback	-	1.0	-	-2.0	-	-2.4	2.28E-03	-46.3

ENSGACG00000016957	*calml4*	calmodulin-like 4	Ensembl_stickleback	-	down	-	1.5	5.64E-02	-8.0	-	0.0
ENSGACG00000013281	*capn5 (2 of 2)*	calpain 5	Ensembl_stickleback	9.28E-02	down	-	up	-	0.0	1.48E-02	up
ENSGACG00000006412	*cnn1*	calponin 1, basic, smooth muscle	Ensembl_stickleback	6.54E-03	down	7.64E-03	down	1.42E-03	down	-	0.0
ENSDARG00000093937	*cnn1b*	calponin 1, basic, smooth muscle, b	Ensembl_zebrafish	-	-1.7	5.21E-02	-5.3	-	-1.3	-	1.4
ENSGACG00000014122	*casq1 (2 of 2)*	calsequestrin 1 (fast-twitch, skeletal muscle)	Ensembl_stickleback	-	-1.1	-	1.3	5.65E-02	down	-	up
ENSDARG00000054456	*clip3*	CAP-GLY domain containing linker protein 3	Ensembl_zebrafish	-	down	-	2.1	-	-1.3	7.77E-02	-6.4
ENSDARG00000056499	*ca6*	carbonic anhydrase VI	Ensembl_zebrafish	-	1.5	-	-2.1	-	-1.1	4.66E-03	37.9
ENSORLG00000014439	*cel (2 of 3)*	carboxyl ester lipase (bile salt-stimulated lipase)	Ensembl_medaka	-	0.0	4.56E-06	-33.0	-	0.0	-	0.0
ENSDARG00000029822	*cel.2*	carboxyl ester lipase, tandem duplicate 2	Ensembl_zebrafish	-	-2.5	4.50E-08	-49.2	-	-1.7	-	6.6
ENSDARG00000021339	*cpa5*	carboxypeptidase A5	Ensembl_zebrafish	-	1.5	1.11E-07	-35.6	-	1.6	-	down
ENSDARG00000045442	*cpb1*	carboxypeptidase B1 (tissue)	Ensembl_zebrafish	-	0.0	1.39E-07	-34.7	-	0.0	-	-1.1
ENSGACG00000015162	*cpb2*	carboxypeptidase B2 (plasma)	Ensembl_stickleback	-	-2.7	-	1.6	-	1.8	2.26E-03	-16.4
ENSORLG00000010823	*ctsc*	cathepsin C	Ensembl_medaka	-	up	-	-1.3	5.66E-03	up	-	-1.9
CX349299	gb|CX349299.1	ccluwtbl015016_0 Coregonus clupeaformis head Coregonus clupeaformis cDNA, mRNA sequence.	EST_others	-	0.0	-	0.0	-	0.0	3.22E-03	down
ENSDARG00000013628	*cd164*	CD164 molecule, sialomucin	Ensembl_zebrafish	-	1.0	-	1.8	4.20E-02	6.2	7.20E-02	6.5
ENSGACG00000017930	*cisd2*	CDGSH iron sulfur domain 2	Ensembl_stickleback	-	2.9	2.45E-03	down	-	2.5	3.74E-02	up
ENSGACG00000004663	*cdca4*	cell division cycle associated 4	Ensembl_stickleback	9.28E-02	down	-	2.1	-	1.6	-	1.0
ENSGACG00000006495	*cdca7l*	cell division cycle associated 7-like	Ensembl_stickleback	-	15.5	-	up	1.59E-02	up	-	0.0
ENSGACG00000009388	*cep290*	centrosomal protein 290kDa	Ensembl_stickleback	-	0.0	-	0.0	1.96E-02	down	-	0.0
ENSDARG00000002365	*cers5*	ceramide synthase 5	Ensembl_zebrafish	-	1.3	-	1.3	-	-1.2	9.95E-02	up
ENSGACG00000002643	*cct5*	chaperonin containing TCP1, subunit 5 (epsilon)	Ensembl_stickleback	-	1.1	-	0.0	-	0.0	8.58E-03	down
ENSGACG00000019847	*cct7*	chaperonin containing TCP1, subunit 7 (eta)	Ensembl_stickleback	3.85E-03	up	-	down	-	-1.0	-	up
ENSGACG00000018739	*cxcl12 (1 of 2)*	chemokine (C-X-C motif) ligand 12	Ensembl_stickleback	-	1.3	-	down	1.43E-09	-65.8	-	2.2
ENSDARG00000055100	*cxcl12b*	chemokine (C-X-C motif) ligand 12b (stromal cell-derived factor 1)	Ensembl_zebrafish	-	-1.2	-	1.4	8.09E-06	-20.4	-	1.1
ENSGACG00000008146	*chn2*	chimerin (chimaerin) 2	Ensembl_stickleback	5.86E-02	up	-	up	-	up	-	up
ENSDARG00000093193	*chia.6*	chitinase, acidic.6	Ensembl_zebrafish	-	-1.1	-	-2.1	-	-2.8	4.66E-03	-13.6
ENSGACG00000017379	*clic2*	chloride intracellular channel 2	Ensembl_stickleback	-	0.0	-	-1.8	4.05E-05	down	-	0.0
ENSGACG00000007280	*clic4*	chloride intracellular channel 4	Ensembl_stickleback	-	-4.0	-	3.7	1.96E-02	down	-	down
ENSGACG00000004855	*cbx7 (1 of 2)*	chromobox homolog 7	Ensembl_stickleback	-	1.2	9.01E-02	7.5	-	up	-	2.2
ENSG00000166002	*c11orf75*	chromosome 11 open reading frame 75	Ensembl_human	-	down	5.52E-06	up	-	-1.3	1.95E-04	up

ENSORLG00000001844	*c17orf67*	chromosome 17 open reading frame 67	Ensembl_medaka	-	-3.6	-	0.0	2.11E-02	-7.4	-	2.1
ENSORLG00000014223	*c4orf33*	chromosome 4 open reading frame 33	Ensembl_medaka	-	1.2	3.54E-02	-5.8	-	-1.3	-	1.3
ENSONIG00000002851	*c9orf16*	chromosome 9 open reading frame 16	Ensembl_nile_tilapia	-	3.0	-	-1.0	-	-1.3	7.68E-02	down
ENSORLG00000004586	*ctrc (2 of 2)*	chymotrypsin C (caldecrin)	Ensembl_medaka	-	0.0	1.10E-07	-37.4	-	up	-	-3.3
ENSDARG00000068680	*ctrl*	chymotrypsin-like	Ensembl_zebrafish	-	0.0	1.39E-07	-41.8	-	0.0	-	1.8
ENSONIG00000003112	*cela3a*	chymotrypsin-like elastase family, member 3A	Ensembl_nile_tilapia	-	0.0	1.82E-03	-19.3	-	0.0	-	0.0
ENSORLG00000006922	*cela1 (2 of 2)*	chymotrypsin-like elastase family, member 1	Ensembl_medaka	-	1.2	1.86E-06	-27.4	-	0.0	-	down
ENSDARG00000017314	*cela1 (1 of 7)*	chymotrypsin-like elastase family, member 1	Ensembl_zebrafish	-	1.2	2.12E-06	-39.5	-	0.0	-	0.0
ENSONIG00000006852	*cela1 (2 of 2)*	chymotrypsin-like elastase family, member 1	Ensembl_nile_tilapia	-	down	1.77E-03	down	-	0.0	-	0.0
ENSDARG00000090428	*ctrb1*	chymotrypsinogen B1	Ensembl_zebrafish	-	0.0	1.35E-07	-46.7	-	0.0	-	down
ENSGACG00000000480	*cotl1*	coactosin-like 1 (Dictyostelium)	Ensembl_stickleback	-	down	3.04E-04	down	5.65E-02	up	-	down
ENSORLG00000013399	*f5*	coagulation factor V (proaccelerin, labile factor)	Ensembl_medaka	-	down	-	0.0	6.99E-02	up	-	-1.3
ENSGACG00000014046	*cc2d2a (1 of 2)*	coiled-coil and C2 domain containing 2A	Ensembl_stickleback	-	-1.3	-	-2.9	5.66E-03	up	-	down
ENSDARG00000028524	*col5a3b*	collagen, type V, alpha 3b	Ensembl_zebrafish	-	-14.4	-	up	5.65E-02	down	-	0.0
213515210	NP_001134256.1	complement C1q-like protein 2	Refseq_proteins	4.90E-02	19.0	-	1.5	1.47E-02	-17.8	-	-1.0
ENSONIG00000016437	*c3 (4 of 4)*	complement component 3	Ensembl_nile_tilapia	-	down	1.27E-05	down	-	-1.4	-	-1.8
ENSGACG00000011303	*coro7*	coronin 7	Ensembl_stickleback	-	-1.9	-	1.4	3.24E-03	down	-	up
CR371595	emb|CR371595.2	CR371595 AGENAE Rainbow trout normalized testis library (tcbi) Oncorhynchus mykiss cDNA clone tcbi0031.o.10 5', mRNA sequence.	EST_others	-	up	-	3.5	4.49E-02	up	-	up
CR373403	emb|CR373403.2	CR373403 AGENAE Rainbow trout normalized testis library (tcbi) Oncorhynchus mykiss cDNA clone tcbi0023.m.23 5', mRNA sequence.	EST_others	1.36E-02	up	-	-7.2	-	-2.3	-	down
ENSONIG00000020925	*crebzf*	CREB/ATF bZIP transcription factor	Ensembl_nile_tilapia	9.89E-02	10.6	-	1.3	-	1.5	-	4.1
113671701	NP_001038787.1	crumbs homolog 3a precursor	Refseq_proteins	-	3.7	-	-2.2	1.96E-02	up	-	-4.6
ENSGACG00000006281	*ctdspl2 (1 of 2)*	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	Ensembl_stickleback	-	-1.4	-	-1.2	4.49E-02	down	-	up
CU069447	emb|CU069447.1	CU069447 AGENAE Rainbow trout multi-tissues library (tcce) Oncorhynchus mykiss cDNA clone tcay0022.o.06 3', mRNA sequence.	EST_others	-	0.0	-	0.0	-	down	4.78E-02	down
ENSGACG00000008425	*cuedc2*	CUE domain containing 2	Ensembl_stickleback	1.11E-07	200.3	-	0.0	-	down	-	7.0
ENSONIG00000003295	*cdk18*	cyclin-dependent kinase 18	Ensembl_nile_tilapia	-	-2.1	-	0.0	6.99E-02	down	-	0.0
375196821	JN739111.1	Cyprinus carpio clone 409854 microsatellite sequence	nt	-	-1.8	6.22E-03	down	-	-1.8	-	down
ENSGACG00000009382	*cth*	cystathionase (cystathionine gamma-lyase)	Ensembl_stickleback	-	-5.9	-	1.1	2.57E-04	-19.4	-	1.0

ENSONIG00000001633	*cox4i2*	cytochrome c oxidase subunit IV isoform 2 (lung)	Ensembl_nile_tilapia	9.61E-03	down	-	-2.1	-	1.8	4.61E-02	6.3
ENSONIG00000001074	*cyp46a1*	cytochrome P450, family 46, subfamily A, polypeptide 1	Ensembl_nile_tilapia	4.68E-03	up	-	2.8	5.78E-03	10.2	-	-1.2
ENSGACG00000017414	*cyp8b1*	cytochrome P450, family 8, subfamily B, polypeptide 1	Ensembl_stickleback	-	-3.1	-	0.0	-	up	8.31E-05	-36.4
ENSDARG00000053068	*cyp8b1*	cytochrome P450, family 8, subfamily B, polypeptide 1	Ensembl_zebrafish	-	0.0	1.87E-02	12.8	-	1.1	-	-1.2
ENSGACG00000011632	*cyth3 (1 of 2)*	cytohesin 3	Ensembl_stickleback	-	-4.0	-	-4.4	6.86E-02	-6.2	-	-3.1
ENSGACG00000008861	*dao*	D-amino-acid oxidase	Ensembl_stickleback	-	0.0	9.01E-02	down	-	down	-	down
41055872	NM_200993.1	Danio rerio zgc:55733 (zgc:55733), mRNA	Refseq_genes	-	-3.2	-	-1.4	-	1.5	2.11E-07	up
ENSGACG00000016060	*ddx21*	DEAD (Asp-Glu-Ala-Asp) box helicase 21	Ensembl_stickleback	-	-16.6	-	-3.8	-	-1.9	1.37E-03	down
ENSGACG00000010201	*dapk2 (2 of 2)*	death-associated protein kinase 2	Ensembl_stickleback	3.13E-08	down	-	0.0	-	0.0	-	down
ENSGACG00000001844	*daxx*	death-domain associated protein	Ensembl_stickleback	2.42E-03	down	-	down	-	2.1	-	-1.8
ENSGACG00000018923	*dock4*	dedicator of cytokinesis 4	Ensembl_stickleback	-	1.4	-	1.3	-	1.1	6.43E-04	-11.7
ENSGACG00000002377	*dhrs7c (2 of 2)*	dehydrogenase/reductase (SDR family) member 7C	Ensembl_stickleback	-	down	-	down	1.04E-02	down	-	0.0
ENSGACG00000008597	*degs2*	delta(4)-desaturase, sphingolipid 2	Ensembl_stickleback	-	1.2	-	5.1	7.29E-04	11.5	-	2.9
ENSGACG00000019427	*dtx4 (1 of 2)*	deltex homolog 4 (Drosophila)	Ensembl_stickleback	-	-1.8	-	1.1	2.43E-02	down	-	down
ENSGACG00000005878	*dnase1*	deoxyribonuclease I	Ensembl_stickleback	-	0.00	1.26E-07	down	-	0.0	-	down
ENSGACG00000015594	*dda1 (2 of 2)*	DET1 and DDB1 associated 1	Ensembl_stickleback	-	down	-	-1.8	1.28E-02	down	-	-4.4
ENSGACG00000018166	*dpysl2 (1 of 2)*	dihydropyrimidinase-like 2	Ensembl_stickleback	-	-6.8	6.40E-02	-24.7	4.39E-02	-30.3	-	-4.3
ENSGACG00000006240	*dip2a*	DIP2 disco-interacting protein 2 homolog A (Drosophila)	Ensembl_stickleback	-	-5.3	-	-3.2	1.22E-03	down	5.14E-04	-28.6
ENSGACG00000000671	*dip2b (2 of 2)*	DIP2 disco-interacting protein 2 homolog B (Drosophila)	Ensembl_stickleback	-	-2.2	-	-1.6	-	-3.1	2.80E-03	-16.8
19171735	AF382036.1	Discocotyle sagittata 28S large subunit ribosomal RNA, partial sequence	nt	8.88E-02	27.2	-	up	-	1.4	-	-1.1
ENSDARG00000062177	*dcbld2*	discoidin, CUB and LCCL domain containing 2	Ensembl_zebrafish	4.69E-02	up	-	up	4.49E-02	up	-	down
ENSORLG00000011807	*dcbld2*	discoidin, CUB and LCCL domain containing 2	Ensembl_medaka	6.54E-03	down	-	-1.2	3.65E-02	down	-	1.0
ENSDARG00000041110	*dnajc3*	DnaJ (Hsp40) homolog, subfamily C, member 3	Ensembl_zebrafish	-	2.7	-	2.6	-	1.5	1.13E-02	9.1
ENSGACG00000016454	*dusp22 (1 of 2)*	dual specificity phosphatase 22	Ensembl_stickleback	-	0.00	-	down	2.28E-03	down	-	down
ENSGACG00000003355	*dynlt3 (1 of 2)*	dynein, light chain, Tctex-type 3	Ensembl_stickleback	9.28E-02	down	-	down	-	1.6	-	up
ENSORLG00000002091	*elf2*	E74-like factor 2 (ets domain transcription factor)	Ensembl_medaka	5.65E-03	down	-	-2.7	-	-3.1	-	1.8
ENSGACG00000003978	*egfl6*	EGF-like-domain, multiple 6	Ensembl_stickleback	-	down	2.87E-03	down	4.39E-02	-28.0	-	0.0
ENSGACG00000015896	*egfl8*	EGF-like-domain, multiple 8	Ensembl_stickleback	-	down	-	-2.8	5.65E-02	down	-	0.0

ENSDARG00000056744	*ela2*	elastase 2	Ensembl_zebrafish	-	0.00	3.21E-07	-30.7	-	0.0	-	down
ENSDARG00000007276	*ela3l*	elastase 3 like	Ensembl_zebrafish	-	0.00	1.10E-07	-46.4	-	0.0	-	down
ENSDARG00000045639	*elavl4*	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	-	0.0
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	-39.3	-	0.0	-	3.7
ENSGACG00000005596	*erlec1*	endoplasmic reticulum lectin 1	Ensembl_stickleback	-	-1.1	-	3.7	3.18E-04	up	-	1.3
269860691	XM_002650019.1	Enterocytozoon bieneusi H348 tubulin alpha chain (EBI_21799) mRNA, complete cds	nt	7.32E-02	up	-	0.0	-	0.0	-	0.0
ENSGACG00000009051	*ephb3 (1 of 2)*	EPH receptor B3	Ensembl_stickleback	-	4.0	4.13E-02	12.6	-	4.0	-	1.5
238817522	FJ443041.1	Ephemerella cornutus 16S ribosomal RNA gene, partial sequence; mitochondrial	nt	-	0.00	1.08E-03	up	-	0.0	-	0.0
ENSGACG00000002632	*epcam*	epithelial cell adhesion molecule	Ensembl_stickleback	-	-1.2	3.54E-02	down	8.30E-03	down	-	up
ENSONIG00000019196	*ect2*	epithelial cell transforming sequence 2 oncogene	Ensembl_nile_tilapia	-	0.00	-	up	3.02E-02	down	-	1.6
225715605	BT079225.1	Esox lucius clone eluc-evq-516-169 Probable pancreatic secretory proteinase inhibitor putative mRNA, complete cds	nt	-	0.00	2.53E-03	-18.3	-	up	-	down
225716561	BT079703.1	Esox lucius clone eluc-evq-517-294 Fucolectin-4 precursor putative mRNA, complete cds	nt	-	0.00	-	1.2	-	0.0	2.72E-05	-25.6
225716185	BT079515.1	Esox lucius clone eluc-evq-538-320 Apolipoprotein O precursor putative mRNA, complete cds	nt	-	up	-	0.0	9.52E-06	down	-	0.0
ENSDARG00000004111	*esr1*	estrogen receptor 1	Ensembl_zebrafish	-	0.00	-	up	-	2.9	1.19E-10	105.2
ENSG00000156508	*eef1a1*	eukaryotic translation elongation factor 1 alpha 1	Ensembl_human	8.70E-06	up	-	0.0	-	0.0	-	0.0
ENSGACG00000008569	*eif2s1*	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	Ensembl_stickleback	-	0.00	1.32E-10	-454.3	-	2.2	-	-1.1
ENSGACG00000013800	*eif2b3*	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	Ensembl_stickleback	2.14E-08	up	-	down	-	down	-	0.0
ENSGACG00000004504	*eif4h*	eukaryotic translation initiation factor 4H	Ensembl_stickleback	-	0.00	1.84E-02	down	-	-1.7	-	up
ENSGACG00000009227	*esyt1 (2 of 2)*	extended synaptotagmin-like protein 1	Ensembl_stickleback	-	-1.9	-	-4.7	6.46E-05	-19.0	-	-1.2
ENSGACG00000018094	*fam129b*	family with sequence similarity 129, member B	Ensembl_stickleback	8.82E-07	-132.5	-	up	-	up	-	down
ENSDARG00000074317	*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	*fam204a*	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
ENSDARG00000010437	*fam46c*	family with sequence similarity 46, member C	Ensembl_zebrafish	-	-4.2	-	1.2	-	-1.9	2.05E-02	11.1

ENSGACG00000004704	*fam65b*	family with sequence similarity 65, member B	Ensembl_stickleback	-	-2.0	-	down	2.47E-02	-6.6	-	up
ENSGACG00000007029	*fancc*	Fanconi anemia, complementation group C	Ensembl_stickleback	5.86E-02	down	-	down	2.85E-09	down	-	down
ENSDARG00000038439	*fabp10a*	fatty acid binding protein 10a, liver basic	Ensembl_zebrafish	-	-1.7	5.44E-02	-25.7	-	-1.4	-	-1.8
ENSGACG00000010321	*fbn3*	fibrillin 3	Ensembl_stickleback	-	-1.4	-	-1.2	8.06E-02	-5.2	-	-4.3
ENSDARG00000008969	*fgb*	fibrinogen, B beta polypeptide	Ensembl_zebrafish	-	4.7	2.66E-02	-30.1	-	2.9	-	-2.0
ENSDARG00000037281	*fgg*	fibrinogen, gamma polypeptide	Ensembl_zebrafish	-	-1.3	1.70E-02	-19.4	-	down	-	-1.7
ENSORLG00000001333	*fscb*	fibrous sheath CABYR binding protein	Ensembl_medaka	-	-2.0	7.81E-02	-6.9	5.97E-02	-8.5	1.96E-02	-15.5
ENSGACG00000013103	*flna (2 of 2)*	filamin A, alpha	Ensembl_stickleback	-	1.3	7.08E-02	-5.6	-	-3.9	-	2.0
301069358	NP_571346.2	forkhead box D1	Refseq_proteins	-	down	2.45E-03	up	-	2.0	-	0.0
ENSGACG00000017029	*foxo4*	forkhead box O4	Ensembl_stickleback	-	-1.0	-	-2.0	1.02E-04	-27.6	-	down
ENSGACG00000007994	*fhod3 (1 of 2)*	formin homology 2 domain containing 3	Ensembl_stickleback	-	0.00	-	down	3.67E-05	down	-	0.0
ENSGACG00000014208	*fmnl1 (2 of 2)*	formin-like 1	Ensembl_stickleback	-	-1.1	-	-1.3	3.17E-02	-8.2	-	down
ENSGACG00000010242	*fhl5*	four and a half LIM domains 5	Ensembl_stickleback	-	down	-	down	3.90E-03	down	-	0.0
ENSGACG00000018742	*fmr1*	fragile X mental retardation 1	Ensembl_stickleback	-	up	2.45E-03	up	-	up	-	0.0
ENSDARG00000089165	*fut9 (14 of 16)*	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	Ensembl_zebrafish	-	-1.2	-	1.9	8.81E-02	14.8	-	up
ENSGACG00000011403	*fh*	fumarate hydratase	Ensembl_stickleback	-	-1.5	9.01E-02	down	-	-1.7	-	down
ENSORLG00000013751	*fundc1*	FUN14 domain containing 1	Ensembl_medaka	4.69E-02	down	-	1.4	6.99E-02	down	5.91E-02	down
ENSGACG00000009962	*gabpb2*	GA binding protein transcription factor, beta subunit 2	Ensembl_stickleback	9.28E-02	down	-	-1.8	-	-2.1	-	-1.2
112419938	BT026755.1	Gasterosteus aculeatus clone CFW26-C06 mRNA sequence	nt	-	-1.0	-	-6.3	6.60E-02	-8.2	-	up
112420062	BT026879.1	Gasterosteus aculeatus clone CFW80-B01 mRNA sequence	nt	-	0.00	-	0.0	-	0.0	1.46E-03	-11.1
112420848	BT027665.1	Gasterosteus aculeatus clone CGX78-D04 mRNA sequence	nt	-	-1.1	-	-4.1	2.28E-03	up	-	up
ENSORLG00000000978	*gatsl3*	GATS protein-like 3	Ensembl_medaka	-	down	-	1.3	8.81E-02	11.9	-	1.0
ENSORLG00000020655	*gle1*	GLE1 RNA export mediator homolog (yeast)	Ensembl_medaka	-	2.0	-	down	8.79E-02	down	-	-2.1
ENSGACG00000005766	*gltscr2*	glioma tumor suppressor candidate region gene 2	Ensembl_stickleback	-	-1.7	-	0.0	6.99E-02	down	-	down
ENSORLG00000002010	*gck*	glucokinase (hexokinase 4)	Ensembl_medaka	-	0.00	-	0.0	-	0.0	1.87E-02	up
ENSDARG00000068006	*gck*	glucokinase (hexokinase 4, maturity onset diabetes of the young 2)	Ensembl_zebrafish	-	0.00	-	down	-	0.0	4.94E-08	42.9
ENSGACG00000011182	*gclm*	glutamate-cysteine ligase, modifier subunit	Ensembl_stickleback	-	1.2	-	-2.0	3.02E-02	down	-	up
ENSGACG00000006959	*qpct*	glutaminyl-peptide cyclotransferase	Ensembl_stickleback	-	down	-	4.9	6.71E-03	-11.0	-	-1.7

ENSGACG00000005698	*gnmt*	glycine N-methyltransferase	Ensembl_stickleback	-	-3.3	-	-5.3	-	-1.2	5.17E-05	-23.2
ENSDARG00000036239	*gatm*	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	Ensembl_zebrafish	-	0.00	-	1.1	3.24E-03	down	-	0.0
ENSGACG00000009501	*grhl3*	grainyhead-like 3 (Drosophila)	Ensembl_stickleback	-	up	-	up	2.75E-04	up	-	up
ENSGACG00000006103	*grem1*	gremlin 1	Ensembl_stickleback	-	down	1.84E-02	up	-	up	-	-1.1
ENSGACG00000020233	*hspb1*	heat shock 27kDa protein 1	Ensembl_stickleback	-	1.2	5.59E-02	down	-	-2.2	-	2.2
ENSDARG00000092362	*hsp70.2*	heat shock cognate 70-kd protein, tandem duplicate 2	Ensembl_zebrafish	5.91E-03	8.9	1.93E-02	7.3	-	1.6	-	-1.3
ENSGACG00000011278	*hectd4 (1 of 2)*	HECT domain containing E3 ubiquitin protein ligase 4	Ensembl_stickleback	-	-1.4	-	-1.0	-	-1.8	3.09E-02	-6.3
ENSGACG00000003389	*hhatl (2 of 2)*	hedgehog acyltransferase-like	Ensembl_stickleback	4.69E-02	down	-	0.0	2.51E-07	down	-	0.0
ENSGACG00000012795	*hhatl (1 of 2)*	hedgehog acyltransferase-like	Ensembl_stickleback	-	0.00	-	0.0	2.43E-02	down	-	0.0
ENSONIG00000012532	*helq*	helicase, POLQ-like	Ensembl_nile_tilapia	9.28E-02	down	-	0.0	-	-1.1	-	down
ENSGACG00000010755	*hltf*	helicase-like transcription factor	Ensembl_stickleback	-	-2.0	-	-2.8	2.75E-04	down	-	-2.9
ENSDARG00000012609	*hpx*	hemopexin	Ensembl_zebrafish	-	-2.3	3.33E-02	-12.0	-	-1.5	-	-1.5
ENSONIG00000017473	*hlcs*	holocarboxylase synthetase (biotin-(proprionyl-CoA-carboxylase (ATP-hydrolysing)) ligase)	Ensembl_nile_tilapia	1.61E-02	down	-	0.0	-	-1.6	-	-1.2
ENSGACG00000009401	*hoxc8*	homeobox C8	Ensembl_stickleback	9.37E-03	-35.8	-	-1.5	3.65E-02	-31.3	-	down
ENSGACG00000010338	*htra1 (1 of 2)*	HtrA serine peptidase 1	Ensembl_stickleback	1.45E-07	127.2	-	down	-	down	-	0.0
ENSORLG00000013140	*habp2*	hyaluronan binding protein 2	Ensembl_medaka	-	down	4.41E-02	down	-	0.0	-	-1.8
ENSGACG00000013673	*hsd3b7*	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	Ensembl_stickleback	-	-2.1	-	1.0	9.50E-02	4.9	2.33E-02	-7.8
260783280	XP_002586704.1	hypothetical protein BRAFLDRAFT_77465	Refseq_proteins	-	-1.5	-	up	9.04E-04	down	-	0.0
156308441	XP_001617664.1	hypothetical protein NEMVEDRAFT_v1g69851	nr	1.25E-07	up	-	0.0	-	0.0	-	0.0
ENSDARG00000096430	*ighv9-1*	immunoglobulin heavy variable 9-1	Ensembl_zebrafish	9.28E-02	down	-	0.0	-	2.6	-	down
ENSONIG00000008551	*ino80d*	INO80 complex subunit D	Ensembl_nile_tilapia	-	-2.9	-	-3.4	3.24E-02	-6.7	-	-1.3
ENSDARG00000011909	*itpr2*	inositol 1,4,5-triphosphate receptor, type 2	Ensembl_zebrafish	-	-1.1	-	1.8	8.78E-02	17.4	-	-2.7
ENSGACG00000000831	*ip6k2 (1 of 2)*	inositol hexakisphosphate kinase 2	Ensembl_stickleback	7.33E-03	8.7	1.51E-02	6.7	-	2.2	1.15E-02	7.4
ENSGACG00000015412	*ipmk*	inositol polyphosphate multikinase	Ensembl_stickleback	-	down	-	12.9	1.70E-04	down	-	1.2
ENSDARG00000014947	*igfbp1a*	insulin-like growth factor binding protein 1a	Ensembl_zebrafish	-	-1.3	-	-1.3	5.65E-02	up	-	-2.2
ENSDARG00000038666	*igfbp1b*	insulin-like growth factor binding protein 1b	Ensembl_zebrafish	-	0.00	-	down	-	down	5.91E-02	-5.4
ENSGACG00000002508	*igfbp5 (1 of 2)*	insulin-like growth factor binding protein 5	Ensembl_stickleback	-	1.1	-	0.0	-	-1.1	2.94E-02	up
ENSDARG00000034043	*irx5a*	iroquois homeobox protein 5a	Ensembl_zebrafish	-	0.00	-	0.0	8.79E-02	down	-	0.0
ENSGACG00000011519	*jph2*	junctophilin 2	Ensembl_stickleback	-	up	-	1.0	-	-2.8	4.60E-03	14.4

ENSGACG00000009872	*kat7 (1 of 2)*	K(lysine) acetyltransferase 7	Ensembl_stickleback	-	-1.6	-	2.0	3.65E-02	down	-	0.0
ENSORLG00000011216	*kansl3*	KAT8 regulatory NSL complex subunit 3	Ensembl_medaka	-	down	-	down	-	-3.1	5.91E-02	down
ENSDARG00000015815	*kdrl*	kinase insert domain receptor like	Ensembl_zebrafish	-	1.4	-	1.5	4.39E-02	21.0	-	-1.4
ENSGACG00000011649	*lace1 (1 of 2)*	lactation elevated 1	Ensembl_stickleback	-	0.00	-	0.0	-	0.0	1.70E-04	up
ENSONIG00000014788	*lrig2*	leucine-rich repeats and immunoglobulin-like domains 2	Ensembl_nile_tilapia	-	1.4	1.49E-02	up	1.50E-04	up	-	-1.1
ENSGACG00000000675	*lta4h*	leukotriene A4 hydrolase	Ensembl_stickleback	-	0.00	-	up	3.67E-05	down	-	up
ENSGACG00000008716	*limk2*	LIM domain kinase 2	Ensembl_stickleback	-	-2.3	-	1.8	3.11E-02	22.4	-	2.6
ENSGACG00000005614	*lmf1*	lipase maturation factor 1	Ensembl_stickleback	-	1.6	4.56E-06	down	-	1.2	-	-1.6
ENSGACG00000019500	*ldlr (2 of 2)*	low density lipoprotein receptor	Ensembl_stickleback	-	up	4.41E-02	down	-	-4.8	-	down
ENSGACG00000011854	*kdm2b (2 of 2)*	lysine (K)-specific demethylase 2B	Ensembl_stickleback	-	-2.4	-	-2.2	1.34E-04	down	-	down
ENSDARG00000013542	*lpgat1*	lysophosphatidylglycerol acyltransferase 1	Ensembl_zebrafish	-	-3.4	-	1.5	-	up	5.61E-03	up
ENSGACG00000018078	*man1b1 (1 of 2)*	mannosidase, alpha, class 1B, member 1	Ensembl_stickleback	-	-1.5	-	-2.4	6.99E-02	down	-	1.3
ENSGACG00000013607	*man1c1*	mannosidase, alpha, class 1C, member 1	Ensembl_stickleback	-	1.1	9.01E-02	down	-	1.5	7.68E-02	up
ENSDARG00000042816	*mmp9*	matrix metalloproteinase 9	Ensembl_zebrafish	-	-1.7	-	-1.5	1.41E-02	-6.6	-	-2.2
ENSDARG00000060808	*mecom*	MDS1 and EVI1 complex locus	Ensembl_zebrafish	3.75E-02	-27.0	-	1.0	-	up	-	-1.1
ENSGACG00000012999	*mep1b (1 of 2)*	meprin A, beta	Ensembl_stickleback	-	down	-	down	9.04E-04	down	-	down
ENSGACG00000015955	*mthfsd*	methenyltetrahydrofolate synthetase domain containing	Ensembl_stickleback	-	-1.5	-	2.9	8.79E-02	down	-	up
ENSDARG00000090044	*mthfd2*	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	Ensembl_zebrafish	-	2.1	-	1.4	-	1.4	1.19E-02	up
ENSDARG00000053087	*mthfr*	methylenetetrahydrofolate reductase (NAD(P)H)	Ensembl_zebrafish	-	1.2	-	-1.7	-	1.2	2.69E-02	28.0
ENSGACG00000016984	*msmo1*	methylsterol monooxygenase 1	Ensembl_stickleback	-	0.00	3.54E-02	up	-	down	-	up
ENSGACG00000005096	*mettl5*	methyltransferase like 5	Ensembl_stickleback	-	-1.1	-	-2.2	8.04E-02	-4.8	-	-1.1
ENSGACG00000006537	*mcph1*	microcephalin 1	Ensembl_stickleback	-	1.5	-	down	1.28E-02	down	-	-2.6
ENSONIG00000009665	*mcph1*	microcephalin 1	Ensembl_nile_tilapia	-	0.00	9.01E-02	down	-	-6.6	-	0.0
ENSONIG00000000210	*mfap4 (8 of 9)*	microfibrillar-associated protein 4	Ensembl_nile_tilapia	-	0.00	1.49E-02	-9.0	-	0.0	-	0.0
ENSGACG00000010541	*mrpl12*	mitochondrial ribosomal protein L12	Ensembl_stickleback	-	5.4	-	1.4	6.99E-02	down	-	-2.2
ENSGACG00000002919	*mrpl30*	mitochondrial ribosomal protein L30	Ensembl_stickleback	-	up	-	-3.0	1.07E-03	down	-	down
ENSGACG00000013019	*mapk8ip3*	mitogen-activated protein kinase 8 interacting protein 3	Ensembl_stickleback	7.43E-04	65.8	-	2.5	-	-2.5	-	4.6
159490	M28397.1	MOTARYBB Tobacco hornworm (M.sexta) arylphorin beta subunit mRNA, complete cds	nt	-	0.00	2.00E-05	up	-	up	-	0.0

ENSGACG00000009336	*mre11a*	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	Ensembl_stickleback	7.32E-02	up	-	2.3	6.84E-03	up	-	1.1
ENSG00000247627	*mtnd4p12*	MT-ND4 pseudogene 12	Ensembl_human	-	down	7.76E-04	down	1.03E-04	down	2.27E-04	-67.2
ENSG00000251544	*mtnd5p12*	MT-ND5 pseudogene 12	Ensembl_human	-	down	-	down	-	down	9.95E-02	down
ENSGACG00000001806	*megf8*	multiple EGF-like-domains 8	Ensembl_stickleback	-	1.0	9.02E-05	up	-	-2.0	-	1.6
ENSGACG00000007818	*mras*	muscle RAS oncogene homolog	Ensembl_stickleback	-	1.0	-	-3.9	3.92E-03	40.7	-	-7.8
ENSGACG00000008124	*myof (1 of 2)*	myoferlin	Ensembl_stickleback	-	up	-	up	-	-1.4	1.33E-14	down
ENSGACG00000000114	*myo18b (1 of 2)*	myosin XVIIIB	Ensembl_stickleback	-	0.00	-	down	3.24E-03	down	-	0.0
ENSGACG00000010907	*myoz1 (1 of 2)*	myozenin 1	Ensembl_stickleback	-	0.00	6.88E-05	down	-	0.0	-	up
ENSDARG00000023369	*mxd*	myxovirus (influenza virus) resistance D	Ensembl_zebrafish	-	-2.5	2.29E-07	31.6	-	-1.4	-	0.0
ENSORLG00000020815	*nans*	N-acetylneuraminic acid synthase	Ensembl_medaka	-	0.00	9.39E-03	up	-	-5.1	-	down
ENSGACG00000002420	*ndufb8*	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	Ensembl_stickleback	-	down	-	0.0	2.21E-03	-16.4	-	-1.6
ENSONIG00000015110	*ndufaf2*	NADH dehydrogenase (ubiquinone) complex I, assembly factor 2	Ensembl_nile_tilapia	-	0.00	-	down	3.65E-02	down	-	0.0
ENSGACG00000020925	*nd1*	NADH dehydrogenase subunit 1	Ensembl_stickleback	2.42E-03	down	1.43E-06	down	8.60E-08	down	1.55E-09	down
ENSGACG00000020947	*nd4*	NADH dehydrogenase subunit 4	Ensembl_stickleback	-	down	-	down	8.79E-02	down	-	down
ENSGACG00000020951	*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
ENSGACG00000014896	*nckap5*	NCK-associated protein 5	Ensembl_stickleback	-	1.3	-	-1.9	-	-3.2	8.58E-03	up
ENSONIG00000017915	*ndfip1 (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
ENSGACG00000013006	*napa*	N-ethylmaleimide-sensitive factor attachment protein, alpha	Ensembl_stickleback	-	down	-	0.0	2.26E-02	-34.4	-	0.0
ENSGACG00000006514	*nsf (1 of 2)*	N-ethylmaleimide-sensitive factor	Ensembl_stickleback	4.19E-04	down	5.07E-03	-40.2	8.79E-02	down	-	0.0
ENSGACG00000014174	*nbeal1*	neurobeachin-like 1	Ensembl_stickleback	1.24E-02	-10.5	-	1.3	-	-1.1	-	-3.4
ENSGACG00000020827	*ncf1*	neutrophil cytosolic factor 1	Ensembl_stickleback	-	-1.4	-	1.9	3.04E-02	-6.8	-	down
ENSGACG00000004210	*nid1 (1 of 2)*	nidogen 1	Ensembl_stickleback	-	0.00	1.13E-04	down	-	up	-	-1.6
ENSGACG00000001588	*ninj1*	ninjurin 1	Ensembl_stickleback	3.75E-08	-199.3	-	-3.1	-	1.5	-	-1.1
ENSDARG00000037958	*nosip*	nitric oxide synthase interacting protein	Ensembl_zebrafish	3.75E-02	down	-	-2.1	-	-3.8	-	2.3
ENSDARG00000044075	*nkx6.2*	NK6 transcription factor related, locus 2	Ensembl_zebrafish	-	0.00	1.45E-02	-9.0	-	up	-	0.0
ENSGACG00000016365	*nfatc3*	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	Ensembl_stickleback	1.34E-08	97.1	-	1.0	-	2.2	-	0.0
ENSDARG00000057741	*nr1h4*	nuclear receptor subfamily 1, group H, member 4	Ensembl_zebrafish	-	0.00	-	1.8	6.04E-02	19.5	-	-1.1
ENSGACG00000012768	*nucb1*	nucleobindin 1	Ensembl_stickleback	-	-1.3	-	-1.5	3.65E-02	down	-	-2.3

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	-	down	-	-5.5
ENSGACG00000019459	*nap1l1*	nucleosome assembly protein 1-like 1	Ensembl_stickleback	-	-4.3	-	up	3.02E-02	down	-	down
ENSDARG00000016256	*nudt3a*	nudix (nucleoside diphosphate linked moiety X)-type motif 3a	Ensembl_zebrafish	-	1.0	2.24E-04	down	3.27E-02	-7.4	-	1.2
1296952	X92804.1	O.mykiss vtg1 gene	nt	-	0.00	-	0.0	-	0.0	9.87E-04	up
ENSGACG00000016390	*odz3 (2 of 2)*	odz, odd Oz/ten-m homolog 3 (Drosophila)	Ensembl_stickleback	-	2.4	-	-2.1	5.07E-02	-9.7	-	down
ES555559	gb|ES555559.1	okis_FCE_L3-12.G09 Coho salmon ZAP Express ovarian library Oncorhynchus kisutch cDNA, mRNA sequence.	EST_others	-	down	-	-3.6	4.94E-04	-27.4	-	-1.1
2258079	AF009794.1	Oncorhynchus gorbuscha microsatellite locus Ogo2, (ga)24	nt	-	down	-	down	3.90E-03	down	-	0.0
164422326	EU325858.1	Oncorhynchus masou formosanus complement factor H1 protein (CFH) mRNA, complete cds	nt	-	0.00	-	0.0	-	0.0	5.91E-02	-16.2
185133427	NM_001124346.1	Oncorhynchus mykiss apolipoprotein E (apoe), mRNA	Refseq_genes	-	1.5	-	-1.8	-	5.0	3.31E-05	up
225705221	BT074033.1	Oncorhynchus mykiss clone omyk-evo-501-128 Leucine-rich repeat-containing protein 42 putative mRNA, complete cds	nt	-	up	2.29E-02	up	-	1.2	-	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	-	0.0
225704491	BT073668.1	Oncorhynchus mykiss clone omyk-evo-509-076 Cytochrome c oxidase subunit VIIa-related protein, mitochondrial precursor putative mRNA, complete cds	nt	-	1.7	-	3.1	6.04E-02	8.1	-	4.6
225705745	BT074295.1	Oncorhynchus mykiss clone omyk-evo-514-224 Tetratricopeptide 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	-	down	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 (LOC100136303), mRNA	Refseq_genes	-	down	-	-8.3	-	-1.4	9.49E-03	-7.2
261245070	NM_001160506.1	Oncorhynchus mykiss fish virus induced TRIM protein (fintrim), mRNA	Refseq_genes	-	-1.3	-	-1.5	7.58E-02	-4.9	-	-1.2
185132277	NM_001124400.1	Oncorhynchus mykiss fucosyltransferase 9 (fut9), 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	-	down	-	-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	-	up	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	-30.9	-	-1.2

185135498	NM_001124308.1	Oncorhynchus mykiss interleukin 13 receptor alpha-2 (LOC100135968), mRNA	Refseq_genes	-	2.5	-	-1.7	9.34E-06	-119.0	-	0.0
34809457	AY386796.1	Oncorhynchus mykiss isolate BamACG-HpaACG tissue-specific MS-AFLP genomic fragment	nt	3.85E-03	down	-	-2.5	4.02E-02	-9.8	-	-4.3
185135324	NM_001124376.1	Oncorhynchus mykiss keratin 13 (k13), mRNA	Refseq_genes	-	1.4	-	6.9	6.99E-02	up	-	1.4
185135579	NM_001124309.1	Oncorhynchus mykiss LECT2 neutrophil chemotactic factor (lect2), mRNA	Refseq_genes	-	down	-	down	1.95E-02	-17.9	-	down
259089112	NM_001165121.1	Oncorhynchus mykiss lipopolysaccharide-induced TNF factor (litaf), mRNA	Refseq_genes	-	1.5	3.04E-04	down	-	2.3	-	-2.3
238231538	NM_001160480.1	Oncorhynchus mykiss mannan-binding lectin H2 (LOC100301642), mRNA	Refseq_genes	-	0.00	-	-2.7	2.82E-04	-13.2	-	down
33414970	AY278452.1	Oncorhynchus mykiss MHC class I antigen (Onmy-UBA) mRNA, Onmy-UBA-*4401 allele, complete cds	nt	2.78E-03	down	2.21E-04	-39.1	7.24E-05	down	1.87E-02	down
14389032	AF375014.1	Oncorhynchus mykiss microsatellite OMM1041 sequence	nt	-	3.4	-	up	1.42E-03	up	-	0.0
40794777	AY518339.1	Oncorhynchus mykiss microsatellite Omy1016UW sequence	nt	-	-3.0	-	-1.9	8.46E-02	-6.9	-	-1.1
387155688	FN824527.1	Oncorhynchus mykiss mRNA for cytokine receptor family member b5 precursor (crfb5 gene)	nt	8.69E-02	9.6	-	0.0	-	-1.6	-	3.7
11863729	AJ303076.1	Oncorhynchus mykiss partial mRNA for Lamin B2 protein	nt	7.42E-04	down	-	-1.7	8.79E-02	-6.0	2.94E-02	down
259089457	NM_001165057.1	Oncorhynchus mykiss SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae) (sumo2), mRNA	Refseq_genes	-	-2.3	-	1.8	1.28E-02	up	-	0.0
185134543	NM_001124290.1	Oncorhynchus mykiss stanniocalcin (LOC100135946), mRNA	Refseq_genes	-	0.00	-	0.0	4.31E-10	down	-	0.0
318065039	HM190266.1	Oncorhynchus mykiss transferrin receptor mRNA, partial cds	nt	-	2.7	4.41E-02	down	-	3.2	-	-1.1
194018416	NM_001129986.1	Oncorhynchus mykiss type II keratin E3 (e3), mRNA	Refseq_genes	-	down	6.22E-03	down	-	0.0	-	0.0
238231355	NM_001160640.1	Oncorhynchus mykiss Vacuolar ATP synthase 16 kDa proteolipid subunit (vatl), mRNA	Refseq_genes	-	down	-	0.0	6.99E-02	down	-	down
185134302	NM_001124285.1	Oncorhynchus mykiss VIG-2 protein (vig-2), mRNA	Refseq_genes	-	-1.6	-	-6.2	6.04E-02	-13.8	-	up
185134310	NM_001124274.1	Oncorhynchus mykiss vitelline envelope protein gamma (LOC100135907), mRNA	Refseq_genes	-	down	-	down	-	0.0	1.49E-09	49.1
259089103	NM_001165118.1	Oncorhynchus mykiss zinc finger, matrin type 2 (zmat2), mRNA	Refseq_genes	3.75E-02	down	-	-1.5	-	-2.1	-	down
185132233	NM_001124600.1	Oncorhynchus mykiss zona pellucida glycoprotein 2.3 (zp2.3), mRNA	Refseq_genes	-	0.00	-	0.0	-	0.0	4.15E-04	up
71381926	DQ025596.1	Oncorhynchus tshawytscha clone Ots.u211.76.64 genomic sequence	nt	-	down	-	down	5.70E-06	down	-	-3.1
24637708	AF527060.1	Oncorhynchus tshawytscha virus-inducible stress protein (VISP) mRNA, complete cds	nt	-	-1.3	-	-2.1	6.27E-02	-5.4	-	1.1
157311696	NM_001105103.1	Oryzias latipes Mhc class I A (orla-uaa), mRNA	Refseq_genes	8.93E-05	-72.6	2.66E-02	-30.7	1.68E-03	down	-	down

225708383	BT075614.1	Osmerus mordax clone omor-eva-506-307 Methyltransferase-like protein 7A precursor putative mRNA, complete cds	nt	-	1.3	-	1.3	-	2.2	1.00E-02	11.2
225706089	BT074467.1	Osmerus mordax clone omor-eva-508-066 Deoxyribonuclease-1 precursor putative mRNA, complete cds	nt	-	0.00	2.85E-02	down	-	0.0	-	0.0
ENSGACG00000004331	*pank4*	pantothenate kinase 4	Ensembl_stickleback	-	down	-	2.4	6.03E-03	-11.3	-	1.4
ENSGACG00000016727	*papd5*	PAP associated domain containing 5	Ensembl_stickleback	8.13E-02	8.9	-	1.1	-	1.2	-	5.6
ENSGACG00000007828	*pon1*	paraoxonase 1	Ensembl_stickleback	-	0.00	-	down	4.67E-03	down	-	19.0
ENSGACG00000007536	*ptms*	parathymosin	Ensembl_stickleback	-	2.2	-	2.5	5.27E-02	5.5	-	up
ENSDARG00000031777	*pparaa*	peroxisome proliferator-activated receptor alpha a	Ensembl_zebrafish	-	-1.6	-	1.3	8.53E-02	6.0	-	1.7
ENSGACG00000009302	*pes1*	pescadillo ribosomal biogenesis factor 1	Ensembl_stickleback	5.86E-02	-15.6	-	0.0	-	0.0	1.70E-04	down
ENSORLG00000006231	*pten*	phosphatase and tensin homolog	Ensembl_medaka	-	0.00	-	1.1	5.65E-02	down	-	0.0
ENSGACG00000011516	*ppap2c (1 of 2)*	phosphatidic acid phosphatase type 2C	Ensembl_stickleback	-	-1.0	-	down	5.65E-02	down	-	-1.6
ENSGACG00000015853	*pigb*	phosphatidylinositol glycan anchor biosynthesis, class B	Ensembl_stickleback	2.00E-02	down	-	0.0	-	0.0	-	down
ENSGACG00000005401	*ptdss1 (2 of 2)*	phosphatidylserine synthase 1	Ensembl_stickleback	2.19E-04	-64.1	-	0.0	-	up	-	up
ENSGACG00000002045	*pde6d*	phosphodiesterase 6D, cGMP-specific, rod, delta	Ensembl_stickleback	-	down	-	0.0	1.70E-04	down	-	down
ENSDARG00000060280	*pde9a (1 of 2)*	phosphodiesterase 9A	Ensembl_zebrafish	-	-2.1	-	-2.8	-	2.8	2.31E-02	down
ENSDARG00000013522	*pck1*	phosphoenolpyruvate carboxykinase 1 (soluble)	Ensembl_zebrafish	-	0.00	-	up	-	3.7	4.39E-03	-11.1
ENSDARG00000009153	*pla2g1b*	phospholipase A2, group IB (pancreas)	Ensembl_zebrafish	-	-1.7	6.16E-05	-19.8	-	-1.0	-	2.2
ENSGACG00000012490	*plcb1 (1 of 2)*	phospholipase C, beta 1 (phosphoinositide-specific)	Ensembl_stickleback	-	1.2	-	1.3	3.68E-02	12.5	-	-1.1
ENSDARG00000037506	*prps1b*	phosphoribosyl pyrophosphate synthetase 1B	Ensembl_zebrafish	-	1.8	9.89E-05	up	-	1.7	-	1.0
ENSGACG00000019001	*pim3*	pim-3 oncogene	Ensembl_stickleback	-	1.1	-	1.0	7.50E-02	5.4	-	up
ENSGACG00000010777	*pls1*	plastin 1	Ensembl_stickleback	-	down	1.08E-03	-9.7	-	0.0	-	1.4
ENSGACG00000016743	*psd4*	pleckstrin and Sec7 domain containing 4	Ensembl_stickleback	5.74E-06	down	-	0.0	3.65E-02	down	6.61E-08	down
ENSGACG00000005254	*plekhm2*	pleckstrin homology domain containing, family M (with RUN domain) member 2	Ensembl_stickleback	-	-7.2	-	1.0	8.87E-02	-7.4	-	-1.5
ENSGACG00000007218	*plk2*	polo-like kinase 2	Ensembl_stickleback	3.04E-05	19.9	-	1.9	-	-1.6	-	-1.9
ENSDARG00000017219	*pabpc1a*	poly A binding protein, cytoplasmic 1 a	Ensembl_zebrafish	1.61E-02	-8.0	1.19E-06	-32.8	2.23E-07	-40.1	2.49E-05	-20.5
ENSGACG00000019366	*polr2a*	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	Ensembl_stickleback	-	-1.0	-	-1.4	1.81E-03	-22.3	-	1.0
ENSG00000129159	*kcnc1*	potassium voltage-gated channel, Shaw-related subfamily, member 1	Ensembl_human	-	down	-	1.0	-	-4.1	5.46E-03	-41.3
ENSGACG00000004944	*pqlc2*	PQ loop repeat containing 2	Ensembl_stickleback	-	-3.3	-	-3.1	4.57E-02	-6.7	-	-1.7

327274185	XM_003221811.1	PREDICTED: Anolis carolinensis synaptopodin-2-like (LOC100567593), mRNA	Refseq_genes	-	down	7.30E-02	-7.0	-	0.0	-	2.8
326678863	XP_001922687.3	PREDICTED: antihemorragic factor cHLP-B	Refseq_proteins	-	1.1	5.49E-02	-15.5	-	-2.7	-	-2.3
410923967	XP_003975453.1	PREDICTED: apolipoprotein D-like	Refseq_proteins	-	0.00	1.43E-06	-39.9	-	0.0	1.35E-02	10.4
410900828	XP_003963898.1	PREDICTED: cadherin-5-like	Refseq_proteins	-	-1.0	-	-1.9	7.67E-02	12.2	-	-1.8
432943847	XP_004083297.1	PREDICTED: cathepsin E-A-like	Refseq_proteins	-	up	-	up	-	-1.4	1.01E-20	up
432882457	XP_004074040.1	PREDICTED: cell division cycle-associated 7-like protein-like	Refseq_proteins	-	down	-	1.1	1.59E-02	down	-	0.0
326671170	XP_003199376.1	PREDICTED: complement C1q-like protein 2-like	Refseq_proteins	-	0.00	-	0.0	-	0.0	3.38E-15	down
348501087	XP_003438102.1	PREDICTED: complement factor H-like	Refseq_proteins	-	0.00	-	0.0	-	0.0	8.65E-13	down
348517015	XP_003446031.1	PREDICTED: C-type lectin domain family 10 member A-like	Refseq_proteins	-	0.00	-	0.0	-	0.0	8.24E-02	-7.4
326669577	XP_001923321.2	PREDICTED: cytochrome P450 2F2-like	Refseq_proteins	-	0.00	5.59E-02	down	-	0.0	4.84E-11	down
348538469	XP_003456713.1	PREDICTED: cytolysin Src-1-like	Refseq_proteins	7.32E-02	down	-	0.0	-	down	-	0.0
326667554	XP_002667068.2	PREDICTED: cytosolic phospholipase A2 gamma	Refseq_proteins	2.78E-03	15.2	-	0.0	-	-1.0	-	down
410932293	XP_003979528.1	PREDICTED: dimethylaniline monooxygenase	Refseq_proteins	-	0.00	2.45E-03	up	-	1.8	-	-1.5
348521084	XP_003448056.1	PREDICTED: E3 ubiquitin/ISG15 ligase TRIM25-like	Refseq_proteins	-	-1.1	-	6.3	4.49E-02	up	-	down
410910654	XP_003968805.1	PREDICTED: endonuclease domain-containing 1 protein-like	Refseq_proteins	-	2.4	8.77E-02	-14.4	-	0.0	-	0.0
348525982	XP_003450500.1	PREDICTED: endonuclease domain-containing 1 protein-like	Refseq_proteins	1.36E-02	8.8	5.59E-02	up	-	up	-	0.0
338718465	XM_001498233.3	PREDICTED: Equus caballus meprin A, alpha (PABA peptide hydrolase) (MEP1A), mRNA	nt	-	0.00	1.60E-12	-243.0	-	0.0	-	up
327269633	XP_003219598.1	PREDICTED: fatty acid-binding protein, adipocyte-like	Refseq_proteins	2.08E-03	up	-	0.0	-	0.0	-	0.0
363738171	XP_001231970.2	PREDICTED: fatty acyl-CoA hydrolase precursor, medium chain isoform 1	Refseq_proteins	-	-1.7	-	-9.3	-	2.2	3.74E-02	down
348525178	XP_003450099.1	PREDICTED: GTPase SLIP-GC-like, partial	Refseq_proteins	-	-1.1	-	-1.0	1.96E-04	down	-	0.0
348539876	XP_003457415.1	PREDICTED: heat shock 70 kDa protein 12A-like	Refseq_proteins	3.56E-06	down	-	0.0	-	0.0	-	0.0
125807411	XP_001343562.1	PREDICTED: hypothetical protein LOC100004199	Refseq_proteins	-	2.5	2.02E-04	-13.5	9.69E-02	5.6	-	down
189517525	XP_001923568.1	PREDICTED: hypothetical protein LOC100149918	Refseq_proteins	-	down	-	down	-	0.0	5.60E-04	11.4
327281562	XP_003225516.1	PREDICTED: hypothetical protein LOC100561123	Refseq_proteins	-	0.00	-	0.0	6.99E-02	down	-	up
348526073	XP_003450545.1	PREDICTED: hypothetical protein LOC100690208	Refseq_proteins	3.46E-03	-13.1	6.88E-05	down	5.66E-03	down	-	up
348526794	XP_003450904.1	PREDICTED: hypothetical protein LOC100696199	Refseq_proteins	-	0.00	-	1.3	-	0.0	2.07E-04	-19.6
348513025	XP_003444043.1	PREDICTED: hypothetical protein LOC100707007	Refseq_proteins	3.15E-02	down	-	0.0	3.65E-02	up	-	up
348539792	XP_003457373.1	PREDICTED: hypothetical protein LOC100709472	Refseq_proteins	1.65E-03	-47.6	1.27E-03	-49.6	-	0.0	-	0.0

348545569	XP_003460252.1	PREDICTED: hypothetical protein LOC100709671	Refseq_proteins	-	down	-	down	4.49E-02	down	-	down
348529410	XP_003452206.1	PREDICTED: hypothetical protein LOC100710425	Refseq_proteins	-	0.00	-	down	-	0.0	4.20E-02	-6.5
68444937	XP_706427.1	PREDICTED: hypothetical protein LOC567961	Refseq_proteins	-	4.4	2.87E-03	up	-	up	-	0.0
125811426	XP_001335256.1	PREDICTED: hypothetical protein LOC795145	Refseq_proteins	2.19E-08	75.4	8.58E-10	-166.1	-	down	-	down
410906097	XP_003966528.1	PREDICTED: insulin receptor substrate 2-like	Refseq_proteins	-	-2.5	-	down	-	-2.8	2.94E-02	down
326674126	XP_003200076.1	PREDICTED: integrin alpha-E-like	Refseq_proteins	-	-1.8	-	1.2	-	-1.5	6.95E-03	down
326665123	XP_691524.5	PREDICTED: interferon-induced guanylate-binding protein 1	Refseq_proteins	-	-1.1	-	1.5	7.71E-05	-88.2	-	up
189514417	XP_001345882.2	PREDICTED: interferon-induced protein 44	Refseq_proteins	-	-7.9	3.54E-02	9.3	-	1.9	-	-7.0
326670954	XP_001336175.4	PREDICTED: interferon-induced protein 44	Refseq_proteins	-	-4.0	2.12E-06	52.4	-	-3.2	-	2.9
432873596	XP_004072295.1	PREDICTED: kallikrein-2-like	Refseq_proteins	1.51E-06	28.5	-	3.6	-	down	-	0.0
348532506	XP_003453747.1	PREDICTED: leucine-rich repeats and immunoglobulin-like domains protein 2	Refseq_proteins	-	down	7.27E-02	down	3.59E-04	down	-	2.3
348507107	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	down
348500648	XM_003437837.1	PREDICTED: Oreochromis niloticus hypothetical protein LOC100692229 (LOC100692229), mRNA	Refseq_genes	-	down	-	0.0	3.02E-02	down	-	up
348523192	XM_003449060.1	PREDICTED: Oreochromis niloticus hypothetical protein LOC100703724 (LOC100703724), mRNA	Refseq_genes	1.36E-02	down	-	-2.0	-	-2.6	-	0.0
348544302	XM_003459573.1	PREDICTED: Oreochromis niloticus hypothetical protein LOC100710022 (LOC100710022), mRNA	Refseq_genes	3.15E-02	down	9.39E-03	down	1.97E-05	down	-	down
348526849	XM_003450884.1	PREDICTED: Oreochromis niloticus protein S100-A11-like (LOC100703730), mRNA	Refseq_genes	-	0.00	-	down	4.86E-03	7.8	-	0.0
348524437	XM_003449682.1	PREDICTED: Oreochromis niloticus transmembrane protein 192-like (LOC100691376), mRNA	Refseq_genes	3.15E-02	up	-	up	4.67E-03	up	-	down
348517992	XP_003446516.1	PREDICTED: protachykinin-like	Refseq_proteins	-	0.00	3.74E-03	-13.5	-	-1.8	-	1.3
348523519	XP_003449271.1	PREDICTED: protection of telomeres protein 1-like	Refseq_proteins	-	-2.4	-	up	-	0.0	9.95E-02	up
348538993	XP_003456974.1	PREDICTED: protein GPR108-like	Refseq_proteins	7.32E-02	down	-	-4.3	-	0.0	-	down
432873602	XP_004072298.1	PREDICTED: putative defense protein 3-like	Refseq_proteins	-	0.00	-	down	-	down	1.21E-02	13.4
301624357	XP_002941477.1	PREDICTED: retinal homeobox protein Rx-like	Refseq_proteins	-	0.00	7.90E-02	-11.7	-	0.0	-	0.0
348516493	XP_003445773.1	PREDICTED: RNA-binding protein 26-like	Refseq_proteins	-	3.2	-	1.0	8.79E-02	down	-	3.7
326663987	XP_003197704.1	PREDICTED: synaptopodin-2	Refseq_proteins	-	0.00	7.34E-02	-6.8	-	0.0	-	down
348506200	XP_003440648.1	PREDICTED: synemin-like	Refseq_proteins	-	4.8	4.41E-02	down	-	2.2	-	up
410924755	XM_003975798.1	PREDICTED: Takifugu rubripes alpha-2-HS-glycoprotein-like (LOC101076681), mRNA	Refseq_genes	-	0.00	-	0.0	-	up	2.29E-18	down

410923730	XM_003975286.1	PREDICTED: Takifugu rubripes glycosylphosphatidylinositol anchor attachment 1 protein-like (LOC101070382), mRNA	Refseq_genes	1.61E-02	down	-	-1.2	-	-3.5	-	-1.1
410919522	XM_003973185.1	PREDICTED: Takifugu rubripes poly(U)-specific endoribonuclease-like (LOC101064652), mRNA	Refseq_genes	-	0.00	5.95E-04	-34.0	-	0.0	-	down
410922242	XM_003974543.1	PREDICTED: Takifugu rubripes UDP-glucuronosyltransferase 2A2-like (LOC101068092), mRNA	Refseq_genes	-	1.2	9.79E-02	-6.9	-	0.0	8.31E-04	down
410926977	XP_003976944.1	PREDICTED: trypsinogen-like protein 3-like, partial	Refseq_proteins	-	up	3.12E-04	-20.6	-	0.0	-	-2.7
348508195	XP_003441640.1	PREDICTED: tsukushin-like	Refseq_proteins	1.36E-02	down	-	1.0	-	1.3	-	-1.5
432926066	XP_004080813.1	PREDICTED: UDP-glucuronosyltransferase 2B31-like	Refseq_proteins	-	0.00	-	down	9.62E-02	8.5	-	1.3
410905289	XP_003966124.1	PREDICTED: urokinase plasminogen activator surface receptor-like	Refseq_proteins	-	-3.3	-	-1.8	4.63E-10	-110.8	-	down
410929355	XP_003978065.1	PREDICTED: WAS/WASL-interacting protein family member 2-like	Refseq_proteins	-	-3.4	2.85E-02	down	-	0.0	-	4.7
ENSDARG00000035350	*ins*	preproinsulin	Ensembl_zebrafish	-	0.00	3.65E-03	-17.3	-	0.0	-	0.0
ENSGACG00000009139	*pfn2 (1 of 2)*	profilin 2	Ensembl_stickleback	-	down	3.51E-04	down	4.49E-02	down	-	down
ENSONIG00000007715	*prlr (1 of 2)*	prolactin receptor	Ensembl_nile_tilapia	-	-1.5	-	-2.1	3.23E-02	8.9	-	0.0
ENSONIG00000009922	*psapl1*	prosaposin-like 1 (gene/pseudogene)	Ensembl_nile_tilapia	-	down	2.07E-03	down	8.21E-08	down	3.74E-02	down
ENSDARG00000017213	*prss35*	protease, serine, 35	Ensembl_zebrafish	-	1.0	-	1.9	7.05E-02	6.5	-	2.7
ENSGACG00000000107	*psmb9 (5 of 5)*	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	Ensembl_stickleback	6.83E-05	up	2.61E-02	9.5	1.04E-02	up	-	0.0
ENSGACG00000019857	*pacsin2*	protein kinase C and casein kinase substrate in neurons 2	Ensembl_stickleback	-	-1.4	-	-1.3	3.02E-02	-8.3	-	9.6
ENSORLG00000015712	*prkch*	protein kinase C, eta	Ensembl_medaka	-	1.7	-	-2.7	2.77E-03	down	-	2.2
ENSDARG00000079585	*pkn3*	protein kinase N3	Ensembl_zebrafish	-	-2.3	-	3.7	2.99E-03	-50.1	-	up
ENSDARG00000089608	*ppp1cbl*	protein phosphatase 1, catalytic subunit, beta isoform, like	Ensembl_zebrafish	-	1.9	-	3.2	1.03E-04	down	-	up
ENSGACG00000005491	*ppp1r21*	protein phosphatase 1, regulatory subunit 21	Ensembl_stickleback	-	1.7	-	1.1	1.08E-03	-29.9	-	up
ENSGACG00000007843	*ptprc*	protein tyrosine phosphatase, receptor type, C	Ensembl_stickleback	-	-1.9	-	-3.2	6.99E-02	-5.8	-	-1.8
ENSGACG00000012481	*ralgapa1*	Ral GTPase activating protein, alpha subunit 1 (catalytic)	Ensembl_stickleback	-	-6.2	-	-2.7	5.07E-02	-29.1	-	-4.1
ENSDARG00000005989	*rgl1*	ral guanine nucleotide dissociation stimulator-like 1	Ensembl_zebrafish	-	-1.5	-	1.7	3.40E-02	12.6	-	2.8
223646095	NP_001138713.1	rapunzel2	Refseq_proteins	-	0.00	5.59E-02	up	-	0.0	-	0.0
ENSGACG00000002543	*rqcd1*	RCD1 required for cell differentiation1 homolog (S. pombe)	Ensembl_stickleback	-	-11.6	9.39E-03	down	1.73E-05	-44.1	-	0.0
ENSDARG00000021869	*rcan2*	regulator of calcineurin 2	Ensembl_zebrafish	-	-1.7	-	-1.3	-	-1.7	8.21E-02	6.1

ENSDARG00000090039	*reck*	reversion-inducing- cysteine-rich protein with kazal motifs	Ensembl_zebrafish	-	-1.4	-	1.3	6.99E-02	up	-	-1.1
ENSGACG00000013298	*arhgdia (1 of 2)*	Rho GDP dissociation inhibitor (GDI) alpha	Ensembl_stickleback	3.85E-03	down	-	83.1	-	1.0	-	up
ENSGACG00000019358	*arhgef15*	Rho guanine nucleotide exchange factor (GEF) 15	Ensembl_stickleback	3.85E-03	down	-	1.2	-	-2.3	-	up
222137251	FJ002822.1	Rhyacophila balcanica voucher RbalL1 16S ribosomal RNA gene, partial sequence; mitochondrial	nt	-	0.00	1.52E-06	123.1	-	0.0	-	0.0
ENSONIG00000002839	*rpp21*	ribonuclease P/MRP 21kDa subunit	Ensembl_nile_tilapia	-	-1.3	-	-1.2	-	1.2	2.30E-02	7.4
ENSGACG00000012811	*rps6ka3*	ribosomal protein S6 kinase, 90kDa, polypeptide 3	Ensembl_stickleback	9.69E-02	5.6	-	2.2	-	1.1	2.74E-06	52.0
ENSORLG00000011879	*rrbp1*	ribosome binding protein 1 homolog 180kDa (dog)	Ensembl_medaka	-	-1.1	-	1.1	-	1.2	8.95E-02	5.5
ENSONIG00000010011	*rrbp1*	ribosome binding protein 1 homolog 180kDa (dog)	Ensembl_nile_tilapia	-	0.00	-	1.2	-	-1.6	1.00E-02	up
ENSMUSG00000026955	2010317E24Rik	RIKEN cDNA 2010317E24 gene	Ensembl_mouse	-	0.00	4.56E-06	down	-	0.0	-	0.0
ENSGACG00000016138	*rnf165 (1 of 2)*	ring finger protein 165	Ensembl_stickleback	-	0.00	4.41E-02	down	9.33E-05	down	-	down
ENSGACG00000005671	*rbms1 (1 of 2)*	RNA binding motif, single stranded interacting protein 1	Ensembl_stickleback	-	down	-	down	3.02E-02	down	-	up
ENSDARG00000045930	*rbpms2 (1 of 2)*	RNA binding protein with multiple splicing 2	Ensembl_zebrafish	-	1.0	7.78E-02	-6.1	-	1.8	-	up
ENSONIG00000008341	*rbfox2 (1 of 2)*	RNA binding protein, fox-1 homolog (C. elegans) 2	Ensembl_nile_tilapia	-	down	-	up	-	down	1.87E-02	up
ENSGACG00000020220	*ruvbl2*	RuvB-like 2 (E. coli)	Ensembl_stickleback	-	0.00	5.75E-05	-15.9	-	0.0	-	0.0
213513492	NM_001140687.1	Salmo salar 40S ribosomal protein S15a (rs15a), mRNA	Refseq_genes	-	1.3	5.59E-02	up	-	1.8	-	down
213513418	NM_001139890.1	Salmo salar 60 kDa lysophospholipase (lpp60), mRNA	Refseq_genes	-	-2.5	-	down	4.41E-02	-9.6	-	-1.6
259155117	NM_001165329.1	Salmo salar adenosine monophosphate deaminase 3 (ampd3), mRNA	Refseq_genes	-	1.1	-	-5.2	8.79E-02	-5.3	-	2.2
291190403	NM_001173641.1	Salmo salar Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A (mgt4a), mRNA	Refseq_genes	-	2.6	-	1.9	8.78E-02	-25.6	-	0.0
213513162	NM_001141362.1	Salmo salar Apolipoprotein C-I (apoc1), mRNA	Refseq_genes	-	-1.0	5.68E-03	-7.8	-	3.6	-	-1.7
291190593	NM_001173915.1	Salmo salar aquaporin 8 (aqp8), mRNA	Refseq_genes	-	0.00	-	1.9	6.99E-02	up	-	0.0
259155215	NM_001165377.1	Salmo salar Beta-adducin (addb), mRNA	Refseq_genes	-	-1.9	-	-2.1	6.99E-02	-6.9	-	1.9
213511949	NM_001140737.1	Salmo salar Bridging integrator 2 (bin2), mRNA	Refseq_genes	-	0.00	-	1.6	2.18E-02	7.2	-	up
185134143	NM_001123580.1	Salmo salar C type lectin receptor B (LOC100136447), mRNA	Refseq_genes	-	down	-	up	-	0.0	9.06E-15	down
213512283	NM_001140113.1	Salmo salar Cadherin-17 (cad17), mRNA	Refseq_genes	-	0.00	1.19E-08	down	3.24E-07	down	-	0.0
213514195	NM_001140522.1	Salmo salar Cathepsin B (catb), mRNA	Refseq_genes	-	0.00	-	0.0	3.02E-02	down	-	0.0

213514355	NM_001140779.1	Salmo salar Cathepsin M (catm), mRNA	Refseq_genes	-	-2.5	-	1.5	1.34E-03	10.6	-	-1.0
226443385	NM_001146421.1	Salmo salar CK046 protein (ck046), mRNA	Refseq_genes	-	down	-	down	6.99E-02	down	-	down
291190368	NM_001173776.1	Salmo salar Clarin-3 (clrn3), mRNA	Refseq_genes	-	0.00	9.39E-03	down	-	0.0	-	0.0
10505157	AF273013.1	Salmo salar clone 01-04L immunoglobulin light chain precursor (IgL) mRNA, complete cds	nt	-	1.1	-	down	1.79E-02	-6.9	-	up
221221511	BT057545.1	Salmo salar clone ssal-evd-529-189 Zymogen granule membrane protein 16 precursor putative mRNA, complete cds	nt	3.43E-12	down	-	0.0	-	0.0	-	0.0
209737133	BT049635.1	Salmo salar clone ssal-eve-504-024 39S ribosomal protein L41, mitochondrial precursor putative mRNA, complete cds	nt	-	-1.1	9.01E-02	down	-	-4.1	-	-1.5
209733395	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
221220955	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
209733843	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
221220457	BT057018.1	Salmo salar clone ssal-eve-547-356 Non-histone chromosomal protein H6 putative mRNA, complete cds	nt	-	0.00	-	down	1.13E-09	down	-	down
209738407	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
221219843	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
221219477	BT056528.1	Salmo salar clone ssal-eve-579-363 PRA1 family protein 3 putative mRNA, complete cds	nt	-	0.00	2.87E-03	down	4.67E-03	down	-	down
209737953	BT050045.1	Salmo salar clone ssal-evf-502-345 Glyceraldehyde-3-phosphate dehydrogenase putative mRNA, complete cds	nt	-	down	6.22E-03	down	-	down	2.26E-03	down
221220267	BT056923.1	Salmo salar clone ssal-evf-504-128 SRA stem-loop-interacting RNA-binding protein, mitochondrial precursor putative mRNA, complete cds	nt	3.75E-02	up	-	up	-	up	-	0.0
221221335	BT057457.1	Salmo salar clone ssal-evf-522-007 Vitamin D3 hydroxylase-associated protein putative mRNA, complete cds	nt	-	-2.0	-	1.9	1.62E-03	-14.2	-	0.0
209731161	BT046649.1	Salmo salar clone ssal-evf-527-292 Mitochondrial 28S ribosomal protein S36 putative mRNA, complete cds	nt	-	1.9	9.01E-02	down	-	-1.8	-	3.1
221221243	BT057411.1	Salmo salar clone ssal-evf-550-301 Eukaryotic translation initiation factor 3 subunit C putative mRNA, complete cds	nt	-	down	-	down	1.18E-04	down	-	down

221220085	BT056832.1	Salmo salar clone ssal-evf-554-043 Butyrophilin subfamily 1 member A1 precursor putative mRNA, complete cds	nt	-	-2.8	-	-4.4	8.30E-03	-21.0	-	-1.3
303663498	BT125368.1	Salmo salar clone ssal-evf-563-255 C8orf40 homolog putative mRNA, complete cds	nt	-	down	-	-4.9	6.99E-02	down	-	0.0
209734397	BT048267.1	Salmo salar clone ssal-plnb-004-066 Gastrotropin putative mRNA, complete cds	nt	-	down	3.07E-10	-273.9	-	up	-	up
221220663	BT057121.1	Salmo salar clone ssal-plnb-027-103 Lectin precursor putative mRNA, complete cds	nt	-	0.00	-	-1.2	-	4.1	1.18E-02	-10.4
304376917	BT050094.2	Salmo salar clone ssal-plnb-506-126 Lipocalin precursor putative mRNA, complete cds	nt	-	-1.4	2.87E-03	down	5.66E-03	down	-	-3.2
209730649	BT046393.1	Salmo salar clone ssal-rgb2-549-178 Testosterone 17-beta-dehydrogenase 3 putative mRNA, complete cds	nt	-	0.00	-	2.0	-	5.2	1.07E-02	-8.3
209738155	BT050146.1	Salmo salar clone ssal-rgb2-565-065 Endonuclease domain-containing 1 protein precursor putative mRNA, complete cds	nt	8.88E-02	27.2	-	0.0	-	0.0	-	0.0
209735875	BT049006.1	Salmo salar clone ssal-rgb2-617-026 Nattectin precursor putative mRNA, complete cds	nt	-	0.00	9.10E-07	-49.4	-	0.0	-	0.0
209730271	BT046204.1	Salmo salar clone ssal-rgb2-641-117 Tetraspanin-8 putative mRNA, complete cds	nt	3.14E-04	up	-	0.0	-	-5.4	5.91E-02	up
224587002	BT071859.1	Salmo salar clone ssal-rgf-002-348 Collagen alpha-3VI chain precursor putative mRNA, pseudogene cds	nt	8.00E-03	down	-	-1.5	8.30E-03	-22.0	-	up
209148888	BT044698.1	Salmo salar clone ssal-rgf-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	BT071893.1	Salmo salar clone ssal-rgf-502-231 unknown large open reading frame mRNA, novel cds	nt	-	-1.1	-	-1.7	4.44E-02	-5.7	-	-1.3
224587090	BT071953.1	Salmo salar clone ssal-rgf-504-369, novel cds	nt	-	down	-	down	6.38E-08	down	-	0.0
223647599	BT058845.1	Salmo salar clone ssal-rgf-507-102 Actin-related protein 2-A putative mRNA, complete cds	nt	3.75E-02	down	-	up	-	-2.9	-	0.0
209154129	BT045035.1	Salmo salar clone ssal-rgf-510-148 Ubiquitin-conjugating enzyme E2 D2 putative mRNA, complete cds	nt	-	down	-	-5.4	3.65E-02	down	-	down
223647861	BT058976.1	Salmo salar clone ssal-rgf-517-215 Stromal cell-derived factor 1 precursor putative mRNA, complete cds	nt	-	-1.9	-	down	8.02E-14	-312.0	-	4.7
223647865	BT058978.1	Salmo salar clone ssal-rgf-517-265 Actin-related protein 2-A putative mRNA, complete cds	nt	-	-1.3	-	-1.3	3.02E-02	-11.7	-	down
224587384	BT072238.1	Salmo salar clone ssal-rgf-517-384 unknown large open reading frame mRNA, novel cds	nt	-	-1.6	6.21E-08	-121.6	9.52E-03	-8.0	-	-5.4
224587388	BT072243.1	Salmo salar clone ssal-rgf-518-093 Proto-oncogene vav putative mRNA, pseudogene cds	nt	-	0.00	-	0.0	1.91E-06	down	-	-1.2
224587400	BT072256.1	Salmo salar clone ssal-rgf-518-306 Myosin-9 putative mRNA, pseudogene cds	nt	-	down	-	down	8.79E-02	down	-	0.0

224587424	BT072278.1	Salmo salar clone ssal-rgf-519-255 Ubiquitin-conjugating enzyme E2 L3 putative mRNA, partial cds	nt	-	1.2	-	3.7	8.09E-06	up	8.31E-04	up
209154931	BT045436.1	Salmo salar clone ssal-rgf-521-193 B-cell receptor-associated protein 31 putative mRNA, complete cds	nt	-	0.00	1.19E-02	down	-	0.0	-	up
224587488	BT072334.1	Salmo salar clone ssal-rgf-521-227 unknown large open reading frame mRNA, novel cds	nt	7.32E-02	up	-	-6.3	-	1.4	-	1.1
223649215	BT059653.1	Salmo salar clone ssal-rgf-521-267 Tripartite motif-containing protein 25 putative mRNA, complete cds	nt	-	-2.0	-	-2.2	4.73E-02	-7.3	-	-5.9
224587510	BT072359.1	Salmo salar clone ssal-rgf-522-242 Biotin--protein ligase putative mRNA, pseudogene cds	nt	3.75E-02	up	-	-1.8	-	-1.7	-	0.0
209155099	BT045520.1	Salmo salar clone ssal-rgf-523-374 max putative mRNA, complete cds	nt	-	0.00	-	down	2.77E-03	down	-	0.0
209155209	BT045575.1	Salmo salar clone ssal-rgf-525-166 Histone chaperone asf1-B putative mRNA, complete cds	nt	-	4.1	-	3.7	3.02E-02	down	-	-1.8
224613399	BT072448.1	Salmo salar clone ssal-rgf-525-359 Transketolase-like protein 2 putative mRNA, partial cds	nt	-	1.1	-	1.1	5.65E-02	-5.1	-	1.1
224613403	BT072459.1	Salmo salar clone ssal-rgf-526-138 Fructose-1,6-bisphosphatase 1 putative mRNA, partial cds	nt	-	down	-	down	9.71E-10	down	-	down
224587622	BT072484.1	Salmo salar clone ssal-rgf-527-126 unknown large open reading frame mRNA, novel cds	nt	-	down	-	down	3.24E-03	down	-	down
224587648	BT072508.1	Salmo salar clone ssal-rgf-528-100 Poly polymerase 14 putative mRNA, pseudogene cds	nt	1.58E-03	-29.2	-	-5.3	4.41E-02	-7.8	-	-2.2
223649117	BT059604.1	Salmo salar clone ssal-rgf-532-019 Actin, cytoplasmic 1 putative mRNA, complete cds	nt	-	-2.5	-	-19.7	7.77E-04	-31.8	-	down
223648461	BT059276.1	Salmo salar clone ssal-rgf-538-059 F-box/LRR-repeat protein 5 putative mRNA, complete cds	nt	-	0.00	-	down	7.67E-02	-14.6	-	down
209156037	BT045989.1	Salmo salar clone ssal-rgf-538-237 Serine/threonine-protein kinase MST4 putative mRNA, complete cds	nt	-	0.00	-	0.0	4.16E-06	down	-	down
224587895	BT072767.1	Salmo salar clone ssal-rgf-539-307 Ras GTPase-activating-like protein IQGAP1 putative mRNA, partial cds	nt	-	1.4	-	-2.0	5.91E-03	-9.9	-	0.0
224587922	BT072796.1	Salmo salar clone ssal-rgf-541-083 unknown large open reading frame mRNA, novel cds	nt	-	-1.2	-	1.4	8.79E-02	up	-	0.0
223672306	BT059975.1	Salmo salar clone ssal-rgg-514-084 Ig kappa chain V-IV region B17 precursor putative mRNA, complete cds	nt	-	down	-	up	8.79E-02	-5.4	-	0.0
223672718	BT060181.1	Salmo salar clone ssal-rgh-507-311 Ig kappa chain V region K29-213 putative mRNA, complete cds	nt	-	down	-	down	1.50E-04	down	-	-1.1
291190370	NM_001173637.1	Salmo salar Clusterin (clus), mRNA	Refseq_genes	-	down	-	down	4.05E-05	down	-	down
213513351	NM_001141001.1	Salmo salar COMM domain-containing protein 9 (comd9), mRNA	Refseq_genes	-	down	-	down	1.07E-03	down	-	down

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	-	-8.7
226442587	NM_001146430.1	Salmo salar Complement component C8 gamma chain (co8g), mRNA	Refseq_genes	-	-1.1	-	2.5	4.44E-02	8.0	-	-1.4
226443114	NM_001146569.1	Salmo salar CU070 protein (cu070), mRNA	Refseq_genes	-	3.4	-	-1.7	6.04E-02	-18.4	-	-1.2
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	131.5
213512966	NM_001139774.1	Salmo salar Epidermis-type lipoxygenase 3 (loxe3), mRNA	Refseq_genes	1.24E-02	8.6	-	-1.4	-	up	-	0.0
194396635	EU643669.1	Salmo salar haplotype Hap_2 NADH dehydrogenase subunit 5 (NADH-5) gene, partial cds; mitochondrial	nt	-	down	9.01E-02	down	3.65E-02	down	7.28E-04	-56.2
213512932	NM_001140849.1	Salmo salar Hepcidin-1 (hepc1), mRNA	Refseq_genes	-	down	-	-2.0	-	-14.6	6.72E-02	-5.2
158702273	EU025707.1	Salmo salar homeobox protein HoxB13ab (HoxB13ab), homeobox protein HoxB10ab (HoxB10ab), homeobox protein HoxB9ab (HoxB9ab), homeobox protien HoxB8ab (HoxB8ab), homeobox protien HoxB7ab (HoxB7ab), homeobox protien HoxB6ab (HoxB6ab), homeobox protien H ...	nt	-	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 interferon 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 CD53 (cd53), mRNA	Refseq_genes	-	up	-	-2.3	8.30E-03	down	-	0.0
218931109	NM_001140986.1	Salmo salar Mannose-specific lectin (asal), mRNA	Refseq_genes	2.16E-05	29.6	-	-2.7	-	down	-	down
213512998	NM_001140457.1	Salmo salar matrix metalloproteinase 9 (mmp9), mRNA	Refseq_genes	-	1.2	-	down	4.41E-02	-12.4	-	-2.2
185132565	NM_001123669.1	Salmo salar metallothionein B (LOC100136581), mRNA	Refseq_genes	9.37E-03	8.2	6.22E-03	7.7	-	2.7	4.46E-02	5.6
25573079	AF504023.1	Salmo salar MHC class I (UBA) mRNA, UBA*0201 allele, partial cds	nt	2.19E-08	down	7.25E-07	-142.8	7.44E-06	down	-	down
363548533	JN897012.1	Salmo salar MHC class I antigen (UBA) mRNA, UBA*4001 allele, complete cds	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	2.60E-08	-57.1
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 myotrophin (mtpn), mRNA	Refseq_genes	-	-1.9	-	down	7.89E-04	down	-	down
259155169	NM_001165355.1	Salmo salar nuclear receptor coactivator 4	Refseq_genes	-	-1.2	-	1.2	-	1.2	3.97E-02	7.0

		(ncoa4), mRNA									
226443008	NM_001146539.1	Salmo salar Nucleoplasmin-like protein NO29 (no29), mRNA	Refseq_genes	-	0.00	-	down	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	-	0.0	-	0.0	4.61E-02	-8.4
329130737	HM133622.1	Salmo salar olfactory receptor family C subfamily 4 member 11 gene, complete cds	nt	-	-7.6	-	-3.4	6.47E-04	-16.4	-	-5.8
213514523	NM_001140090.1	Salmo salar PDZ domain-containing protein 1 (pdzd1), mRNA	Refseq_genes	-	0.00	7.73E-07	down	2.75E-04	down	-	0.0
304555577	NM_001195198.1	Salmo salar Phospholemman (plm), mRNA	Refseq_genes	-	down	6.16E-05	down	6.99E-02	down	-	down
213513391	NM_001140288.1	Salmo salar Polypyrimidine tract-binding protein 1 (ptbp1), mRNA	Refseq_genes	-	-4.3	3.54E-02	down	8.25E-07	down	-	down
226443419	NM_001146429.1	Salmo salar Proheparin-binding EGF-like growth factor (hbegf), mRNA	Refseq_genes	-	down	-	up	1.96E-02	down	-	0.0
213513082	NM_001141336.1	Salmo salar Pyrroline-5-carboxylate reductase 2 (p5cr2), mRNA	Refseq_genes	-	1.4	-	3.0	-	-1.6	1.31E-03	13.0
226443273	NM_001146626.1	Salmo salar Ran-binding protein 10 (rbp10), mRNA	Refseq_genes	-	1.2	-	0.0	-	2.2	9.95E-02	9.0
213512635	NM_001140741.1	Salmo salar Rhamnose-binding lectin (sal), mRNA	Refseq_genes	-	2.0	2.06E-02	6.9	-	up	-	0.0
213514719	NM_001141345.1	Salmo salar S100-A16 (s10ag), mRNA	Refseq_genes	-	-3.0	2.29E-02	down	-	up	-	0.0
213515517	NM_001140898.1	Salmo salar Sclerostin domain-containing protein 1 (sosd1), mRNA	Refseq_genes	-	-13.5	-	1.5	4.39E-02	-15.2	-	-1.1
213512394	NM_001141358.1	Salmo salar SCO4629 (y4629), mRNA	Refseq_genes	9.61E-03	down	-	-1.1	-	-1.1	-	0.0
291190832	NM_001173937.1	Salmo salar Selenide, water dikinase 1 (sps1), mRNA	Refseq_genes	-	1.7	-	-2.1	5.28E-02	-6.4	-	3.6
185133566	NM_001123692.1	Salmo salar serum albumin 2 (LOC100136922), mRNA	Refseq_genes	-	1.0	1.03E-03	-13.4	-	-1.6	-	-1.5
185133997	NM_001123569.1	Salmo salar serum lectin isoform 1 precursor (LOC100136435), mRNA	Refseq_genes	-	up	-	-1.1	1.98E-02	6.7	-	up
213514919	NM_001141637.1	Salmo salar Sporozoite surface protein 2 (ssp2), mRNA	Refseq_genes	-	-4.2	8.47E-02	-7.3	3.98E-02	-6.6	2.27E-02	-25.6
213513389	NM_001140261.1	Salmo salar Transcobalamin-2 (tco2), mRNA	Refseq_genes	-	-9.4	-	-1.1	8.45E-06	down	-	1.2
291190285	NM_001173882.1	Salmo salar Tropomodulin-3 (tmod3), mRNA	Refseq_genes	-	0.00	-	0.0	6.84E-03	down	-	up
185135858	NM_001123711.1	Salmo salar trypsin IA (trp-ia), mRNA	Refseq_genes	-	0.00	2.24E-04	down	-	0.0	-	0.0
213514129	NM_001139633.1	Salmo salar upstream transcription factor 1 (usf1), mRNA	Refseq_genes	-	down	-	1.0	3.02E-02	down	-	down
185135317	NM_001123588.1	Salmo salar zonadhesin-like (LOC100136455), mRNA	Refseq_genes	-	up	1.95E-04	-17.0	-	4.6	-	2.0
7769634	AF228581.1	Salmo trutta IgM-B heavy chain constant region mRNA, partial cds	nt	-	3.0	9.01E-02	up	-	-1.4	-	1.7
164510790	AM262766.1	Salmo trutta partial mRNA for MHC class I heavy chain, Satr-UBA*2801 allele (uba gene)	nt	6.67E-04	down	2.07E-03	down	-	0.0	-	down

4102912	AF017232.1	Salvelinus namaycush transposon Tsn1-3 transposase (Tsn1) pseudogene, complete sequence	nt	-	-1.6	7.27E-02	down	-	-1.4	-	1.1
ENSGACG00000001474	*sar1b*	SAR1 homolog B (S. cerevisiae)	Ensembl_stickleback	-	-4.8	-	0.0	1.60E-02	-37.0	-	-3.6
ENSDARG00000069983	CU929159.1	scinderin like a	Ensembl_zebrafish	-	-1.1	-	-1.8	1.31E-05	down	-	2.0
ENSGACG00000016757	*sec24b*	SEC24 family, member B (S. cerevisiae)	Ensembl_stickleback	-	-1.1	-	down	9.04E-04	down	-	-1.4
ENSGACG00000000830	*sec61a1 (2 of 2)*	Sec61 alpha 1 subunit (S. cerevisiae)	Ensembl_stickleback	-	1.5	-	-1.2	6.84E-03	down	-	1.2
ENSDARG00000090286	*serpina1*	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	Ensembl_zebrafish	-	2.4	6.39E-03	-15.7	-	-1.4	-	-1.7
ENSDARG00000021208	*serpind1*	serine (or cysteine) proteinase inhibitor, clade D (heparin cofactor), member 1	Ensembl_zebrafish	-	2.3	7.81E-02	-23.2	-	-3.2	-	-1.4
ENSGACG00000007719	*serinc2 (1 of 2)*	serine incorporator 2	Ensembl_stickleback	-	down	-	down	1.28E-02	down	-	down
ENSGACG00000007834	*srsf5*	serine/arginine-rich splicing factor 5	Ensembl_stickleback	-	-1.9	-	-3.0	1.77E-03	-27.3	-	-2.2
ENSORLG00000016512	LOC100144362	serotransferrin precursor	Ensembl_medaka	-	-1.1	1.67E-02	-8.5	1.81E-03	-11.6	-	1.3
ENSGACG00000010973	*sgk1*	serum/glucocorticoid regulated kinase 1	Ensembl_stickleback	-	2.2	-	-4.1	-	0.0	4.42E-20	-862.7
ENSONIG00000011932	*sbf1*	SET binding factor 1	Ensembl_nile_tilapia	-	down	-	down	5.07E-02	-28.3	-	-2.1
ENSGACG00000014971	*sdr42e1*	short chain dehydrogenase/reductase family 42E, member 1	Ensembl_stickleback	2.42E-03	up	-	1.3	-	0.0	-	0.0
ENSDARG00000095304	si:ch211-207c6.2	si:ch211- 207c6.2	Ensembl_zebrafish	-	-3.8	-	0.0	4.41E-02	-12.4	-	up
ENSDARG00000073742	si:ch73-103b2.3	si:ch73- 103b2.3	Ensembl_zebrafish	-	0.00	4.50E-08	-38.7	-	up	-	-2.8
ENSDARG00000093374	si:ch73-18b11.1	si:ch73- 18b11.1	Ensembl_zebrafish	-	down	-	2.8	3.65E-02	down	-	-1.0
ENSDARG00000058719	si:dkey-119f1.1	si:dkey-119f1.1	Ensembl_zebrafish	-	-3.6	-	1.0	-	-2.8	1.00E-02	16.4
ENSDARG00000060325	si:dkey-179j5.2	si:dkey-179j5.2	Ensembl_zebrafish	-	0.00	-	0.0	-	up	1.18E-10	up
ENSDARG00000094929	si:dkey-7f3.15	si:dkey-7f3.15	Ensembl_zebrafish	-	down	-	1.6	-	up	4.66E-06	42.9
ENSDARG00000068515	si:zfos-1762d12.1	si:zfos- 1762d12.1	Ensembl_zebrafish	-	-1.5	-	1.5	4.52E-02	8.3	-	1.6
ENSGACG00000002914	*neu1*	sialidase 1 (lysosomal sialidase)	Ensembl_stickleback	-	up	1.58E-02	-32.8	-	up	-	up
ENSGACG00000016749	*srp72*	signal recognition particle 72kDa	Ensembl_stickleback	-	1.6	-	up	3.65E-02	up	-	up
ENSORLG00000006430	*srprb*	signal recognition particle receptor, B subunit	Ensembl_medaka	-	1.0	9.01E-02	up	-	0.0	-	1.3
ENSONIG00000012851	*sin3a (1 of 2)*	SIN3 transcription regulator homolog A (yeast)	Ensembl_nile_tilapia	-	0.00	-	down	4.67E-03	down	-	up
ENSGACG00000008432	*six1*	SIX homeobox 1	Ensembl_stickleback	-	3.6	-	-1.1	8.79E-02	-97.0	-	3.2
ENSDARG00000052578	*c6ast4*	six-cysteine containing astacin protease 4	Ensembl_zebrafish	-	0.00	2.12E-06	-23.4	-	0.0	-	down
BQ036199	gb|BQ036199.1	SL3-0294 Atlantic Salmon liver SSH Salmo salar cDNA clone SL3-0294, mRNA sequence.	EST_others	-	down	-	0.0	-	0.0	2.57E-15	down
ENSGACG00000016411	*slit3*	slit homolog 3 (Drosophila)	Ensembl_stickleback	-	0.00	-	down	5.51E-02	-8.9	-	up

ENSDARG00000071430	*smyhc1*	slow myosin heavy chain 1	Ensembl_zebrafish	2.44E-03	-27.0	-	1.6	-	-1.5	-	0.0
ENSGACG00000015581	*sumo1*	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	Ensembl_stickleback	-	-1.1	-	-3.6	2.24E-02	-14.4	-	1.2
DW592332	gb|DW592332.1	smus1-016AE03.g1_#0016.0 DIAS_SMUS Salmo salar cDNA 5', mRNA sequence.	EST_others	-	4.1	-	-1.3	3.65E-02	up	-	up
ENSONIG00000004201	*slc12a9*	solute carrier family 12 (potassium/chloride transporters), member 9	Ensembl_nile_tilapia	-	1.6	-	13.6	3.67E-05	down	-	-1.3
ENSDARG00000013855	*slc12a3*	solute carrier family 12 (sodium/chloride transporters), member 3	Ensembl_zebrafish	-	1.3	-	1.3	7.27E-02	4.8	-	up
ENSGACG00000007935	*slc16a4*	solute carrier family 16, member 4 (monocarboxylic acid transporter 5)	Ensembl_stickleback	-	0.00	1.49E-02	down	1.42E-03	down	-	down
ENSGACG00000010985	*slc2a2*	solute carrier family 2 (facilitated glucose transporter), member 2	Ensembl_stickleback	-	up	-	-1.5	-	1.6	8.09E-02	-7.9
ENSGACG00000019384	*slc2a4*	solute carrier family 2 (facilitated glucose transporter), member 4	Ensembl_stickleback	-	down	5.07E-03	-39.2	8.60E-08	down	-	down
ENSONIG00000013596	*slc24a6*	solute carrier family 24 (sodium/lithium/calcium exchanger), member 6	Ensembl_nile_tilapia	-	1.9	-	-1.3	1.68E-03	down	5.91E-02	down
ENSGACG00000015473	*slc25a36 (2 of 2)*	solute carrier family 25 (pyrimidine nucleotide carrier), member 36	Ensembl_stickleback	-	up	-	up	-	-28.1	5.61E-03	up
ENSGACG00000005439	*slc35e2b*	solute carrier family 35, member E2B	Ensembl_stickleback	-	-1.1	-	12.6	1.96E-03	-19.2	-	down
ENSGACG00000016873	*slc39a2*	solute carrier family 39 (zinc transporter), member 2	Ensembl_stickleback	-	-1.6	-	down	8.30E-03	-18.4	-	0.0
ENSGACG00000007949	*slc48a1*	solute carrier family 48 (heme transporter), member 1	Ensembl_stickleback	-	-1.8	-	-4.6	1.08E-03	-29.6	-	3.7
ENSGACG00000004673	*snx5*	sorting nexin 5	Ensembl_stickleback	-	up	-	0.0	5.84E-02	-7.9	-	down
ENSGACG00000006733	*spc24*	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Ensembl_stickleback	-	0.00	-	0.0	4.50E-02	-10.5	-	up
ENSGACG00000020699	*spag7*	sperm associated antigen 7	Ensembl_stickleback	-	1.1	-	-1.9	8.67E-02	-7.6	-	1.1
ENSGACG00000013537	*s1pr1*	sphingosine-1-phosphate receptor 1	Ensembl_stickleback	-	2.1	-	-1.2	1.85E-07	up	-	-1.2
ENSGACG00000008317	*skap2*	src kinase associated phosphoprotein 2	Ensembl_stickleback	3.75E-02	down	-	1.9	-	-1.1	-	down
ENSGACG00000011185	*sox9 (2 of 2)*	SRY (sex determining region Y)-box 9	Ensembl_stickleback	-	0.00	-	4.1	1.96E-02	up	-	-3.3
ENSGACG00000016008	*st6galnac6*	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1, 3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6	Ensembl_stickleback	-	-1.4	-	1.3	5.07E-02	-9.0	-	-1.1
ENSORLG00000018292	*stab2*	stabilin 2	Ensembl_medaka	-	-1.1	-	3.7	-	-1.2	9.95E-02	12.2
ENSORLG00000000328	*stc1 (2 of 2)*	stanniocalcin 1	Ensembl_medaka	-	down	-	up	2.36E-18	down	-	0.0
ENSDARG00000058476	*stc1l*	stanniocalcin 1, like	Ensembl_zebrafish	-	down	-	up	2.30E-12	down	-	0.0
ENSDARG00000033662	*scd*	stearoyl-CoA desaturase (delta-9-desaturase)	Ensembl_zebrafish	-	1.2	-	3.5	-	1.0	8.55E-10	54.2
ENSDARG00000024026	*sdf2*	stromal cell-derived factor 2	Ensembl_zebrafish	-	-1.2	-	1.3	-	1.8	5.55E-02	5.5
ENSGACG00000020581	*sod1*	superoxide dismutase 1, soluble	Ensembl_stickleback	1.15E-02	down	6.61E-04	down	2.28E-03	down	1.89E-03	down

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	-	0.00	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	-	-1.1
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	-	0.00	2.29E-02	up	-	down	-	2.1
ENSGACG00000003136	*syt11*	synaptotagmin XI	Ensembl_stickleback	-	-1.0	8.90E-08	down	-	-2.8	-	-1.3
288548571	GU569096.1	Taenia pisiformis mitochondrion, complete genome	nt	-	0.00	6.59E-03	8.6	-	0.0	-	0.0
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	-	0.00	-	0.0	6.99E-02	down	-	0.0
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
ENSDARG00000008407	*tspan7b*	tetraspanin 7b	Ensembl_zebrafish	-	-3.0	-	-2.5	5.07E-02	-14.4	-	up
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	-	0.00	-	0.0	-	up	1.57E-20	up
ENSGACG00000016986	*trip4*	thyroid hormone receptor interactor 4	Ensembl_stickleback	1.61E-02	up	-	up	-	-1.0	-	up
ENSDARG00000002909	*tjp3*	tight junction protein 3	Ensembl_zebrafish	-	1.2	-	1.1	1.59E-02	11.6	2.14E-02	12.3
ENSGACG00000003028	*timp2 (2 of 2)*	TIMP metallopeptidase inhibitor 2	Ensembl_stickleback	-	0.00	-	down	2.75E-04	down	-	0.0
ENSORLG00000012522	*tsta3*	tissue specific transplantation antigen P35B	Ensembl_medaka	2.00E-02	down	3.88E-05	down	-	0.0	-	0.0
ENSDARG00000063420	*tox4 (2 of 2)*	TOX high mobility group box family member 4	Ensembl_zebrafish	-	-15.1	6.40E-02	23.9	-	4.7	-	down
ENSGACG00000017200	*taldo1*	transaldolase 1	Ensembl_stickleback	-	down	2.29E-02	down	-	-1.6	-	0.0
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	-	up
ENSGACG00000015584	*tmed2*	transmembrane emp24 domain trafficking protein 2	Ensembl_stickleback	-	0.00	-	0.0	8.79E-02	down	-	0.0
ENSGACG00000016363	*tmed9*	transmembrane emp24 protein transport domain containing 9	Ensembl_stickleback	-	1.8	-	-2.7	6.04E-03	-22.0	-	up
ENSGACG00000004023	*tmem106c*	transmembrane protein 106C	Ensembl_stickleback	-	0.00	1.71E-02	-15.7	-	0.0	-	down
ENSGACG00000009084	*tmem136 (2 of 2)*	transmembrane protein 136	Ensembl_stickleback	2.50E-02	down	-	up	8.79E-02	up	-	0.0

ENSGACG00000013071	*tmem161a*	transmembrane protein 161A	Ensembl_stickleback	-	up	5.69E-02	-5.4	-	0.0	3.31E-05	up
ENSGACG00000016548	*tmem38b*	transmembrane protein 38B	Ensembl_stickleback	4.11E-07	43.7	-	1.1	-	-1.3	-	5.6
ENSGACG00000003118	*tmem42*	transmembrane protein 42	Ensembl_stickleback	-	-4.4	-	0.0	2.01E-17	up	-	down
ENSGACG00000004640	*tmem64*	transmembrane protein 64	Ensembl_stickleback	-	-1.8	-	-4.3	-	-5.3	2.31E-02	down
ENSGACG00000015841	*tnpo1*	transportin 1	Ensembl_stickleback	-	down	-	down	3.24E-03	down	-	-1.1
ENSGACG00000007382	*trim36*	tripartite motif containing 36	Ensembl_stickleback	-	-7.5	-	-4.0	8.81E-02	-10.2	-	-7.6
ENSDARG00000028027	*trim63*	tripartite motif containing 63	Ensembl_zebrafish	-	-1.7	-	1.0	2.69E-02	-16.5	-	down
ENSGACG00000004198	*tnnc2 (1 of 2)*	troponin C type 2 (fast)	Ensembl_stickleback	-	-6.2	1.17E-03	-12.4	3.31E-04	-12.8	1.38E-03	-11.1
ENSDARG00000042993	*try*	trypsin	Ensembl_zebrafish	-	1.2	1.73E-07	-32.3	-	-1.1	-	down
229366578	*acq58269.1*	Trypsin precursor	nr	3.04E-05	19.4	-	0.0	-	0.0	-	0.0
ENSONIG00000003233	*tdrd3*	tudor domain containing 3	Ensembl_nile_tilapia	-	-1.5	-	1.6	5.65E-02	up	-	-3.3
ENSGACG00000009537	*tpcn1*	two pore segment channel 1	Ensembl_stickleback	-	1.4	-	-4.7	-	2.2	9.97E-03	-9.0
ENSDARG00000036832	*cyt1l*	type I cytokeratin, enveloping layer, like	Ensembl_zebrafish	-	1.1	3.95E-03	9.4	-	2.6	-	1.0
ENSGACG00000005854	*uchl5*	ubiquitin carboxyl-terminal hydrolase L5	Ensembl_stickleback	-	down	-	0.0	4.49E-02	up	-	up
ENSDARG00000087495	*usp2 (2 of 3)*	ubiquitin specific peptidase 2	Ensembl_zebrafish	-	2.4	-	2.2	3.36E-02	6.6	-	1.7
ENSGACG00000011028	*usp36*	ubiquitin specific peptidase 36	Ensembl_stickleback	1.08E-02	-34.3	2.07E-03	down	1.42E-03	down	2.53E-05	-90.0
ENSDARG00000007714	*ube2q1*	ubiquitin-conjugating enzyme E2Q (putative) 1	Ensembl_zebrafish	-	-3.7	3.54E-02	up	-	1.4	-	0.0
ENSDARG00000011537	*ugt2a5*	UDP glucuronosyltransferase 2 family, polypeptide A5	Ensembl_zebrafish	-	down	-	down	1.91E-07	down	-	-1.6
ENSDARG00000039501	*ugt2a6*	UDP glucuronosyltransferase 2 family, polypeptide A6	Ensembl_zebrafish	-	0.00	-	down	4.36E-09	down	-	0.0
ENSORLG00000007327	*galntl4*	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	Ensembl_medaka	-	down	-	0.0	1.96E-02	down	-	0.0
ENSGACG00000009985	*unc45b*	unc-45 homolog B (C. elegans)	Ensembl_stickleback	-	1.8	-	up	6.59E-02	-5.5	-	-6.7
ENSDARG00000078382	CABZ01075938.1	Uncharacterize d protein	Ensembl_zebrafish	-	-1.6	6.21E-08	up	9.52E-06	up	5.91E-02	up
ENSDARG00000087843	CABZ01092722.1	Uncharacterized protein	Ensembl_zebrafish	-	-1.1	-	3.0	-	1.3	2.50E-02	-6.9
ENSDARG00000088309	*ct573337.1*	Uncharacterized protein	Ensembl_zebrafish	3.75E-02	8.5	-	up	-	up	-	0.0
116517246	NP_001070844.1	uncharacterized protein LOC559260 precursor	Refseq_proteins	-	1.2	-	1.0	2.26E-02	24.6	-	2.8
158534007	NP_001103579.1	uncharacterized protein LOC561171 precursor	Refseq_proteins	-	0.00	-	down	-	0.0	8.84E-12	-20469.0
ENSGACG00000017435	*upf3b*	UPF3 regulator of nonsense transcripts homolog B (yeast)	Ensembl_stickleback	2.50E-02	down	-	0.0	1.50E-04	down	-	0.0
ENSGACG00000014740	*utp18*	UTP18 small subunit (SSU) processome component homolog (yeast)	Ensembl_stickleback	-	up	-	0.0	1.28E-02	up	-	0.0

ENSGACG00000005430	*crk (1 of 2)*	v-crk sarcoma virus CT10 oncogene homolog (avian)	Ensembl_stickleback	4.69E-02	down	-	-1.6	-	1.4	-	down
ENSGACG00000005867	*vsx2*	visual system homeobox 2	Ensembl_stickleback	7.32E-02	down	-	1.0	-	1.8	-	-1.2
ENSORLG00000016336	*vmo1*	vitelline membrane outer layer 1 homolog (chicken)	Ensembl_medaka	-	0.00	9.89E-05	-17.4	-	up	-	-2.2
ENSDARG00000055809	*vtg2*	vitellogenin 2	Ensembl_zebrafish	-	-1.2	-	2.7	-	-1.5	9.15E-33	20268.3
ENSDARG00000092419	*vtg7*	vitellogenin 7	Ensembl_zebrafish	-	-1.5	-	-1.6	-	-1.4	2.57E-15	317.5
ENSGACG00000007380	*wdr61*	WD repeat domain 61	Ensembl_stickleback	1.36E-02	down	3.54E-02	down	-	0.0	-	down
ENSORLG00000005229	*wls*	wntless homolog (Drosophila)	Ensembl_medaka	-	2.8	-	-1.2	9.04E-04	down	-	down
ENSGACG00000019114	*xrcc6bp1*	XRCC6 binding protein 1	Ensembl_stickleback	7.95E-05	23.6	-	up	-	-1.0	-	down
ENSGACG00000020724	*yipf5*	Yip1 domain family, member 5	Ensembl_stickleback	-	down	-	down	3.65E-02	down	-	up
238943009	CU695216.16	Zebrafish DNA sequence from clone CH73-348N11 in linkage group 3, complete sequence	nt	-	1.3	1.76E-04	up	-	5.1	-	1.2
156764000	CU464084.9	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
ENSDARG00000093844	zgc:136461	zgc:136461	Ensembl_zebrafish	-	down	2.78E-07	-34.5	-	0.0	-	down
ENSDARG00000079274	zgc:66382	zgc:66382	Ensembl_zebrafish	-	down	4.52E-06	-20.9	-	1.4	-	down
ENSGACG00000015779	*zfhx3*	zinc finger homeobox 3	Ensembl_stickleback	-	1.0	4.30E-03	down	4.65E-02	-7.9	3.74E-02	down
ENSGACG00000002418	*zfhx4*	zinc finger homeobox 4	Ensembl_stickleback	-	-3.9	-	-6.0	-	-1.7	6.34E-11	-403.4
ENSGACG00000002626	*znf423*	zinc finger protein 423	Ensembl_stickleback	-	-16.1	1.49E-02	down	1.98E-03	-53.9	-	down
ENSGACG00000016481	*znf710 (1 of 2)*	zinc finger protein 710	Ensembl_stickleback	-	up	-	up	3.02E-02	up	-	3.2
ENSGACG00000010661	*znf750*	zinc finger protein 750	Ensembl_stickleback	-	-1.1	9.89E-05	down	-	up	-	down
ENSGACG00000005282	*zcchc11*	zinc finger, CCHC domain containing 11	Ensembl_stickleback	-	1.3	-	-1.4	-	2.2	5.72E-03	-9.7
ENSGACG00000009457	*zranb2*	zinc finger, RAN-binding domain containing 2	Ensembl_stickleback	-	1.0	-	down	-	-2.1	5.91E-02	up
ENSGACG00000005043	*zwilch*	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 02RT117K06 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 3', 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	1349293 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	EST_others	-	1.3	4.12E-02	-11.4	-	-2.0	-	1.4

		cDNA clone 10RT#3_145E18 5', mRNA sequence.									
ENSGACG00000012314	*nt5dc2*	5'-nucleotidase domain containing 2	Ensembl_stickleback	-	down	7.27E-02	down	9.04E-04	down	-	down
CA350320	gb|CA350320.1	621050 NCCCWA 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	643965 NCCCWA 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	654297 NCCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT34F22_D_C11 5', mRNA sequence.	EST_others	-	-3.6	9.01E-02	down	-	3.0	-	down
CA383249	gb|CA383249.1	663393 NCCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT13C10_C_B05 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 3prim, 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	-	-1.9	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	-	down
BX866879	emb|BX866879.3	BX866879 tcba Oncorhynchus mykiss cDNA clone tcba0026.f.12 5prim, mRNA sequence.	EST_others	-	-1.7	-	up	-	up	1.19E-02	up
BX871489	emb|BX871489.2	BX871489 tcbk Oncorhynchus mykiss cDNA clone tcbk0008.d.18 5prim, mRNA sequence.	EST_others	-	-1.1	5.82E-03	-10.2	-	up	-	down
ENSGACG00000000665	ENSGACG00000000665	ENSGACT00000000858	Ensembl_stickleback	-	down	-	down	3.11E-02	-32.4	3.24E-02	-29.2
ENSGACG00000001046	ENSGACG00000001046	ENSGACT00000001352	Ensembl_stickleback	-	0.00	5.20E-03	up	-	up	-	0.0
ENSGACG00000001103	ENSGACG00000001103	ENSGACT00000001428	Ensembl_stickleback	8.33E-04	-53.1	-	1.1	-	-1.3	-	2.3
ENSGACG00000002397	ENSGACG00000002397	ENSGACT00000003154	Ensembl_stickleback	-	-1.2	-	down	-	-17.9	5.56E-10	up
ENSGACG00000003684	ENSGACG00000003684	ENSGACT00000004857	Ensembl_stickleback	2.50E-02	down	-	1.1	-	1.4	9.95E-02	up

ENSGACG00000003787	ENSGACG00000003787	ENSGACT00000004984	Ensembl_stickleback	-	1.0	4.56E-06	up	-	0.0	-	up
ENSGACG00000004988	ENSGACG00000004988	ENSGACT00000006645	Ensembl_stickleback	-	down	-	0.0	1.95E-02	-34.6	1.00E-02	down
ENSGACG00000005457	ENSGACG00000005457	ENSGACT00000007232	Ensembl_stickleback	-	up	1.20E-06	128.1	-	up	-	down
ENSGACG00000005610	ENSGACG00000005610	ENSGACT00000007471	Ensembl_stickleback	-	-1.4	7.31E-06	-20.2	-	-1.1	-	1.2
ENSGACG00000006023	ENSGACG00000006023	ENSGACT00000007994	Ensembl_stickleback	-	1.3	-	3.7	2.43E-02	up	-	0.0
ENSGACG00000006109	ENSGACG00000006109	ENSGACT00000008146	Ensembl_stickleback	-	-2.6	7.81E-02	-6.9	3.76E-02	-6.3	9.93E-06	-36.5
ENSGACG00000006376	ENSGACG00000006376	ENSGACT00000008463	Ensembl_stickleback	-	-3.3	2.28E-02	-9.6	-	-1.4	-	-2.1
ENSGACG00000006658	ENSGACG00000006658	ENSGACT00000008841	Ensembl_stickleback	7.32E-02	up	2.85E-02	up	-	-1.1	-	0.0
ENSGACG00000007518	ENSGACG00000007518	ENSGACT00000010009	Ensembl_stickleback	-	2.6	-	up	8.30E-03	down	5.91E-02	down
ENSGACG00000007857	ENSGACG00000007857	ENSGACT00000010455	Ensembl_stickleback	-	0.00	-	0.0	1.07E-03	down	-	0.0
ENSGACG00000007990	ENSGACG00000007990	ENSGACT00000010603	Ensembl_stickleback	2.78E-03	down	-	1.3	3.90E-03	down	-	down
ENSGACG00000008104	ENSGACG00000008104	ENSGACT00000010748	Ensembl_stickleback	-	-1.4	1.36E-03	-11.0	-	1.7	-	-1.8
ENSGACG00000008362	ENSGACG00000008362	ENSGACT00000011076	Ensembl_stickleback	-	0.00	-	down	-	up	3.31E-05	down
ENSGACG00000008527	ENSGACG00000008527	ENSGACT00000011292	Ensembl_stickleback	-	up	-	0.0	-	0.0	4.66E-03	down
ENSGACG00000008544	ENSGACG00000008544	ENSGACT00000011317	Ensembl_stickleback	1.61E-02	down	-	1.6	-	-1.6	-	-1.2
ENSGACG00000008811	ENSGACG00000008811	ENSGACT00000011669	Ensembl_stickleback	-	0.00	-	0.0	8.30E-03	down	-	0.0
ENSGACG00000009769	ENSGACG00000009769	ENSGACT00000012954	Ensembl_stickleback	-	down	-	up	-	down	3.46E-09	990.0
ENSGACG00000010278	ENSGACG00000010278	ENSGACT00000013605	Ensembl_stickleback	-	-1.1	-	down	4.99E-02	-8.7	-	-3.1
ENSGACG00000010455	ENSGACG00000010455	ENSGACT00000013842	Ensembl_stickleback	1.27E-03	28.4	-	0.0	-	up	-	0.0
ENSGACG00000011411	ENSGACG00000011411	ENSGACT00000015161	Ensembl_stickleback	-	-6.8	-	-1.7	7.05E-02	-13.1	-	-5.4
ENSGACG00000011761	ENSGACG00000011761	ENSGACT00000015587	Ensembl_stickleback	-	2.8	1.19E-02	up	-	-8.0	-	up
ENSGACG00000012223	ENSGACG00000012223	ENSGACT00000016209	Ensembl_stickleback	-	up	9.01E-02	up	-	-1.9	-	-1.4
ENSGACG00000012735	ENSGACG00000012735	ENSGACT00000016852	Ensembl_stickleback	-	down	6.21E-08	down	-	down	-	up

ENSGACG00000012810	ENSGACG00000012810	ENSGACT00000016961	Ensembl_stickleback	-	1.1	-	0.0	2.75E-04	down	-	0.0
ENSGACG00000012940	ENSGACG00000012940	ENSGACT00000017168	Ensembl_stickleback	9.44E-05	up	2.33E-05	51.6	-	-1.3	-	-12.1
ENSGACG00000013362	ENSGACG00000013362	ENSGACT00000017700	Ensembl_stickleback	-	down	-	down	1.04E-02	down	-	down
ENSGACG00000013443	ENSGACG00000013443	ENSGACT00000017812	Ensembl_stickleback	-	down	-	0.0	8.79E-02	down	-	2.1
ENSGACG00000013510	ENSGACG00000013510	ENSGACT00000017897	Ensembl_stickleback	-	-2.5	-	0.0	-	-5.5	9.86E-13	up
ENSGACG00000013819	ENSGACG00000013819	ENSGACT00000018284	Ensembl_stickleback	-	2.5	-	1.0	3.90E-03	up	-	2.6
ENSGACG00000014561	ENSGACG00000014561	ENSGACT00000019250	Ensembl_stickleback	-	0.00	4.56E-06	-21.0	-	up	-	-2.2
ENSGACG00000014922	ENSGACG00000014922	ENSGACT00000019782	Ensembl_stickleback	-	down	-	down	6.81E-04	down	4.78E-02	down
ENSGACG00000015113	ENSGACG00000015113	ENSGACT00000019973	Ensembl_stickleback	1.53E-03	down	1.20E-06	down	4.79E-06	down	-	-5.7
ENSGACG00000016237	ENSGACG00000016237	ENSGACT00000021465	Ensembl_stickleback	-	1.1	-	1.2	9.52E-06	up	-	0.0
ENSGACG00000016744	ENSGACG00000016744	ENSGACT00000022145	Ensembl_stickleback	-	0.00	-	7.5	-	up	5.91E-02	down
ENSGACG00000017541	ENSGACG00000017541	ENSGACT00000023221	Ensembl_stickleback	-	-1.6	3.51E-09	-180.7	-	1.2	-	up
ENSGACG00000017983	ENSGACG00000017983	ENSGACT00000023805	Ensembl_stickleback	-	down	-	0.0	8.60E-08	-110.3	-	0.0
ENSGACG00000018030	ENSGACG00000018030	ENSGACT00000023870	Ensembl_stickleback	-	-5.1	-	-2.6	1.25E-04	-41.5	-	-2.2
ENSGACG00000018802	ENSGACG00000018802	ENSGACT00000024909	Ensembl_stickleback	-	0.00	9.86E-07	down	1.28E-06	down	-	down
ENSGACG00000019767	ENSGACG00000019767	ENSGACT00000026179	Ensembl_stickleback	-	0.00	-	up	6.85E-02	-12.0	-	down
ENSGACG00000020439	ENSGACG00000020439	ENSGACT00000027081	Ensembl_stickleback	1.08E-02	-34.4	1.08E-03	up	-	-5.5	-	down
ENSGACG00000020467	ENSGACG00000020467	ENSGACT00000027116	Ensembl_stickleback	-	0.00	-	down	3.59E-04	down	7.28E-04	down
ENSGACG00000020921	ENSGACG00000020921	ENSGACT00000027713	Ensembl_stickleback	2.14E-06	down	7.73E-07	-65.9	3.05E-10	-226.8	7.38E-10	-303.9
ENSONIG00000002827	ENSONIG00000002827	ENSONIT00000003544	Ensembl_nile_tilapia	-	up	6.22E-03	up	-	down	-	-1.0
ENSONIG00000004540	ENSONIG00000004540	ENSONIT00000005718	Ensembl_nile_tilapia	-	-1.2	-	2.9	-	-1.7	2.31E-02	down
ENSONIG00000007219	ENSONIG00000007219	ENSONIT00000009107	Ensembl_nile_tilapia	-	-1.4	2.12E-06	55.2	-	2.8	-	-1.1
ENSONIG00000009825	ENSONIG00000009825	ENSONIT00000012355	Ensembl_nile_tilapia	-	0.00	-	-2.1	-	5.1	3.37E-15	225.1

ENSONIG00000011792	ENSONIG00000011792	ENSONIT00000014857	Ensembl_nile_tilapia	-	0.00	2.37E-03	-18.5	-	0.0	-	0.0
ENSONIG00000013985	ENSONIG00000013985	ENSONIT00000017595	Ensembl_nile_tilapia	-	1.1	-	-1.6	5.07E-02	20.1	-	2.3
ENSONIG00000017323	ENSONIG00000017323	ENSONIT00000021866	Ensembl_nile_tilapia	-	-1.5	-	-4.0	1.30E-02	-12.0	-	-1.4
ENSONIG00000019573	ENSONIG00000019573	ENSONIT00000024660	Ensembl_nile_tilapia	-	-1.3	-	-1.4	-	-2.0	7.68E-02	down
ENSORLG00000000460	ENSORLG00000000460	ENSORLT00000000568	Ensembl_medaka	-	0.00	-	2.1	7.87E-07	143.3	-	-5.8
ENSORLG00000001173	ENSORLG00000001173	ENSORLT00000001443	Ensembl_medaka	-	1.1	-	3.7	-	1.2	7.68E-02	down
ENSORLG00000001190	ENSORLG00000001190	ENSORLT00000001466	Ensembl_medaka	-	1.3	6.31E-02	6.1	-	down	-	-2.2
ENSORLG00000003700	ENSORLG00000003700	ENSORLT00000004613	Ensembl_medaka	-	-2.5	-	down	-	0.0	3.47E-03	-44.5
ENSORLG00000010522	ENSORLG00000010522	ENSORLT00000013192	Ensembl_medaka	-	0.00	-	0.0	-	0.0	6.43E-04	up
ENSORLG00000011293	ENSORLG00000011293	ENSORLT00000014151	Ensembl_medaka	-	0.00	4.90E-02	9.7	-	0.0	-	0.0
ENSORLG00000011321	ENSORLG00000011321	ENSORLT00000014185	Ensembl_medaka	-	0.00	6.16E-05	down	-	2.1	-	-1.9
ENSORLG00000012785	ENSORLG00000012785	ENSORLT00000016011	Ensembl_medaka	-	-4.9	-	-3.7	1.17E-02	-39.9	-	down
ENSORLG00000013333	ENSORLG00000013333	ENSORLT00000016712	Ensembl_medaka	-	0.00	-	0.0	-	0.0	1.13E-12	up
ENSORLG00000019280	ENSORLG00000019280	ENSORLT00000024015	Ensembl_medaka	1.36E-03	21.0	-	up	-	up	-	0.0
ENSORLG00000020091	ENSORLG00000020091	ENSORLT00000024932	Ensembl_medaka	1.61E-02	down	-	down	-	-1.5	-	down
EV367322	gb|EV367322.1	EST_cclu_evb_703099 ccluevb mixed_tissue Coregonus clupeaformis cDNA Coregonus clupeaformis cDNA clone cclu_evb_12_91_rev 3', mRNA sequence.	EST_others	-	down	-	down	1.28E-02	down	-	down
EV368845	gb|EV368845.1	EST_cclu_evb_704787 ccluevb mixed_tissue Coregonus clupeaformis cDNA Coregonus clupeaformis cDNA clone cclu_evb_14_243_rev 3', mRNA sequence.	EST_others	-	-1.7	-	up	1.09E-02	-10.4	-	0.0
EV370019	gb|EV370019.1	EST_cclu_evb_706182 ccluevb mixed_tissue Coregonus clupeaformis cDNA Coregonus clupeaformis cDNA clone cclu_evb_16_102_rev 3', mRNA sequence.	EST_others	-	1.5	-	-2.4	8.79E-02	-8.6	-	up
EV370268	gb|EV370268.1	EST_cclu_evb_706314 ccluevb mixed_tissue Coregonus clupeaformis cDNA Coregonus clupeaformis cDNA clone cclu_evb_16_234_rev 3', mRNA sequence.	EST_others	-	7.7	6.31E-02	14.6	-	4.6	-	6.5
FK872811	gb|FK872811.1	EST_crog_evp_897819 crog_evp Caligus	EST_others	-	2.2	-	4.1	2.99E-03	9.4	-	2.8

		rogercresseyi cDNA clone crog_evp_506_315_fwd 5', mRNA sequence.									
FK872812	gb|FK872812.1	EST_crog_evp_904731 crog_evp Caligus rogercresseyi cDNA clone crog_evp_506_315_rev 5', mRNA sequence.	EST_others	8.88E-02	-22.8	-	0.0	-	-1.4	-	0.0
FK882798	gb|FK882798.1	EST_crog_evp_908098 crog_evp Caligus rogercresseyi cDNA clone crog_evp_520_226_rev 5', mRNA sequence.	EST_others	-	2.6	7.27E-02	down	-	-1.4	-	down
FK869364	gb|FK869364.1	EST_crog_evp_915567 crog_evp Caligus rogercresseyi cDNA clone crog_evp_502_015_fwd 5', mRNA sequence.	EST_others	-	0.00	7.64E-03	down	2.28E-03	down	-	down
FK879202	gb|FK879202.1	EST_crog_evp_916574 crog_evp Caligus rogercresseyi cDNA clone crog_evp_515_254_rev 5', mRNA sequence.	EST_others	3.75E-02	down	-	down	-	up	-	0.0
GW640860	gb|GW640860.1	EST_lsaA_evu_1215038 lsaAevu mixed_tissue Lepeophtheirus salmonis (Atlantic Canada) cDNA Lepeophtheirus salmonis cDNA clone lsaA_evu_506_284 3', mRNA sequence.	EST_others	-	5.9	-	-1.1	8.30E-03	down	-	1.7
GE839897	gb|GE839897.1	EST_omyk_evo_818548 omykevo WBC Oncorhynchus mykiss cDNA Oncorhynchus mykiss cDNA clone omyk_evo_513_148 3', mRNA sequence.	EST_others	-	-1.6	-	-1.3	1.82E-03	-14.9	-	1.5
GE835715	gb|GE835715.1	EST_omyk_evo_830394 omykevo WBC Oncorhynchus mykiss cDNA Oncorhynchus mykiss cDNA clone omyk_evo_507_282 5', mRNA sequence.	EST_others	-	4.7	-	-2.6	4.49E-02	up	-	0.0
EL553118	gb|EL553118.1	EST_otsh_evc_1287 otshevc mixed_tissue Oncorhynchus tshawytscha cDNA Oncorhynchus tshawytscha cDNA clone otsh_evc_005_046_fwd 3', mRNA sequence.	EST_others	-	-1.7	-	-2.6	-	up	2.48E-03	11.5
EG791873	gb|EG791873.1	EST_ssal_evd_12006 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_514_352_fwd 5', mRNA sequence.	EST_others	-	-1.8	-	-1.2	6.16E-02	-10.0	-	1.5
EG793024	gb|EG793024.1	EST_ssal_evd_13041 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_516_121_rev 3', mRNA sequence.	EST_others	-	down	-	0.0	4.49E-02	down	-	0.0
EG795706	gb|EG795706.1	EST_ssal_evd_15456 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_519_242_rev 3', mRNA sequence.	EST_others	-	up	-	0.0	5.85E-04	down	-	down
EG804652	gb|EG804652.1	EST_ssal_evd_1707 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_006_336_fwd 5', mRNA sequence.	EST_others	2.08E-03	down	-	-2.0	3.02E-05	-21.9	1.37E-03	down
EG807134	gb|EG807134.1	EST_ssal_evd_17813 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_522_310_fwd 5', mRNA sequence.	EST_others	-	3.1	9.89E-05	up	-	1.9	-	-1.2
EG822862	gb|EG822862.1	EST_ssal_evd_24557 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone	EST_others	-	up	1.49E-02	down	-	0.0	-	0.0

		ssal_evd_531_353_fwd 5', mRNA sequence.									
EG824531	gb|EG824531.1	EST_ssal_evd_26059 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_533_360_fwd 5', mRNA sequence.	EST_others	5.86E-02	down	-	1.0	-	-1.9	-	0.0
EG824683	gb|EG824683.1	EST_ssal_evd_26196 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_534_047_rev 3', mRNA sequence.	EST_others	-	-2.4	1.84E-02	down	-	-2.3	-	down
EG806136	gb|EG806136.1	EST_ssal_evd_26841 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_535_004_rev 3', mRNA sequence.	EST_others	-	0.00	5.59E-02	down	2.75E-04	down	-	down
EG785970	gb|EG785970.1	EST_ssal_evd_42158 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_556_188_fwd 5', mRNA sequence.	EST_others	1.18E-03	down	2.85E-02	down	4.63E-10	down	-	down
EG776240	gb|EG776240.1	EST_ssal_evd_51400 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_569_098_fwd 5', mRNA sequence.	EST_others	4.99E-10	88.9	-	up	-	up	-	0.0
EG801892	gb|EG801892.1	EST_ssal_evd_58485 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_578_355_fwd 5', mRNA sequence.	EST_others	-	-1.0	-	1.9	-	down	1.00E-02	up
EG802309	gb|EG802309.1	EST_ssal_evd_58862 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_579_175_rev 3', mRNA sequence.	EST_others	-	4.1	-	9.2	8.79E-02	down	-	up
EG803435	gb|EG803435.1	EST_ssal_evd_610 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssal_evd_004_040_fwd 5', mRNA sequence.	EST_others	-	1.1	-	up	2.24E-02	-14.3	-	0.0
EG835764	gb|EG835764.1	EST_ssal_eve_10967 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_514_345_fwd 5', mRNA sequence.	EST_others	-	-1.3	-	down	2.51E-04	-74.5	-	-2.2
EG838512	gb|EG838512.1	EST_ssal_eve_1553 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_501_070_rev 3', mRNA sequence.	EST_others	2.20E-02	8.1	-	1.0	-	0.0	-	up
EG855707	gb|EG855707.1	EST_ssal_eve_16329 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_522_062_fwd 5', mRNA sequence.	EST_others	1.15E-02	up	-	0.0	3.02E-02	down	-	0.0
EG879755	gb|EG879755.1	EST_ssal_eve_17542 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_523_359_fwd 5', mRNA sequence.	EST_others	-	down	-	0.0	2.43E-02	down	-	0.0
EG879910	gb|EG879910.1	EST_ssal_eve_17556 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_523_367_rev 3', mRNA sequence.	EST_others	-	3.7	-	-1.3	1.96E-02	up	-	1.4
EG881910	gb|EG881910.1	EST_ssal_eve_17736 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_524_075_fwd 5', mRNA sequence.	EST_others	-	down	3.54E-02	down	-	0.0	-	0.0
EG876254	gb|EG876254.1	EST_ssal_eve_19989 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_527_074_rev 3', mRNA sequence.	EST_others	3.75E-02	down	2.85E-02	down	-	-4.5	-	1.8

EG878528	gb|EG878528.1	EST_ssal_eve_22035 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_529_368_fwd 5', mRNA sequence.	EST_others	1.27E-03	11.8	-	up	-	1.8	-	0.0
EG880230	gb|EG880230.1	EST_ssal_eve_23568 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_532_046_fwd 5', mRNA sequence.	EST_others	-	2.7	-	-1.2	6.99E-02	up	-	-2.9
EG881131	gb|EG881131.1	EST_ssal_eve_24379 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_533_077_rev 3', mRNA sequence.	EST_others	-	down	-	6.7	9.52E-06	down	-	0.0
EG882237	gb|EG882237.1	EST_ssal_eve_25374 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_534_203_fwd 5', mRNA sequence.	EST_others	-	21.3	-	up	6.47E-04	33.0	-	4.9
EG882682	gb|EG882682.1	EST_ssal_eve_25775 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_535_024_rev 3', mRNA sequence.	EST_others	-	down	-	down	8.79E-02	down	-	down
EG866124	gb|EG866124.1	EST_ssal_eve_27704 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_537_252_fwd 5', mRNA sequence.	EST_others	-	-1.4	-	-1.2	5.77E-02	-5.7	-	down
EG867991	gb|EG867991.1	EST_ssal_eve_29384 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_539_349_fwd 5', mRNA sequence.	EST_others	-	1.5	-	-1.2	2.93E-06	up	-	2.0
EG868203	gb|EG868203.1	EST_ssal_eve_29575 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_540_067_fwd 5', mRNA sequence.	EST_others	-	4.1	-	2.5	2.99E-03	-24.2	-	up
EG869982	gb|EG869982.1	EST_ssal_eve_31176 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_542_125_rev 3', mRNA sequence.	EST_others	7.42E-04	down	-	down	-	0.0	-	0.0
EG870274	gb|EG870274.1	EST_ssal_eve_31439 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_542_264_fwd 5', mRNA sequence.	EST_others	-	4.3	-	down	-	-1.2	1.48E-02	up
EG840326	gb|EG840326.1	EST_ssal_eve_3187 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_503_137_fwd 5', mRNA sequence.	EST_others	-	5.6	-	down	8.79E-02	down	-	0.0
EG840695	gb|EG840695.1	EST_ssal_eve_3520 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_503_306_fwd 5', mRNA sequence.	EST_others	-	1.2	-	-1.7	7.46E-02	-6.0	-	1.0
EG844851	gb|EG844851.1	EST_ssal_eve_37660 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_551_105_fwd 5', mRNA sequence.	EST_others	5.73E-03	-11.1	-	up	-	0.0	-	0.0
EG833455	gb|EG833455.1	EST_ssal_eve_45402 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_561_291_rev 3', mRNA sequence.	EST_others	-	0.00	4.41E-02	up	1.96E-02	down	-	-4.3
EG859641	gb|EG859641.1	EST_ssal_eve_52969 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_572_066_rev 3', mRNA sequence.	EST_others	-	-1.7	-	-3.1	2.33E-02	-10.8	-	-1.1
EG860536	gb|EG860536.1	EST_ssal_eve_53774 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone	EST_others	-	down	-	down	2.43E-02	down	-	down

		ssal_eve_573_104_rev 3', mRNA sequence.									
EG849257	gb|EG849257.1	EST_ssal_eve_6723 ssaleve thyroid Salmo salar cDNA Salmo salar cDNA clone ssal_eve_508_052_rev 3', mRNA sequence.	EST_others	-	-2.7	-	down	6.99E-02	down	-	0.0
EG907993	gb|EG907993.1	EST_ssal_evf_10351 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_512_085_rev 3', mRNA sequence.	EST_others	-	0.00	-	0.0	7.05E-02	-26.3	-	0.0
EG908200	gb|EG908200.1	EST_ssal_evf_10537 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_512_182_rev 3', mRNA sequence.	EST_others	-	-2.9	-	-1.4	3.24E-03	down	-	3.5
EG908809	gb|EG908809.1	EST_ssal_evf_11085 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_513_091_rev 3', mRNA sequence.	EST_others	-	down	-	down	4.54E-05	down	-	down
EG911244	gb|EG911244.1	EST_ssal_evf_13277 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_516_098_fwd 5', mRNA sequence.	EST_others	-	-2.5	-	-1.8	5.01E-02	-6.8	-	up
EG912415	gb|EG912415.1	EST_ssal_evf_14331 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_517_261_rev 3', mRNA sequence.	EST_others	-	0.00	-	-3.4	-	-1.6	7.68E-02	down
EG913326	gb|EG913326.1	EST_ssal_evf_15151 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_518_298_fwd 5', mRNA sequence.	EST_others	-	0.00	-	down	3.65E-02	down	-	down
EG914877	gb|EG914877.1	EST_ssal_evf_16547 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_520_246_fwd 5', mRNA sequence.	EST_others	-	2.8	-	1.0	4.22E-03	-13.1	-	1.0
EG942150	gb|EG942150.1	EST_ssal_evf_17594 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_522_020_fwd 5', mRNA sequence.	EST_others	-	2.4	-	down	7.56E-02	-6.0	-	down
EG922711	gb|EG922711.1	EST_ssal_evf_1797 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_006_217_fwd 5', mRNA sequence.	EST_others	-	down	-	0.0	3.11E-02	-15.9	-	0.0
EG935627	gb|EG935627.1	EST_ssal_evf_19632 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_524_301_fwd 5', mRNA sequence.	EST_others	3.15E-02	down	-	-1.1	7.15E-02	-5.1	-	-1.1
EG937327	gb|EG937327.1	EST_ssal_evf_21163 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_526_319_fwd 5', mRNA sequence.	EST_others	-	-1.5	2.85E-02	down	-	1.1	-	1.3
EG937416	gb|EG937416.1	EST_ssal_evf_21243 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_526_359_fwd 5', mRNA sequence.	EST_others	-	0.00	-	2.9	4.49E-02	up	-	1.9
EG942312	gb|EG942312.1	EST_ssal_evf_25650 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_533_370_fwd 5', mRNA sequence.	EST_others	-	-12.9	-	down	2.07E-03	-13.1	-	-5.4
EG899717	gb|EG899717.1	EST_ssal_evf_2676 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_501_329_rev 3', mRNA sequence.	EST_others	-	down	-	-1.4	3.54E-02	7.2	-	down

EG926272	gb|EG926272.1	EST_ssal_evf_28802 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_538_075_rev 3', mRNA sequence.	EST_others	-	0.00	-	down	2.43E-02	down	-	down
EG903128	gb|EG903128.1	EST_ssal_evf_2983 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_502_106_rev 3', mRNA sequence.	EST_others	-	down	5.20E-03	down	2.70E-08	down	-	down
EG928582	gb|EG928582.1	EST_ssal_evf_30881 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_540_380_rev 3', mRNA sequence.	EST_others	-	down	-	down	5.65E-02	down	-	down
EG931057	gb|EG931057.1	EST_ssal_evf_33109 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_544_009_fwd 5', mRNA sequence.	EST_others	-	down	-	0.0	-	down	3.00E-03	-15.0
EG932783	gb|EG932783.1	EST_ssal_evf_34663 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_546_047_fwd 5', mRNA sequence.	EST_others	-	-1.1	-	1.3	-	-1.7	5.91E-02	up
EG889573	gb|EG889573.1	EST_ssal_evf_3563 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_503_025_rev 3', mRNA sequence.	EST_others	-	1.6	4.41E-02	up	-	3.3	-	up
EG934489	gb|EG934489.1	EST_ssal_evf_36198 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_548_077_fwd 5', mRNA sequence.	EST_others	9.28E-02	up	-	up	-	up	-	down
EG898924	gb|EG898924.1	EST_ssal_evf_37933 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_550_226_fwd 5', mRNA sequence.	EST_others	1.53E-03	down	-	down	2.73E-05	down	1.18E-03	down
EG901696	gb|EG901696.1	EST_ssal_evf_40428 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_553_372_rev 3', mRNA sequence.	EST_others	-	-2.5	-	1.0	1.60E-02	-18.6	-	down
EG902053	gb|EG902053.1	EST_ssal_evf_40749 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_554_152_rev 3', mRNA sequence.	EST_others	-	1.0	-	-2.1	3.65E-02	down	-	0.0
EG885127	gb|EG885127.1	EST_ssal_evf_43515 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_558_059_rev 3', mRNA sequence.	EST_others	2.00E-02	down	-	-2.5	-	-1.6	-	1.3
EG885488	gb|EG885488.1	EST_ssal_evf_43840 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_558_225_rev 3', mRNA sequence.	EST_others	-	-2.5	-	-3.0	2.28E-03	down	-	-2.7
EG886211	gb|EG886211.1	EST_ssal_evf_44490 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_559_176_rev 3', mRNA sequence.	EST_others	-	up	-	0.0	2.73E-05	-103.6	-	down
EG888853	gb|EG888853.1	EST_ssal_evf_46868 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_562_243_fwd 5', mRNA sequence.	EST_others	-	1.5	2.07E-03	down	-	2.2	-	1.7
EG889122	gb|EG889122.1	EST_ssal_evf_47111 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_562_369_rev 3', mRNA sequence.	EST_others	-	0.00	-	-3.7	6.99E-02	down	-	-2.0
EG890543	gb|EG890543.1	EST_ssal_evf_48390 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone	EST_others	-	down	-	down	4.20E-04	down	-	0.0

		ssal_evf_564_275_rev 3', mRNA sequence.									
EG893526	gb|EG893526.1	EST_ssal_evf_51075 ssalevf 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	-7.1	-	down
EG917093	gb|EG917093.1	EST_ssal_evf_56281 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_575_185_rev 3', mRNA sequence.	EST_others	-	down	-	down	2.77E-03	down	-	up
EG917122	gb|EG917122.1	EST_ssal_evf_56307 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_575_198_fwd 5', mRNA sequence.	EST_others	-	-3.3	1.50E-03	down	1.61E-05	down	-	1.1
EG918173	gb|EG918173.1	EST_ssal_evf_57254 ssalevf 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	10.2	-	2.5
EG918652	gb|EG918652.1	EST_ssal_evf_57684 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_577_153_fwd 5', mRNA sequence.	EST_others	-	down	-	down	8.78E-02	-24.8	-	-2.2
EG920601	gb|EG920601.1	EST_ssal_evf_59439 ssalevf 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	down	-	0.0
EG904422	gb|EG904422.1	EST_ssal_evf_7136 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_507_333_fwd 5', mRNA sequence.	EST_others	-	0.00	-	0.0	1.59E-02	down	-	0.0
EG907324	gb|EG907324.1	EST_ssal_evf_9748 ssalevf mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_evf_511_154_fwd 5', mRNA sequence.	EST_others	-	0.00	-	1.2	6.84E-03	up	-	23.1
DW532716	gb|DW532716.1	EST_ssal_plnb_1352 plnb Salmo salar cDNA clone ssal_plnb_011_015_fwd 3', mRNA sequence.	EST_others	-	0.00	3.98E-06	-37.4	-	0.0	-	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	-	0.00	6.22E-03	down	-	0.0	-	0.0
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
DY692525	gb|DY692525.1	EST_ssal_plnb_5435 ssalplnb mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_plnb_025_377_fwd 3', mRNA sequence.	EST_others	5.86E-02	down	5.59E-02	down	-	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	-	0.00	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	-	0.00	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

DW557640	gb|DW557640.1	EST_ssal_rgb2_22059 rgb2 Salmo salar cDNA clone ssal_rgb2_535_331_rev 5', mRNA sequence.	EST_others	-	-1.3	-	-2.1	6.85E-02	-11.0	-	-4.3
DW565146	gb|DW565146.1	EST_ssal_rgb2_29565 rgb2 Salmo salar cDNA clone ssal_rgb2_547_373_rev 5', mRNA sequence.	EST_others	5.86E-02	down	-	down	3.59E-04	-27.7	-	1.8
DW565771	gb|DW565771.1	EST_ssal_rgb2_30190 rgb2 Salmo salar cDNA clone ssal_rgb2_548_373_rev 5', mRNA sequence.	EST_others	-	0.00	-	8.7	7.05E-02	18.8	-	0.0
DW566521	gb|DW566521.1	EST_ssal_rgb2_30940 rgb2 Salmo salar cDNA clone ssal_rgb2_550_051_rev 5', mRNA sequence.	EST_others	-	down	9.39E-03	down	-	down	-	0.0
DW567486	gb|DW567486.1	EST_ssal_rgb2_31905 rgb2 Salmo salar cDNA clone ssal_rgb2_551_261_rev 5', mRNA sequence.	EST_others	-	3.2	-	6.8	3.92E-03	12.8	-	-1.1
DW568758	gb|DW568758.1	EST_ssal_rgb2_33177 rgb2 Salmo salar cDNA clone ssal_rgb2_553_284_rev 5', mRNA sequence.	EST_others	6.54E-03	down	7.76E-04	down	8.45E-06	down	-	0.0
DW570084	gb|DW570084.1	EST_ssal_rgb2_34503 rgb2 Salmo salar cDNA clone ssal_rgb2_555_329_fwd 3', mRNA sequence.	EST_others	-	0.00	3.65E-03	-17.2	-	0.0	-	down
DW539469	gb|DW539469.1	EST_ssal_rgb2_3888 rgb2 Salmo salar cDNA clone ssal_rgb2_507_270_rev 5', mRNA sequence.	EST_others	-	-4.2	-	down	6.99E-02	up	-	up
DW575959	gb|DW575959.1	EST_ssal_rgb2_40378 rgb2 Salmo salar cDNA clone ssal_rgb2_565_232_fwd 3', mRNA sequence.	EST_others	-	-6.9	-	up	4.49E-02	down	-	0.0
DW576807	gb|DW576807.1	EST_ssal_rgb2_41226 rgb2 Salmo salar cDNA clone ssal_rgb2_566_338_rev 5', mRNA sequence.	EST_others	-	2.4	-	-6.2	1.36E-02	-19.3	-	-1.1
DW577325	gb|DW577325.1	EST_ssal_rgb2_41744 rgb2 Salmo salar cDNA clone ssal_rgb2_567_258_rev 5', mRNA sequence.	EST_others	-	down	-	down	7.89E-04	down	-	down
DW578341	gb|DW578341.1	EST_ssal_rgb2_42760 rgb2 Salmo salar cDNA clone ssal_rgb2_569_121_rev 5', mRNA sequence.	EST_others	-	1.2	3.54E-02	down	-	up	-	down
DW581115	gb|DW581115.1	EST_ssal_rgb2_45534 rgb2 Salmo salar cDNA clone ssal_rgb2_573_258_rev 5', mRNA sequence.	EST_others	-	2.1	-	3.5	1.96E-03	up	-	up
DY697537	gb|DY697537.1	EST_ssal_rgb2_53276 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_586_071_fwd 3', mRNA sequence.	EST_others	-	0.00	-	0.0	3.02E-02	down	-	0.0
DW541038	gb|DW541038.1	EST_ssal_rgb2_5457 rgb2 Salmo salar cDNA clone ssal_rgb2_510_041_rev 5', mRNA sequence.	EST_others	-	down	-	down	3.65E-02	down	-	down
DY701339	gb|DY701339.1	EST_ssal_rgb2_57078 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone	EST_others	-	down	-	down	7.24E-05	down	-	down

		ssal_rgb2_592_062_fwd 3', mRNA sequence.									
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	-	0.0	-	down
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	-	-2.7	-	-1.1
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	-	up	-	up	1.57E-03	up
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	-	down	-	0.0	4.39E-02	-15.2	-	0.0
DY715711	gb|DY715711.1	EST_ssal_rgb2_71451 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_615_305_rev 5', mRNA sequence.	EST_others	-	up	3.88E-05	up	-	-1.7	7.28E-04	up
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	-	0.0	-	up
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	-13.0	-	down
DY726856	gb|DY726856.1	EST_ssal_rgb2_82595 ssalrgb2 mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_rgb2_635_205_fwd 3', mRNA sequence.	EST_others	1.81E-04	up	-	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	-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	-15.2	-	up
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
GE767884	gb|GE767884.1	EST_ssal_rgf_835799 ssalrgf mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgf_002_311 3', mRNA sequence.	EST_others	-	-2.1	5.59E-02	down	5.88E-06	-48.9	-	down

GE775959	gb|GE775959.1	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	gb|GE780214.1	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	gb|GE795073.1	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	gb|GE783177.1	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	gb|GE794330.1	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	gb|GE792696.1	EST_ssal_rgf_869097 ssalrgf mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgf_536_009 3', mRNA sequence.	EST_others	-	-1.5	2.18E-02	-6.3	-	1.0	-	1.9
GE793450	gb|GE793450.1	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
GO044564	gb|GO044564.1	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
GO045464	gb|GO045464.1	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	gb|GO045318.1	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
GO054151	gb|GO054151.1	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	gb|GO055970.1	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	gb|GO063143.1	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	gb|GO064603.1	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	gb|GO061981.1	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	gb|GO057448.1	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

		ssal_rgh_508_026 3', mRNA sequence.									
GO057929	gb|GO057929.1	EST_ssal_rgh_1083694 ssalrgh 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	-	down
GO062248	gb|GO062248.1	EST_ssal_rgh_1083855 ssalrgh 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	-	-1.6
GO059796	gb|GO059796.1	EST_ssal_rgh_1086096 ssalrgh 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	-	down
GO064045	gb|GO064045.1	EST_ssal_rgh_1086921 ssalrgh 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	-25.5	-	down
GO058122	gb|GO058122.1	EST_ssal_rgh_1088428 ssalrgh mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_509_076 5', mRNA sequence.	EST_others	-	0.00	5.59E-02	up	-	0.0	-	-1.4
GO059623	gb|GO059623.1	EST_ssal_rgh_1089059 ssalrgh mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_511_323 3', mRNA sequence.	EST_others	-	down	-	down	5.66E-03	down	-	down
GO060238	gb|GO060238.1	EST_ssal_rgh_1090227 ssalrgh mixed_tissue full-length Salmo salar cDNA Salmo salar cDNA clone ssal_rgh_512_339 3', mRNA sequence.	EST_others	-	-3.2	-	-7.9	2.51E-04	-37.3	-	0.0
EG757222	gb|EG757222.1	EST_ssal_sjb_5903 ssalsjb mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_sjb_013_245_fwd 3', mRNA sequence.	EST_others	-	down	-	0.0	3.76E-02	-11.4	-	0.0
EG757601	gb|EG757601.1	EST_ssal_sjb_6246 ssalsjb mixed_tissue Salmo salar cDNA Salmo salar cDNA clone ssal_sjb_014_052_rev 5', mRNA sequence.	EST_others	-	-1.2	-	1.1	4.79E-06	up	-	1.7
BF228600	gb|BF228600.1	EST00311 Atlantic salmon Lambda Zap Express brain cDNA library Salmo salar cDNA clone BNM-134 5', mRNA sequence.	EST_others	-	up	-	1.9	8.79E-02	up	-	0.0
CK873433	gb|CK873433.1	SGP134561 Atlantic salmon Brain cDNA library Salmo salar cDNA clone HJ6-0532 5', mRNA sequence.	EST_others	-	-2.5	7.27E-02	up	-	1.3	-	1.4
CK873617	gb|CK873617.1	SGP134767 Atlantic salmon Brain cDNA library Salmo salar cDNA clone HJ6-0878 5', mRNA sequence.	EST_others	-	0.00	-	0.0	-	0.0	1.36E-04	down
CK876604	gb|CK876604.1	SGP137887 Atlantic salmon Eye cDNA library Salmo salar cDNA clone OY4-0782 5', mRNA sequence.	EST_others	-	3.6	-	2.4	-	down	7.44E-07	60.1
CK893686	gb|CK893686.1	SGP153778 Atlantic salmon Spleen cDNA library Salmo salar cDNA clone MI6-0365 5', mRNA sequence.	EST_others	-	1.2	-	-10.2	2.47E-02	-11.3	-	1.0
CK899155	gb|CK899155.1	SGP162743 Atlantic salmon Testis cDNA library Salmo salar cDNA clone MG4-1507 5', mRNA sequence.	EST_others	-	down	-	down	5.66E-03	down	-	down

CK885162	gb|CK885162.1	SGP165529 Atlantic salmon Intestine cDNA library Salmo salar cDNA clone T4-0448 5', mRNA sequence.	EST_others	-	0.00	-	-1.5	2.73E-05	down	-	-1.0
CN181335	gb|CN181335.1	SGP169629 Atlantic salmon Intestine cDNA library Salmo salar cDNA clone TH5-0120 5', mRNA sequence.	EST_others	-	-3.2	7.85E-02	5.2	-	1.2	-	-1.2
DW471606	gb|DW471606.1	SGP285723 Atlantic salmon Spleen cDNA library Salmo salar cDNA clone MI5-1529 5', mRNA sequence.	EST_others	-	-3.4	-	-16.5	5.30E-03	-16.4	-	down
DW469525	gb|DW469525.1	SGP297862 Atlantic salmon Testis cDNA library Salmo salar cDNA clone MG4-2653 5', mRNA sequence.	EST_others	-	-4.8	-	down	7.05E-02	-17.0	-	down
DW472356	gb|DW472356.1	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	-	0.0
DW473174	gb|DW473174.1	SGP314039 Atlantic salmon Spleen cDNA library Salmo salar cDNA clone MI5-3285 5', mRNA sequence.	EST_others	-	up	7.64E-03	down	-	-6.3	-	0.0
DW473451	gb|DW473451.1	SGP314316 Atlantic salmon Spleen cDNA library Salmo salar cDNA clone MI5-3605 5', mRNA sequence.	EST_others	-	0.00	-	1.0	2.27E-04	down	-	0.0
GT129117	gb|GT129117.1	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	1.00E-02	up
CB501817	gb|CB501817.1	ssalga508249 head Salmo salar cDNA, mRNA sequence.	EST_others	4.69E-02	down	-	0.0	-	0.0	-	0.0
CA037858	gb|CA037858.1	ssallna007071 liver Salmo salar cDNA, mRNA sequence.	EST_others	-	0.00	-	0.0	-	down	8.31E-04	down
CK990829	gb|CK990829.1	ssallna008094 liver Salmo salar cDNA, mRNA sequence.	EST_others	-	0.00	-	0.0	-	0.0	7.68E-02	down
CK991140	gb|CK991140.1	ssallna014053 liver Salmo salar cDNA, mRNA sequence.	EST_others	-	0.00	-	0.0	-	0.0	3.69E-05	down
CA039316	gb|CA039316.1	ssalnwh003073 whole Salmo salar cDNA, mRNA sequence.	EST_others	-	0.00	2.04E-04	-65.3	-	0.0	-	0.0
CA038580	gb|CA038580.1	ssalnwh008031 whole Salmo salar cDNA, mRNA sequence.	EST_others	1.61E-02	down	-	-1.1	-	0.0	-	-3.6
CB511060	gb|CB511060.1	ssalnwh507328 whole Salmo salar cDNA, mRNA sequence.	EST_others	-	0.00	-	down	6.99E-02	down	-	up
CA042597	gb|CA042597.1	ssalplnb501369 gut Salmo salar cDNA, mRNA sequence.	EST_others	-	3.2	-	1.9	3.65E-02	7.3	-	up
CA768031	gb|CA768031.1	ssalplnb510330 gut Salmo salar cDNA, mRNA sequence.	EST_others	7.32E-02	down	-	down	3.59E-04	down	-	0.0
CA042008	gb|CA042008.1	ssalplnb512301 gut Salmo salar cDNA, mRNA sequence.	EST_others	-	-1.6	5.49E-02	5.4	-	2.8	-	1.6
CA054965	gb|CA054965.1	ssalrga510050 mixed_tissue Salmo salar cDNA,	EST_others	-	-1.7	-	1.3	7.56E-02	6.4	-	5.4

		mRNA sequence.									
CA056117	gb|CA056117.1	ssalrgb504092 mixed_tissue Salmo salar cDNA, mRNA sequence.	EST_others	-	down	-	down	3.90E-03	down	-	down
CA057792	gb|CA057792.1	ssalrgb507133 mixed_tissue Salmo salar cDNA, mRNA sequence.	EST_others	-	down	-	-5.1	1.62E-03	-15.2	-	down
CA054786	gb|CA054786.1	ssalrgb511065 mixed_tissue Salmo salar cDNA, mRNA sequence.	EST_others	-	down	-	down	5.65E-02	down	-	down
CX353553	gb|CX353553.1	ssalrgb515206_rev_0 mixed_tissue Salmo salar cDNA, mRNA sequence.	EST_others	-	down	-	down	1.42E-03	down	-	down
CA054240	gb|CA054240.1	ssalrgb517113 mixed_tissue Salmo salar cDNA, mRNA sequence.	EST_others	-	down	-	down	1.96E-03	down	-	0.0
CX357249	gb|CX357249.1	ssalrgb526112_rev_0 mixed_tissue Salmo salar cDNA, mRNA sequence.	EST_others	-	up	-	-4.0	1.96E-02	down	5.60E-04	down
CA058601	gb|CA058601.1	ssalrgb544140 mixed_tissue Salmo salar cDNA, mRNA sequence.	EST_others	-	-6.8	5.76E-04	25.9	-	-2.5	-	down
CB517802	gb|CB517802.1	ssalrgb549316 mixed_tissue Salmo salar cDNA, mRNA sequence.	EST_others	-	3.4	-	down	1.59E-02	down	-	-2.2
CB516646	gb|CB516646.1	ssalrgb555042 mixed_tissue Salmo salar cDNA, mRNA sequence.	EST_others	-	down	-	down	1.59E-02	down	-	0.0
CA049024	gb|CA049024.1	ssalsrkc010094 kidney Salmo salar cDNA, mRNA sequence.	EST_others	-	0.00	-	down	2.43E-02	down	-	up
CB499373	gb|CB499373.1	ssalsrkc016061 kidney Salmo salar cDNA, mRNA sequence.	EST_others	-	down	-	down	2.51E-04	down	-	down
Locus_34577	-	-	-	-	2.1	-	-1.2	-	up	9.83E-03	14.2
Locus_32303	-	-	-	-	0.00	-	0.0	-	0.0	1.15E-02	-34.3
Locus_99680	-	-	-	-	0.00	-	down	-	0.0	1.15E-02	-35.6
Locus_9039	-	-	-	-	-4.3	-	-1.6	-	1.1	9.95E-02	down
Locus_112355	-	-	-	-	0.00	-	0.0	-	0.0	1.19E-02	down
Locus_44033	-	-	-	-	0.00	-	-5.9	-	up	5.91E-02	up
Locus_99603	-	-	-	-	0.00	-	0.0	-	0.0	3.22E-03	up
Locus_22516	-	-	-	-	up	-	1.2	-	1.4	3.74E-02	up
Locus_99354	-	-	-	-	down	-	up	-	up	4.73E-22	up
Locus_36047	-	-	-	-	1.0	-	1.0	1.28E-02	down	-	down
Locus_215	-	-	-	-	2.4	5.78E-02	-7.5	-	-1.3	-	-2.1
Locus_109383	-	-	-	-	-2.5	-	3.9	3.41E-02	-11.7	-	-1.2
Locus_17197	-	-	-	-	1.7	2.87E-03	down	-	-1.1	-	-1.1
Locus_91597	-	-	-	-	-1.2	6.48E-02	5.8	-	-1.4	-	1.1
Locus_16875	-	-	-	-	1.2	9.01E-02	-9.5	-	1.3	-	1.9

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	-	0.0
Locus_63842	-	-	-	3.78E-06	down	-	0.0	-	0.0	-	0.0
Locus_42919	-	-	-	9.35E-14	up	-	0.0	-	0.0	-	0.0
Locus_43483	-	-	-	3.91E-08	up	-	0.0	-	0.0	-	0.0
Locus_43115	-	-	-	1.45E-07	up	-	0.0	-	0.0	-	0.0
Locus_45068	-	-	-	2.87E-07	up	-	0.0	-	0.0	-	0.0
Locus_43319	-	-	-	8.82E-07	up	-	0.0	-	0.0	-	0.0
Locus_47644	-	-	-	2.14E-06	up	-	0.0	-	0.0	-	0.0
Locus_45727	-	-	-	5.37E-06	up	-	0.0	-	0.0	-	0.0
Locus_43795	-	-	-	8.08E-06	up	-	0.0	-	0.0	-	0.0
Locus_80358	-	-	-	1.21E-04	up	-	0.0	-	0.0	-	0.0
Locus_46093	-	-	-	7.42E-04	up	-	0.0	-	0.0	-	0.0
Locus_80642	-	-	-	1.15E-02	up	-	0.0	-	0.0	-	0.0
Locus_81054	-	-	-	1.61E-02	up	-	0.0	-	0.0	-	0.0
Locus_80712	-	-	-	7.32E-02	up	-	0.0	-	0.0	-	0.0
Locus_56467	-	-	-	-	2.8	-	1.0	6.04E-02	19.6	-	0.0
Locus_52222	-	-	-	-	4.7	2.56E-02	10.2	-	up	-	0.0
Locus_90954	-	-	-	-	0.00	9.17E-02	21.3	-	0.0	-	0.0
Locus_21308	-	-	-	3.14E-17	up	-	down	-	0.0	-	0.0
Locus_52406	-	-	-	-	0.00	1.03E-05	up	-	0.0	-	0.0
Locus_43970	-	-	-	1.76E-07	up	-	0.0	-	0.0	-	up
Locus_21331	-	-	-	2.80E-15	up	-	0.0	-	0.0	-	up