Table S1. Expression data tables of significant genes not presented in main figures

Α	Unstream	signaling	genes during	osmotic stress	s in	Gillichthys	mirahilis

				Significant expression	
Gene product	Putative function during osmotic stress	Functional category	Osmotic stress	Time	Max fold change
ransforming growth factor β (TGF-β) II receptor	Propagation of transforming growth factor β signaling	Signaling	Нуро	12	1.68±0.10
Prostaglandin E2 synthase	Regulation of prostaglandin production – water permeability	Signaling	Hyper	12	-1.25±0.08
stradiol-17-β dehydrogenase	Regulation of estradiol production	Signaling	Нуро	12	-1.61±0.10
leural derived orphan receptor1 (NOR-1)	Regulation of steroid receptor activity	Signaling	Hyper	4, 12	1.52±0.11
roline rich nuclear receptor coactivator 2 (PNRC-2)	Activation of nuclear receptors	Signaling	Hyper	4	1.57±0.16
disintegrin and metalloproteinase (ADAM) 17 recursor	Regulation of tumor necrosis factor signaling	Signaling	Hyper	2, 4	-1.30±0.07
Class 1 helical cytokine receptor	Cytokine signal transduction	Signaling	Hyper	12	-1.59±0.08
GTP cyclohydrolase 1	Regulation of nitrous oxide production	Signaling	Hyper	2	1.54±0.10
legulator of G-protein signaling 14	Regulation of G-protein receptor signal transduction	Signaling	Hyper	12	-1.39±0.08
Short chain dehydrogenase/reductase	Regulation of steroid hormone activity	Signaling	Hyper / Hypo	1/2	-1.39±0.10 / -1.37±0.0
-2-HS glycoprotein	Regulation of insulin like growth factor-1 signaling	Signaling	Нуро	2	-1.49±0.07
Pellino 1	Scaffold protein for intracellular receptors	Signaling	Нуро	2	-1.67±0.06
Receptor-associated protein of the synapse	Stabilization of transmembrane receptors	Signaling	Нуро	2	-1.49±0.07
Retinoid X receptor β	Regulation of steroid receptor activity	Signaling	Нуро	2	1.61±0.08
Scavenger receptor class B, member 2	Regulation of cell adhesion	Signaling	Нуро	2	1.46±0.10
Cenotropic and polytropic retrovirus receptor	G-protein receptor signal transduction	Signaling	Нуро	12	1.36±0.06
yn tyrosine kinase eceptor type tyrosine protein phosphatase $\gamma$ (RPTP $\gamma$ ) lyotubularin-related protein 14 casein kinase II $\beta$ subunit (CKII- $\beta$ ) CY-1 like protein rotein arginine methyltransferase 5 isoform 1	Propagation of receptor tyrosine kinase signal transduction Regulation of receptor tyrosine kinase signal transduction Regulation of phosphatidylinositol production Putative osmosensor – kinase activity-multiple substrates Kinase activity – regulation of protein transport JAK/STAT signal transduction	Signaling Signaling Signaling Signaling Signaling Signaling	Hyper Hyper Hyper Hyper Hypo Hypo	1 1 1 12 1 2	1.27±0.09 -1.35±0.07 -1.54±0.07 -1.32±010 -1.59±0.06 1.34±0.06
C. Osmotic effectors during osmotic stress in Gillichthys	mirabilis – Ion homeostasis				
System N amino acid transporter 1 (SNAT-1)	Sodium ion transport	Ion homeostasis	Hyper	4, 12	1.96±0.07
arbonic anhydrase	Regulation of hydrogen ion homeostasis – pH regulation	Ion homeostasis	Hyper	1, 4	1.92±0.16
odium/sialic acid co-transporter	Sodium ion transport	Ion homeostasis	Hyper	4	-1.45±0.08
Potassium channel auxillary subunit	Potassium ion transport	Ion homeostasis	Нуро	2	-1.67±0.12
Osmotic effectors during osmotic stress in Gillichthys	mirabilis – Organic osmolytes				
Arginase II precursor	Regulation of urea production	Osmolyte	Hyper	4	2.10±0.24
E. Osmotic effectors during osmotic stress in Gillichthys	mirabilis - Cytoskeleton	•	71		
5kDa erythrocyte membrane protein	Stablization of cell shape through cytoskeletal membrane linkages	Cytoskeleton	Hyper	12	1.33±0.12
IID1 interacting protein	Stabilization of microtubules	Cytoskeleton	Hyper	2	-1.64±0.06
ebulin	Bind and stabilize F-actin	Cytoskeleton	Hyper	2, 4, 12	2.02±0.23
nkyrin-repeat domain containing protein 40	Regulation of cytoskeletal – membrane protein interactions	Cytoskeleton	Нуро	12	-1.23±0.07
	÷	,			
Shroom 2	Regulation of cell shape <i>via</i> F-actin interaction	Cytoskeleton	Hypo	1	-1.23±0.07

Numb-binding protein 2 Numb-binding protein 3 Numb-binding protein 3 Numb-binding protein 4		2				
Myosin light chain 1	Kelch and BTB domain containing protein 2	Adaptor protein for ubiquitin ligases regulating cell shape	Cytoskeleton	Нуро	4, 12	-1.32±0.07
receipt a montality process of the p	Numb-binding protein 2	Regulation of cytoskeletal – membrane protein interactions	Cytoskeleton	Нуро	12	1.38±0.07
Analysin 2 Regulation of cytoskeletal — membrane protein interactions	Myosin light chain 1	. , ,	Cytoskeleton	Нуро	1	1.27±0.09
E. Demolic offectors during osmotic stross in Gillichthys mirabilis — Extracellular matrix  Buildous peraphsigoid antiqen 1  Linker protein mediating cytoskeletal-ECM interaction Insular protein mediating cytoskeletal-ECM integral protein cross- Insular protein mediating cytoskeletal-ECM integral protein cytoskeletal-ECM interaction Insular protein mediating cytoskeletal-ECM integral protein protei	Plectin 1	Stabilization of cytoskeletal intermediate filament network	Cytoskeleton	Нуро	12	1.42±0.08
Bullous pemphigoid antigen 1 Linker protein mediating cytoskeletal-ECM Interaction Regulation of cell adhesion - catalyzes protein cross- ECM Hyper 2,4 1,326,009 Tubuloimferstital neghritis antigen procursor Regulation of cell adhesion - catalyzes protein cross- ECM Hyper 12 1,880,011 Tubuloimferstital neghritis antigen procursor Regulation of cell adhesion via integrin interaction ECM Hyper 12 1,880,011 ECM Hyper 2,4 1,1540,09 Fibrinogen, a chain Regulation of cell adhesion via integrin interaction Regulation of cell adhesion via firmation ECM Hyper 2 1,1540,09 Fibrinogen, a chain Regulation of cell adhesion via firmation of librin ECM Hyper 2,1 1,1544,008 RECM Hyper 12 1,1544,008 RECM Hyper 2,4 1,12 1,1544,008 RECM Hyper 3,12 1,132 Recommendation of the ECM Hyper 3,12 1,132 Recommendation of the ECM Hyper 3,132 Recommendation of	Ankyrin 2	Regulation of cytoskeletal – membrane protein interactions	Cytoskeleton	• •	2, 4	-1.59±0.05
Bullous pemphigoid antigen 1 Linker protein mediating cytoskeletal-ECM Interaction Regulation of cell adhesion - catalyzes protein cross- ECM Hyper 2,4 1,326,009 Tubuloimferstital neghritis antigen procursor Regulation of cell adhesion - catalyzes protein cross- ECM Hyper 12 1,880,011 Tubuloimferstital neghritis antigen procursor Regulation of cell adhesion via integrin interaction ECM Hyper 12 1,880,011 ECM Hyper 2,4 1,1540,09 Fibrinogen, a chain Regulation of cell adhesion via integrin interaction Regulation of cell adhesion via firmation ECM Hyper 2 1,1540,09 Fibrinogen, a chain Regulation of cell adhesion via firmation of librin ECM Hyper 2,1 1,1544,008 RECM Hyper 12 1,1544,008 RECM Hyper 2,4 1,12 1,1544,008 RECM Hyper 3,12 1,132 Recommendation of the ECM Hyper 3,12 1,132 Recommendation of the ECM Hyper 3,132 Recommendation of	F. Osmotic effectors during osmotic stress in Gillichth	ys mirabilis – Extracellular matrix				
Tubulointersitial nephritis antigen precursor Regulation of cell adhesion via integrin interaction ECM Hyper   12   1.80±0.11 [Gm. 40e12] Sa parvin   Regulation of cell adhesion via integrin interaction   ECM Hypo   2   -1.45±0.09   Fibrinogon, a Chain   Regulation of cell adhesion via integrin interaction   ECM Hypo   2   -1.75±0.06   Fibrinogon, a Chain   Regulation of cell adhesion via formation of fibrin   ECM Hypo   2   -1.75±0.06   Fibrinogon, a Chain   Regulation of adhesion, migration and tissue organization   ECM Hyper / Hypo   1/12   -1.28±0.09   Fibrinogon, a Chain   Regulation of adhesion, migration and tissue organization   ECM Hyper / Hypo   1/2   -1.28±0.00   Fibrinogon, a Chain   Regulation of the ECM Stabilization of the ECM Hyper   ECM Hyper   1/2   -1.28±0.00   Fibrinogon, a Chain   Regulation of the ECM ECM Hyper   1/2   -1.28±0.00   Fibrinogon, a Chain   Regulation of the ECM ECM Hyper   1/2   -1.69±0.05   Fibrinogon, a Chain   Regulation of the ECM ECM Hyper   1/2   -1.69±0.05   Fibrinogon   Regulation of the ECM ECM Hyper   1/2   -1.59±0.09 / 1.42±0.00   Fibrinogon   Regulation of the ECM ECM Hyper   1/2   -1.59±0.09 / 1.42±0.00   Fibrinogon   Regulation of the ECM ECM Hyper   1/2   -1.59±0.00 / 1.79±0.00   Fibrinogon   Regulation of the ECM EcM Hyper   1/2   -1.59±0.00 / 1.79±0.00   Fibrinogon   Regulation of the ECM EcM Hyper   1/2   -1.59±0.00 / 1.79±0.00   Fibrinogon   Regulation of the ECM EcM Hyper   1/2   -1.59±0.00 / 1.79±0.00   Fibrinogon   Regulation of the ECM EcM Hyper   1/2   -1.59±0.00 / 1.79±0.00   Fibrinogon   Regulation of calcium ion acid availability   Regulation of the ECM Hyper   1/2   -1.43±0.00 / 1.79±0.00   Fibrinogon   Regulation of calcium ion availability   Calcium homeostasis   Hyper   1/2   -1.43±0.00 / 1.79±0.00   Fibrinogon   Regulation of calcium ion availability   Calcium homeostasis   Hyper   1/2   -1.59±0.00   Fibrinogon   Regulation of calcium ion availability   Calcium homeostasis   Hyper   1/2   -1.59±0.00   Fibrinogon   Regulation of chromosomal reco	Bullous pemphigoid antigen 1		ECM	Hyper	2	1.32±0.09
Gim_40o12	Tissue transglutaminase	, ,	ECM	Hyper	2, 4	1.88±0.01
Fibringogn, a chain	Tubulointerstitial nephritis antigen precursor (Gm_40e12)	Regulation of cell adhesion via integrin interaction	ECM	Hyper	12	1.80±0.11
Laminin p-1 chain precursor Regulation of adhesion, migration and tissue organization Putative somosensor – anti-adhesive properties RCM Hyper 12 -1.54±0.08 / -1.59±0.00 RCM Hyper 12 -1.28±0.09 RCM Hyper 12 -1.28±0.09 RCM Hyper 12 -1.69±0.05 RCM Hyper 14 -1.69±0.05 RCM Hyper 15 -1.69±0.05 RCM Hyper 17 -1.69±0.05 RCM Hyper 18 -1.69±0.05 RCM Hyper 19 -1.69±0.05 RCM	α parvin	Regulation of cell adhesion via integrin interaction	ECM	Нуро	2	-1.45±0.09
Muclin-4 Putative osmosensor - anti-adhesive properties ECM Hyper 12 -1.28±0.09 inter-ut typsin inhibitor heavy chain 3 (Gm_AB08) Stabilization of the ECM ECM Hypo 2, 4, 12 -1.67±0.06 inter-ut typsin inhibitor heavy chain 3A Stabilization of the ECM ECM Hypo 2, 4, 12 -1.69±0.05 inter-ut typsin inhibitor heavy chain 3A Stabilization of the ECM ECM Hypo 2, 4, 12 -1.69±0.05 inter-ut typsin inhibitor heavy chain 3A Stabilization of the ECM ECM Hypo 2, 4, 12 -1.69±0.05 inter-ut typsin inhibitor heavy chain 3A Stabilization of the ECM ECM Hypo 1, 12, 4 -1.39±0.09 (-1.42±0.05 ECM Hypor Aprecursor Broad specificity proteolytic activity a. a. metabolism Hyper (Hypo 1, 12, 4 -1.39±0.09 (-1.79±0.05 ECM Hypor) (Fig. 4) -1.59±0.07 (Fig. 4) -1.69±0.07 (Fig. 4) -1.69	Fibrinogen, α chain	Regulation of cell adhesion via formation of fibrin	ECM	Нуро	2	-1.75±0.06
Mucin-4 Putative osmosensor - anti-adhesive properties ECM Hyper 12 -1.2240.09 inter-a trypsin inhibitor heavy chain 3 (Gm_AB08) Stabilization of the ECM ECM Hypo 2, 4 -1.6740.06 inter-a trypsin inhibitor heavy chain 3 (Gm_AB08) Stabilization of the ECM ECM Hypo 2, 4, 12 -1.6940.05  G. Osmotic effectors during osmotic stress in Gillichthys mirabilis - Amino acid metabolism  Pepsin A precursor  Broad specificity proteolytic activity a. a. metabolism Hyper / Hypo 1/2, 4 -1.3940.09 / -1.4240.07  Prosine animotransferase Regulation of free amino acid availability a. a. metabolism Hyper / Hypo 1/1 -1.5940.07 / -1.7940.07  Prosine animotransferase Regulation of free amino acid availability a. a. metabolism Hyper / Hypo 1/1 -1.5940.07 / -1.7940.07  Prosine animotransferase Regulation of free amino acid availability a. a. metabolism Hyper / Hypo 1/2 -1.4340.06 / -1.6740.18  H. Osmotic effectors during osmotic stress in Gillichthys mirabilis - Calcium in homeostasis  Propertine P450 24A1 (Gm_CD22) Regulation of vitamin D synthesis Calcium homeostasis Hyper 1/2 -2.1360.13  Providence P450 24A1 (Gm_CD22) Regulation of calcium in availability Calcium homeostasis Hyper 1/2 -2.1360.13  Providence P450 24A1 (Gm_CD22) Regulation of calcium in availability Calcium homeostasis Hyper 1/2 -2.1360.13  Providence P450 24A1 (Gm_CD22) Regulation of calcium in availability Calcium homeostasis Hyper 1/2 -2.1360.13  Providence P450 24A1 (Gm_CD22) Regulation of calcium in availability Calcium homeostasis Hyper 1/2 -2.1360.13  Providence P450 24A1 (Gm_CD22) Regulation of calcium in availability Calcium homeostasis Hyper 1/2 -2.16740.11  Providence P450 24A1 (Gm_CD22) Regulation of calcium in availability Calcium homeostasis Hyper 1/4 (Regulation of Acidium	•	Regulation of adhesion, migration and tissue organization	ECM		1 / 12	-1.54±0.08 / -1.59±0.05
Inter-a typsin inhibitor heavy chain 3 (Gm_AB08) Stabilization of the ECM ECM Hypo 2, 4, 1-1,67±0.06 ECM Hypo 2, 4, 1-1,67±0.05 stabilization of the ECM ECM Hypo 2, 4, 12 -1,69±0.05 eCM Hypo 1,10	Mucin-4		ECM		12	-1.28±0.09
Ca. Osmotic effectors during osmotic stress in <i>Gillichthys mirabilis</i> — Amino acid metabolism  Pepsin A precursor  Broad specificity proteolytic activity a. a.a. metabolism Hyper / Hypo 1 / 2, 4	Intra-α trypsin inhibitor heavy chain 3 (Gm. AB08)	Stabilization of the ECM	ECM		2. 4	-1.67±0.06
Pepsin A procursor Regulation of free amino acid availability a.a. metabolism Hyper / Hypo 1 / 2, 4 -1.39±0.09 / -1.42±0.07 Hrosine aminotransferase Regulation of free amino acid availability a.a. metabolism Hyper / Hypo 1 / 1 -1.59±0.07 / -1.79±0.07 Hyposine aminotransferase Regulation of free amino acid availability Alanine-glyoxalate amino transferase Glyoxylate metabolism Alanine-glyoxalate amino transferase Glyoxylate metabolism Hyper / Hypo 2 / 2, 12 -1.43±0.06 / -1.67±0.15 H, Osmotic effectors during osmotic stress in Gillichthys mirabilis – Calcium ion homeostasis Cytochrome P450 24A1 (Gm_CD22) Regulation of vitamin D synthesis Cytochrome P450 24A1 (Gm_CD22) Regulation of calcium deposition in otolith Glacium homeostasis Hyper 1 2 -2.13±0.13 Grancalcin Regulation of calcium availability Calcium homeostasis Hypo 1 2 -1.49±0.07 Parvalburuin-like protein Regulation of calcium ion availability Calcium homeostasis Hypo 2 -1.59±0.07 Eloxomati interacting molecule Regulation of calcium ion availability Calcium homeostasis Hypo 1 2 -1.67±0.11  L Osmotic effectors during osmotic stress in Gillichthys mirabilis – Cell cycle Growth arrest and DNA damage inducible protein 45 Regulation of chromosomal recombination Cell cycle Hypo 2 -1.67±0.10  GADD45) RAD 54 Regulation of chromatin structure Cell cycle Hypo 2 2 2.96±0.26  Kelch-like protein 13 Adaptor protein for ubiquitin ligases regulating cell cycle Cell cycle Hyper 1 2 -1.54±0.07  Eloposide induced 2.4 mRNA isoform 1 Induction of apoptosis Cell cycle Hyper 1 1 -1.56±0.07  Hyper 1 2 -1.58±0.07  Hyper 1 2 -1.58±0.07  Hyper 1 2 -1.58±0.07  Hyper 1 3 -1.59±0.07  Hyper 1 4 1.61±0.06  Evotransferrin I ron homeostasis Hyper / Hypo 2, 1, 2	Inter-α trypsin inhibitor heavy chain 3A	Stabilization of the ECM	ECM	• • •		-1.69±0.05
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Threonine dearminase Regulation of free amino acid availability a.a. a. metabolism Hyper 2 1.53±0.15 Alanine-glyoxalate amino transferase Glyoxylate metabolism a.a. metabolism Hyper / Hypo 2 / 2 , 12 -1.43±0.06 / -1.67±0.15 Alanine-glyoxalate amino transferase Glyoxylate metabolism Calcium for a.a. metabolism Hyper 4, 12 -1.43±0.06 / -1.67±0.15 Alanine-glyoxalate amino transferase Glyoxylate metabolism on homeostasis  Hyper 4, 12 -1.55±0.08 Calcium homeostasis Hyper 12 -2.13±0.13 Cancalcin Regulation of calcium for calcium for oxidity Calcium homeostasis Hyper 12 -2.13±0.13 Cancalcin Regulation of calcium ion availability Calcium homeostasis Hypo 12 -1.49±0.07 Alarvalbumin-like protein Regulation of calcium ion availability Calcium homeostasis Hypo 12 -1.67±0.11 Calcium homeostasis Hypo 2 -1.67±0.10 Calcium homeostasis Hypo 2 -1.67±0.00 Calcium homeostasis Hypo 2 -1.67±0.00 Calcium homeostasis Calcium homeostasis Calcium homeostasis Hypo 2 -1.67±0.00 Calcium homeostasis Hypo 2 -1.67±0.00 Calcium homeostasis Calcium homeostasis Hypo 2 -1.67±0.00 Calcium homeostasis Hypo 2 -1.67±0.00 Calcium homeostasis Calcium homeostasis Hypo 2 -1.67±0.00 Calcium homeostasis Hypo 2 -1.67±0.00 Calcium homeostasis Calcium homeostasis Hypor Calcium homeostasis Calcium homeostasis Hypor Calcium homeostasis Hypor Calcium homeostasis Calcium homeosta	•	, ,, ,		,, ,,	,	
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Myeloid leukemia differentiation protein Regulation of cell proliferation Cell cycle Hyper 4 1.62±0.14  J. Osmotic effectors during osmotic stress in <i>Gillichthys mirabilis</i> – Iron homeostasis  Serotransferrin I Iron homeostasis Hypo 4 -1.61±0.06  Serotransferrin I precursor (Gm_AK17) Iron ion transport Iron homeostasis Hyper / Hypo 2, 12 / 2, 4, 12 -1.28±0.06 / -1.67±0.06  Feline leukemia virus subgroup C receptor related Exporter of cytoplasmic heme Iron homeostasis Hyper 12 -1.49±0.10  protein	Etoposide induced 2.4 mRNA isoform 1	Induction of apoptosis	Cell cycle	Hyper	1	-1.56±0.07
J. Osmotic effectors during osmotic stress in <i>Gillichthys mirabilis</i> – Iron homeostasis  Serotransferrin I Iron homeostasis Hypo 4 –1.61±0.06  Serotransferrin I precursor (Gm_AK17) Iron ion transport Iron homeostasis Hyper / Hypo 2, 12 / 2, 4, 12 –1.28±0.06 / –1.67±0.06  Feline leukemia virus subgroup C receptor related Exporter of cytoplasmic heme Iron homeostasis Hyper 12 –1.49±0.10  protein	Histone H1 family, member 0	Regulation of chromatin structure	Cell cycle	Hyper	4, 12	-1.89±0.08
Serotransferrin I Iron homeostasis Hypo 4 -1.61±0.06 Serotransferrin I precursor (Gm_AK17) Iron ion transport Iron homeostasis Hyper / Hypo 2, 12 / 2, 4, 12 -1.28±0.06 / -1.67±0.06 Feline leukemia virus subgroup C receptor related Exporter of cytoplasmic heme Iron homeostasis Hyper 12 -1.49±0.10 protein	Myeloid leukemia differentiation protein	Regulation of cell proliferation	Cell cycle	Hyper	4	1.62±0.14
Serotransferrin I Iron homeostasis Hypo 4 -1.61±0.06 Serotransferrin I precursor (Gm_AK17) Iron ion transport Iron homeostasis Hyper / Hypo 2, 12 / 2, 4, 12 -1.28±0.06 / -1.67±0.06 Feline leukemia virus subgroup C receptor related Exporter of cytoplasmic heme Iron homeostasis Hyper 12 -1.49±0.10 protein	L Cematic affactors during asmatic stress in Cilliabth	ve mirabilie – Iron homooetasis				
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Feline leukemia virus subgroup C receptor related Exporter of cytoplasmic heme Iron homeostasis Hyper 12 -1.49±0.10 protein		·			•	
protein	. , – ,	•				
Hemopexin-like protein Iron ion transport Iron homeostasis Hyper 12 1.52±0.08	protein	ехронег от суюріавнію пеніе				
	Hemopexin-like protein	Iron ion transport	Iron homeostasis	Hyper	12	1.52±0.08

K. Osmotic effectors during osmotic stress in <i>Gillichth</i> y $\gamma$ interferon lysosomal thiol reductase	Facilitates protein unfolding for degradation in lysosome	Molecular degradation	Hyper	12	-1.49±0.07
Cytochrome P450 1A1 (Gm_BM11)	Oxidation of steroids or fatty acids	Molecular degradation	Hyper / Hypo	4, 12 / 1, 2, 4	1.87±0.30 / 2.58±0.18
Microsomal glutathione S transferase	Remediation of oxidative stress	Molecular degradation	Нуро	2	-1.22±0.06
Myeloperoxidase precursor	Anti-apoptotic properties responsive to oxidative stress	Molecular degradation	Hyper	2	1.57±0.07
Arylsulfatase A precursor	Desulfation of lipid rafts-may reduce Na <sup>+</sup> , K <sup>+</sup> -ATPase	Molecular degradation	Нуро	12	2.00±0.15
Aryiounatase A precursor	activity	Moleculai degradation	Пуро	12	2.0010.13
Peroxisomal N1-acetyl-spermine oxidase	Regulation of polyamine homoestasis	Molecular degradation	Нуро	12	-1.37±0.06
L. Osmotic effectors during osmotic stress in Gillichthy	vs mirabilis – Protein synthesis				
40S ribosomal protein S8	Regulation of protein synthesis	Protein synthesis	Hyper	2	-1.64±0.05
40S ribosomal protein 27A	Regulation of protein synthesis	Protein synthesis	Нуро	1	1.70±0.12
60S ribosomal protein L38	Regulation of protein synthesis	Protein synthesis	Нуро	1	1.90±0.15
Ribosomal protein L7	Regulation of protein synthesis	Protein synthesis	Нуро	2, 12	-1.89±0.07
Eukaryotic translation initiation factor 4 γ 2	Regulation of translation initiation	Protein synthesis	Hyper	4, 12	1.92±0.13
AA Oomeakin official and district contact of the character of the characte	ve minabilia. Duakain kuaffiakin s				
M. Osmotic effectors during osmotic stress in Gillichth	·	Drotoin troffiction	Hunor / Llime :	1.0/1.0	-1.67±0.07 / -1.96±0.07
Mannose receptor C type 2 (Gm_Al03)	Regulation of receptor mediated endocytosis	Protein trafficking	Hyper / Hypo	1, 2 / 1, 2	
β 1, 3 galactosyl transferase 7	Regulation of post-translational protein glycosylation	Protein trafficking	Hyper / Hypo	1/4	-1.20±0.07 / -1.37±0.06
Secretory carrier-associated membrane protein 1 (Gm_34d11)	Carrier of recycled protein to the cell surface	Protein trafficking	Hyper / Hypo	4, 12 / 1, 2	-1.25±0.10 / 1.22±0.07
ADP-ribosylation factor-like protein 8	Small GTPase affecting protein transport	Protein trafficking	Hyper	12	-1.35±0.08
Hermansky-pudlak syndrome 1	Regulation of intracellular protein sorting	Protein trafficking	Hyper	2, 4	-1.30±0.07
x 1, 3 glucosyl-transferase 8	Regulation of post-translational protein glycosylation	Protein trafficking	Hyper	12	1.23±0.08
ΓBC1 domain family member 17	Small GTPase affecting protein transport	Protein trafficking	Hyper	1	1.50±0.08
Vacuolar sorting protein 45A	Regulation of vesicle - mediated transport through Golgi	Protein trafficking	Нуро	2	-1.32±0.09
Protein disulfide isomerase A6 precursor	Rearrangement of disulfide bonds in proteins	Protein trafficking	Нуро	1	-1.19±0.06
N. Osmotic effectors during osmotic stress in Gillichth	ve mirahilie – Protoniveie				
Elastase 1 precursor	Hydrolysis of proteins-possibly IGFBP-1	Proteolysis	Hyper / Hypo	2/4	-1.49±0.07 / -1.62±0.06
Serine protease inhibitor clade A member 1	Elastase inhibitor	Proteolysis	Hyper	2	-1.43±0.07 / -1.02±0.00
Elastase 4-like protein	Hydrolysis of proteins-possibly IGFBP-1	Proteolysis	Нуро	2	-1.39±0.07
RING finger protein 87	Ubiquitin ligase activity	Proteolysis	Hyper	12	-1.37±0.08
Till d linger protein of	Obiquini ngase activity	1 Toteorysis	Пурег	12	-1.07 ±0.00
O. Osmotic effectors during osmotic stress in Gillichth	· •	<del>-</del>			1.00.0.10
Butyrate response factor 2 (Gm_15e01)	Regulation of the response to growth factors	Transcription regulation	Hyper	2, 4	1.82±0.18
CCAAT/enhancer binding protein Δ (Gm_14h20)	Regulation of the response to MAPK signaling	Transcription regulation	Hyper	2, 4	3.24±0.35
C-ets-2 protein	Regulation of the response to MAPK signaling	Transcription regulation	Hyper	12	-1.85±0.09
Hepatic leukemia factor	Regulation of the repsonse to cytokine signaling	Transcription regulation	Hyper	4, 12	2.48±0.22
Nucler factor interleukin 3 regulated (Gm_17e08)	Regulation of the response to growth factors	Transcription regulation	Hyper	4, 12	1.66±0.14
Sox 21	Regulation of cellular differentiation events	Transcription regulation	Hyper	1	-1.49±0.08
Tob1 protein (Gm_AC09)	Cell growth regulation – anti-proliferative activity	Transcription regulation	Hyper	4, 12	1.77±0.10
Franscription factor Sp1	Regulation of the response to MAPK signaling	Transcription regulation	Hyper	4, 12	-1.32±0.10
Chick ovalbumin upstream promoter (COUP) ranscription factor	Regulation of the response to glucocorticoids	Transcription regulation	Нуро	4	-1.33±0.07
•	Transcriptional regulation of stress responsive genes	Transcription regulation	Нуро	12	1.50±0.10
General negative regulator of transcription subunit 1			75-	<del>-</del>	
General negative regulator of transcription subunit 1 Nucleolar protein 11		Transcription regulation	Hypo	1	-1.56±0.05
General negative regulator of transcription subunit 1 Nucleolar protein 11 Something about silencing protein 10	Regulation of rRNA transcription  Promotion of gene silencing-chromatin structure	Transcription regulation Transcription regulation	Нуро Нуро	1 1	-1.56±0.05 -1.35±0.06

Apolipoprotein L	Regulation of cholesterol production	Cholesterol metabolism	Hyper	1	1.66±0.24
Apolipoprotein A	Regulation of cholesterol production	Cholesterol metabolism	Нуро	4	-1.43±0.05
Cholesteryl ester transfer protein precursor	Transport of cholesterol	Cholesterol metabolism	Нуро	2	-1.35±0.06
Q. Osmotic effectors during osmotic stress in Gillichthys	s mirabilis – Energy/Metabolism				_
6-phosphofructo-2-kinase/fructose 2,6 bisphosphatase	Aerobic carbohydrate metabolism	Energy/metabolism	Hyper	12	2.02±0.13
4 (Gm_BN17)					
Adenine nucleotide translocator S598	ATP transport	Energy/metabolism	Hyper	1	-1.52±0.08
Elongation of very long chain fatty acids 3	Lipid biosynthesis	Energy/metabolism	Hyper	4, 12	1.85±0.18
NADH dehydrogenase subunit 1	Electron transport – ATP production	Energy/metabolism	Hyper	1, 4, 12	-1.75±0.07
Succinate dehydrogenase complex subunit A	Aerobic carbohydrate metabolism	Energy/metabolism	Hyper	1	-1.31±0.07
Butyrophilin 2A2 (Gm_46i15)	Lipid metabolism	Energy/metabolism	Hyper	12	-1.39±0.08
γ-butyrobetaine dioxygenase	Carnitine biosynthesis – lipid metabolism	Energy/metabolism	Hyper / Hypo	1 / 4	-1.39±0.07 / -1.52±0.05
Glycerophosphoryl phosphodiesterase 2	Glycerol metabolism – lipid metabolism	Energy/metabolism	Hyper / Hypo	12 / 1	-1.47±0.08 / -1.43±0.05
Lactate dehydrogenase A chain (Gm_DI16)	Anaerobic carbohydrate metabolism	Energy/metabolism	Hyper / Hypo	4 / 12	1.54±0.09 / -1.75±0.07
C1q adipose specific protein	Lipid metabolism	Energy/metabolism	Hyper / Hypo	12 / 1, 2, 4	-1.47±0.08 / -1.85±0.05
Cytochrome c oxidase subunit 1 (Gm_10c18)	Electron transport – ATP production	Energy/metabolism	Hyper / Hypo	1, 2, 12	-1.92±0.05 / -1.69±0.13
Glycerol-3-phosphate dehydrogenase	Glycerol metabolism - lipid metabolism	Energy/metabolism	Нуро	4	-1.25±0.07
Lysosomal α mannosidase precursor	Lysosomal carbohydrate metabolism	Energy/metabolism	Нуро	12	1.24±0.06
Facilitated glucose transporter	Glucose transport	Energy/metabolism	Нуро	12	-1.64±0.13
Very long chain acyl-CoA synthetase	Lipid metabolism	Energy/metabolism	Нуро	4	-1.12±0.09

## NOTES:

- -In cases of a single gene represented by multiple significant features (those proceeded by a clone ID) the feature with the strongest P-value was displayed
- -Putative functions during osmotic stress and functional categories were assigned based upon data contained with the Gene Ontology database, UniProt and the primary literature Abbreviations

Hyper = significant during hyperosmotic stress

Hypo = significant during hypo-osmotic stress

ECM = extracellular matrix

a.a. = amino acid