

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

A. Upstream signaling genes during osmotic stress in <i>Gillichthys mirabilis</i>					
Gene product	Putative function during osmotic stress	Functional category	Osmotic stress	Significant expression Time	Max fold change
Transforming growth factor β (TGF- β) II receptor	Propagation of transforming growth factor β signaling	Signaling	Hypo	12	1.68 \pm 0.10
Prostaglandin E2 synthase	Regulation of prostaglandin production – water permeability	Signaling	Hyper	12	-1.25 \pm 0.08
Estradiol-17- β dehydrogenase	Regulation of estradiol production	Signaling	Hypo	12	-1.61 \pm 0.10
Neural derived orphan receptor1 (NOR-1)	Regulation of steroid receptor activity	Signaling	Hyper	4, 12	1.52 \pm 0.11
Proline rich nuclear receptor coactivator 2 (PNRC-2)	Activation of nuclear receptors	Signaling	Hyper	4	1.57 \pm 0.16
A disintegrin and metalloproteinase (ADAM) 17 precursor	Regulation of tumor necrosis factor signaling	Signaling	Hyper	2, 4	-1.30 \pm 0.07
Class 1 helical cytokine receptor	Cytokine signal transduction	Signaling	Hyper	12	-1.59 \pm 0.08
GTP cyclohydrolase 1	Regulation of nitrous oxide production	Signaling	Hyper	2	1.54 \pm 0.10
Regulator of G-protein signaling 14	Regulation of G-protein receptor signal transduction	Signaling	Hyper	12	-1.39 \pm 0.08
Short chain dehydrogenase/reductase	Regulation of steroid hormone activity	Signaling	Hyper / Hypo	1/2	-1.39 \pm 0.10 / -1.37 \pm 0.06
α -2-HS glycoprotein	Regulation of insulin like growth factor-1 signaling	Signaling	Hypo	2	-1.49 \pm 0.07
Pellino 1	Scaffold protein for intracellular receptors	Signaling	Hypo	2	-1.67 \pm 0.06
Receptor-associated protein of the synapse	Stabilization of transmembrane receptors	Signaling	Hypo	2	-1.49 \pm 0.07
Retinoid X receptor β	Regulation of steroid receptor activity	Signaling	Hypo	2	1.61 \pm 0.08
Scavenger receptor class B, member 2	Regulation of cell adhesion	Signaling	Hypo	2	1.46 \pm 0.10
Xenotropic and polytropic retrovirus receptor	G-protein receptor signal transduction	Signaling	Hypo	12	1.36 \pm 0.06
B. Signal transduction genes during osmotic stress in <i>Gillichthys mirabilis</i>					
Lyn tyrosine kinase	Propagation of receptor tyrosine kinase signal transduction	Signaling	Hyper	1	1.27 \pm 0.09
Receptor type tyrosine protein phosphatase γ (RPTP γ)	Regulation of receptor tyrosine kinase signal transduction	Signaling	Hyper	1	-1.35 \pm 0.07
Myotubularin-related protein 14	Regulation of phosphatidylinositol production	Signaling	Hyper	1	-1.54 \pm 0.07
Casein kinase II β subunit (CKII- β)	Putative osmosensor – kinase activity-multiple substrates	Signaling	Hyper	12	-1.32 \pm 0.10
SCY-1 like protein	Kinase activity – regulation of protein transport	Signaling	Hypo	1	-1.59 \pm 0.06
Protein arginine methyltransferase 5 isoform 1	JAK/STAT signal transduction	Signaling	Hypo	2	1.34 \pm 0.06
C. Osmotic effectors during osmotic stress in <i>Gillichthys mirabilis</i> – Ion homeostasis					
System N amino acid transporter 1 (SNAT-1)	Sodium ion transport	Ion homeostasis	Hyper	4, 12	1.96 \pm 0.07
Carbonic anhydrase	Regulation of hydrogen ion homeostasis – pH regulation	Ion homeostasis	Hyper	1, 4	1.92 \pm 0.16
Sodium/sialic acid co-transporter	Sodium ion transport	Ion homeostasis	Hyper	4	-1.45 \pm 0.08
Potassium channel auxiliary subunit	Potassium ion transport	Ion homeostasis	Hypo	2	-1.67 \pm 0.12
D. Osmotic effectors during osmotic stress in <i>Gillichthys mirabilis</i> – Organic osmolytes					
Arginase II precursor	Regulation of urea production	Osmolyte	Hyper	4	2.10 \pm 0.24
E. Osmotic effectors during osmotic stress in <i>Gillichthys mirabilis</i> – Cytoskeleton					
55kDa erythrocyte membrane protein	Stabilization of cell shape through cytoskeletal membrane linkages	Cytoskeleton	Hyper	12	1.33 \pm 0.12
MID1 interacting protein	Stabilization of microtubules	Cytoskeleton	Hyper	2	-1.64 \pm 0.06
Nebulin	Bind and stabilize F-actin	Cytoskeleton	Hyper	2, 4, 12	2.02 \pm 0.23
Ankyrin-repeat domain containing protein 40	Regulation of cytoskeletal – membrane protein interactions	Cytoskeleton	Hypo	12	-1.23 \pm 0.07
Shroom 2	Regulation of cell shape via F-actin interaction	Cytoskeleton	Hypo	1	-1.23 \pm 0.07
BTB (PDZ) domain containing protein 14	Regulation of cytoskeletal – membrane protein interactions	Cytoskeleton	Hypo	12	3.06 \pm 0.06

Kelch and BTB domain containing protein 2	Adaptor protein for ubiquitin ligases regulating cell shape	Cytoskeleton	Hypo	4, 12	-1.32±0.07
Numb-binding protein 2	Regulation of cytoskeletal – membrane protein interactions	Cytoskeleton	Hypo	12	1.38±0.07
Myosin light chain 1	Mediate cell contractile events – possibly during cell motility	Cytoskeleton	Hypo	1	1.27±0.09
Plectin 1	Stabilization of cytoskeletal intermediate filament network	Cytoskeleton	Hypo	12	1.42±0.08
Ankyrin 2	Regulation of cytoskeletal – membrane protein interactions	Cytoskeleton	Hypo	2, 4	-1.59±0.05

F. Osmotic effectors during osmotic stress in *Gillichthys mirabilis* – Extracellular matrix

Bullous pemphigoid antigen 1	Linker protein mediating cytoskeletal-ECM interaction	ECM	Hyper	2	1.32±0.09
Tissue transglutaminase	Regulation of cell adhesion – catalyzes protein cross-linking	ECM	Hyper	2, 4	1.88±0.01
Tubulointerstitial nephritis antigen precursor (Gm_40e12)	Regulation of cell adhesion via integrin interaction	ECM	Hyper	12	1.80±0.11
α parvin	Regulation of cell adhesion via integrin interaction	ECM	Hypo	2	-1.45±0.09
Fibrinogen, α chain	Regulation of cell adhesion via formation of fibrin	ECM	Hypo	2	-1.75±0.06
Laminin β-1 chain precursor	Regulation of adhesion, migration and tissue organization	ECM	Hyper / Hypo	1 / 12	-1.54±0.08 / -1.59±0.05
Mucin-4	Putative osmosensor – anti-adhesive properties	ECM	Hyper	12	-1.28±0.09
Intra-α trypsin inhibitor heavy chain 3 (Gm_AB08)	Stabilization of the ECM	ECM	Hypo	2, 4	-1.67±0.06
Inter-α trypsin inhibitor heavy chain 3A	Stabilization of the ECM	ECM	Hypo	2, 4, 12	-1.69±0.05

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	-1.39±0.09 / -1.42±0.05
Tyrosine aminotransferase	Regulation of free amino acid availability	a.a. metabolism	Hyper / Hypo	1 / 1	-1.59±0.07 / -1.79±0.06
Threonine deaminase	Regulation of free amino acid availability	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±0.13

H. Osmotic effectors during osmotic stress in *Gillichthys mirabilis* – Calcium ion homeostasis

Cytochrome P450 24A1 (Gm_CD22)	Regulation of vitamin D synthesis	Calcium homeostasis	Hyper	4, 12	1.55±0.08
Otopetrin	Regulation of calcium deposition in otolith	Calcium homeostasis	Hyper	12	-2.13±0.13
Grancalcin	Regulation of calcium ion availability	Calcium homeostasis	Hypo	12	-1.49±0.07
Parvalbumin-like protein	Regulation of calcium ion availability	Calcium homeostasis	Hypo	2	-1.59±0.07
Stromal interacting molecule	Regulation of calcium ion availability	Calcium homeostasis	Hypo	12	-1.67±0.11

I. Osmotic effectors during osmotic stress in *Gillichthys mirabilis* – Cell cycle

Growth arrest and DNA damage inducible protein 45 (GADD45)	Regulation of cell cycle arrest	Cell cycle	Hypo	2	-1.67±0.10
RAD 54	Regulation of chromosomal recombination	Cell cycle	Hypo	2, 4	-1.47±0.09
Histone H2B	Regulation of chromatin structure	Cell cycle	Hypo	2	2.96±0.26
Kelch-like protein 13	Adaptor protein for ubiquitin ligases regulating cell cycle	Cell cycle	Hyper	12	-1.54±0.07
Etoposide induced 2.4 mRNA isoform 1	Induction of apoptosis	Cell cycle	Hyper	1	-1.56±0.07
Histone H1 family, member 0	Regulation of chromatin structure	Cell cycle	Hyper	4, 12	-1.89±0.08
Myeloid leukemia differentiation protein	Regulation of cell proliferation	Cell cycle	Hyper	4	1.62±0.14

J. Osmotic effectors during osmotic stress in *Gillichthys mirabilis* – Iron homeostasis

Serotransferrin I	Iron ion transport	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±0.05
Feline leukemia virus subgroup C receptor related protein	Exporter of cytoplasmic heme	Iron homeostasis	Hyper	12	-1.49±0.10
Hemopexin-like protein	Iron ion transport	Iron homeostasis	Hyper	12	1.52±0.08

K. Osmotic effectors during osmotic stress in *Gillichthys mirabilis* – Molecular degradation

γ 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	Hypo	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 ⁺ , K ⁺ -ATPase activity	Molecular degradation	Hypo	12	2.00±0.15
Peroxisomal N1-acetyl-spermine oxidase	Regulation of polyamine homeostasis	Molecular degradation	Hypo	12	-1.37±0.06

L. Osmotic effectors during osmotic stress in *Gillichthys 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	Hypo	1	1.70±0.12
60S ribosomal protein L38	Regulation of protein synthesis	Protein synthesis	Hypo	1	1.90±0.15
Ribosomal protein L7	Regulation of protein synthesis	Protein synthesis	Hypo	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

M. Osmotic effectors during osmotic stress in *Gillichthys mirabilis* – Protein trafficking

Mannose receptor C type 2 (Gm_AI03)	Regulation of receptor mediated endocytosis	Protein trafficking	Hyper / Hypo	1, 2 / 1, 2	-1.67±0.07 / -1.96±0.07
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
α 1, 3 glucosyl-transferase 8	Regulation of post-translational protein glycosylation	Protein trafficking	Hyper	12	1.23±0.08
TBC1 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	Hypo	2	-1.32±0.09
Protein disulfide isomerase A6 precursor	Rearrangement of disulfide bonds in proteins	Protein trafficking	Hypo	1	-1.19±0.06

N. Osmotic effectors during osmotic stress in *Gillichthys mirabilis* – Proteolysis

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	-1.64±0.07
Elastase 4-like protein	Hydrolysis of proteins-possibly IGFBP-1	Proteolysis	Hypo	2	-1.39±0.08
RING finger protein 87	Ubiquitin ligase activity	Proteolysis	Hyper	12	-1.37±0.08

O. Osmotic effectors during osmotic stress in *Gillichthys mirabilis* – Transcription regulation

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 response to cytokine signaling	Transcription regulation	Hyper	4, 12	2.48±0.22
Nuclear 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
Transcription factor Sp1	Regulation of the response to MAPK signaling	Transcription regulation	Hyper	4, 12	-1.32±0.10
Chick ovalbumin upstream promoter (COUP) transcription factor	Regulation of the response to glucocorticoids	Transcription regulation	Hypo	4	-1.33±0.07
General negative regulator of transcription subunit 1	Transcriptional regulation of stress responsive genes	Transcription regulation	Hypo	12	1.50±0.10
Nucleolar protein 11	Regulation of rRNA transcription	Transcription regulation	Hypo	1	-1.56±0.05
Something about silencing protein 10	Promotion of gene silencing-chromatin structure	Transcription regulation	Hypo	1	-1.35±0.06
Zinc fingers and homeoboxes 3	Repression of transcription	Transcription regulation	Hypo	12	-1.54±0.07

P. Osmotic effectors during osmotic stress in *Gillichthys mirabilis* – Cholesterol metabolism

Apolipoprotein L	Regulation of cholesterol production	Cholesterol metabolism	Hyper	1	1.66±0.24
Apolipoprotein A	Regulation of cholesterol production	Cholesterol metabolism	Hypo	4	-1.43±0.05
Cholesteryl ester transfer protein precursor	Transport of cholesterol	Cholesterol metabolism	Hypo	2	-1.35±0.06

Q. Osmotic effectors during osmotic stress in *Gillichthys mirabilis* – Energy/Metabolism

6-phosphofructo-2-kinase/fructose 2,6 bisphosphatase 4 (Gm_BN17)	Aerobic carbohydrate metabolism	Energy/metabolism	Hyper	12	2.02±0.13
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	Hypo	4	-1.25±0.07
Lysosomal α mannosidase precursor	Lysosomal carbohydrate metabolism	Energy/metabolism	Hypo	12	1.24±0.06
Facilitated glucose transporter	Glucose transport	Energy/metabolism	Hypo	12	-1.64±0.13
Very long chain acyl-CoA synthetase	Lipid metabolism	Energy/metabolism	Hypo	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