

1 **Supplementary information**2 **Transcriptome profiling reveals exposure to predicted end-of-century**  
3 **ocean acidification as a stealth stressor for Atlantic cod larvae**4  
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15 Oslo, Postboks 1066, NO-0316 Oslo, Norway16 \*Corresponding author: [fmittermayer@geomar.de](mailto:fmittermayer@geomar.de)17 Table 1: Results of a linear mixed model for dry weight of 5 and 15 dph cod larvae, including tank as a  
18 random factor

Larval age	Response	Fixed factor	F	DF(num)	DF(denum)	p-value
5 dph	Dry weight	Larval $p\text{CO}_2$ (ambient/increased)	6.0045	1	3.725	0.075
15 dph	Dry weight	Larval $p\text{CO}_2$ (ambient/increased)	2.0643	1	3	0.246

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21 *Table 2. Summary of samples, treatments, sequencing and assignment results. # presents number,*  
 22 *SD is standard deviation. Read values refer to single reads, raw reads are total number of reads per*  
 23 *sampling category, and filtered reads are average per sample.*

Treatment	Age (dph)	# Samples	RAW READS DE-MULTIPLEXED			FILTERED READS USED IN DEANALYSIS		ASSIGNED UNIQUELY TO THE REF. TRANSCRIPTOME	
			Sum	Mean #	SD	Mean #	SD	Mean %	SD
Ambient pCO <sub>2</sub>	6	8	5.1*10 <sup>8</sup>	6.4*10 <sup>7</sup>	1.8*10 <sup>5</sup>	6.4*10 <sup>7</sup>	1.8*10 <sup>5</sup>	70.58	1.00
High pCO <sub>2</sub>	6	8	5.3*10 <sup>8</sup>	6.6*10 <sup>7</sup>	2.8*10 <sup>5</sup>	6.5*10 <sup>7</sup>	2.8*10 <sup>5</sup>	70.52	0.96
Ambient pCO <sub>2</sub>	13	8	6.2*10 <sup>8</sup>	7.8*10 <sup>7</sup>	24.3*10 <sup>5</sup>	7.7*10 <sup>7</sup>	24.2*10 <sup>5</sup>	71.11	0.75
High pCO <sub>2</sub>	13	8	5.2*10 <sup>8</sup>	6.5*10 <sup>7</sup>	4.8*10 <sup>5</sup>	6.4*10 <sup>7</sup>	4.7*10 <sup>5</sup>	71.29	1.35
Ambient pCO <sub>2</sub>	36	8	6.9*10 <sup>8</sup>	8.6*10 <sup>7</sup>	28.5*10 <sup>5</sup>	8.4*10 <sup>7</sup>	28.2*10 <sup>5</sup>	61.23	2.88
High pCO <sub>2</sub>	36	8	5.4*10 <sup>8</sup>	6.7*10 <sup>7</sup>	2.8*10 <sup>5</sup>	6.7*10 <sup>7</sup>	2.7*10 <sup>5</sup>	70.51	2.92
Total		48	34.1*10 <sup>8</sup>	7.1*10 <sup>7</sup>		7.0*10 <sup>7</sup>		69.20	

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26 *Table 3a. Loadings of first principal component, 25 main contributing genes to first principle*  
 27 *component in Figure 3*

GENE	CONTRIBUTION TO PC 1 IN %
MYOSIN HEAVY CHAIN. FAST SKELETAL MUSCLE ( <i>CYPRINUS CARPIO</i> )	0.388066021
KLHL38 KELCH-LIKE PROTEIN 38 ( <i>DANIO RERIO</i> )	0.371193025
FBXO32 F-BOX ONLY PROTEIN 32 ( <i>SUS SCROFA</i> )	0.302487707
MYOSIN HEAVY CHAIN. FAST SKELETAL MUSCLE ( <i>CYPRINUS CARPIO</i> )	0.301755979
PROTEIN OF UNKNOWN FUNCTION	0.237395845
GAMMA-CRYSTALLIN M3 ( <i>CYPRINUS CARPIO</i> )	0.223435332
PROTEIN OF UNKNOWN FUNCTION	0.218408605
LADDERLECTIN ( <i>ONCORHYNCHUS MYKISS</i> )	0.217564849
FAM134B RETICULOPHAGY RECEPTOR FAM134B ( <i>MUS MUSCULUS</i> )	0.198892372
PROTEIN OF UNKNOWN FUNCTION	0.182636968
PROTEIN OF UNKNOWN FUNCTION	0.181408566
MYOSIN HEAVY CHAIN. FAST SKELETAL MUSCLE ( <i>CYPRINUS CARPIO</i> )	0.175043319
ARRDC2 ARRESTIN DOMAIN-CONTAINING PROTEIN 2 ( <i>HOMO SAPIENS</i> )	0.170943549
IGFBP1 INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN 1 ( <i>BOS TAURUS</i> )	0.170560436
VCAN VERSICAN CORE PROTEIN ( <i>GALLUS GALLUS</i> )	0.168464054
EXOSC6 EXOSOME COMPLEX COMPONENT MTR3 ( <i>DANIO RERIO</i> )	0.162277631
UCP2 MITOCHONDRIAL UNCOUPLING PROTEIN 2 ( <i>MUS MUSCULUS</i> )	0.161029997
VISININ ( <i>GALLUS GALLUS</i> )	0.160272963
BNIP3 BCL2/ADENOVIRUS E1B 19 KDA PROTEIN-INTERACTING PROTEIN 3 ( <i>MUS MUSCULUS</i> )	0.159401846
VERRUCOTOXIN SUBUNIT BETA ( <i>SYNANCEIA VERRUCOSA</i> )	0.154615965
C4 COMPLEMENT C4 ( <i>RATTUS NORVEGICUS</i> )	0.15237641
HMGCS1 HYDROXYMETHYLGLUTARYL-COA SYNTHASE. CYTOPLASMIC ( <i>GALLUS GALLUS</i> )	0.1502471
COL9A3 COLLAGEN ALPHA-3(IX) CHAIN ( <i>GALLUS GALLUS</i> )	0.149620902
CYP51A1 LANOSTEROL 14-ALPHA DEMETHYLASE ( <i>MACACA FASCICULARIS</i> )	0.145205011

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29 *Table 3b. Loadings of first principal component, 25 main contributing genes to second principle*  
 30 *component in Figure 3*

GENE	CONTRIBUTION TO PC 2 IN %
ES1 ES1 PROTEIN. MITOCHONDRIAL ( <i>DANIO RERIO</i> )	0.631738076
MYOSIN HEAVY CHAIN. FAST SKELETAL MUSCLE ( <i>CYPRINUS CARPIO</i> )	0.518263622
MRC1 MACROPHAGE MANNOSE RECEPTOR 1 ( <i>HOMO SAPIENS</i> )	0.357842258
HCEA HIGH CHORIOLYTIC ENZYME 1 ( <i>ORYZIAS LATIPES</i> )	0.315547116
PROTEIN OF UNKNOWN FUNCTION	0.292950430
IMPA1 INOSITOL MONOPHOSPHATASE 1 ( <i>BOS TAURUS</i> )	0.284643925
C3 COMPLEMENT C3 (FRAGMENT) ( <i>ONCORHYNCHUS MYKISS</i> )	0.282401366
COL10A1 COLLAGEN ALPHA-1(X) CHAIN ( <i>GALLUS GALLUS</i> )	0.246564047
EXOSC6 EXOSOME COMPLEX COMPONENT MTR3 ( <i>DANIO RERIO</i> )	0.228810163
PROTEIN OF UNKNOWN FUNCTION	0.201614736
PROTEIN OF UNKNOWN FUNCTION	0.186421801
PEG3 PATERNALLY-EXPRESSED GENE 3 PROTEIN ( <i>BOS TAURUS</i> )	0.179113111
ELASTASE-1 ( <i>SALMO SALAR</i> )	0.179070813
RPL31 60S RIBOSOMAL PROTEIN L31 ( <i>PARALICHTHYS OLIVACEUS</i> )	0.177788248
ENTPD5 ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 5 ( <i>GALLUS GALLUS</i> )	0.177782763
COL1A2 COLLAGEN ALPHA-2(I) CHAIN ( <i>RATTUS NORVEGICUS</i> )	0.176887258
VCAN VERSICAN CORE PROTEIN ( <i>GALLUS GALLUS</i> )	0.174817539
CKMT1 CREATINE KINASE U-TYPE. MITOCHONDRIAL ( <i>GALLUS GALLUS</i> )	0.173735764
LECT2 LEUKOCYTE CELL-DERIVED CHEMOTAXIN-2 ( <i>HOMO SAPIENS</i> )	0.169742346
CELA3B CHYMOTRYPSIN-LIKE ELASTASE FAMILY MEMBER 3B ( <i>MUS MUSCULUS</i> )	0.164459664
INTERMEDIATE FILAMENT PROTEIN ON3 ( <i>CARASSIUS AURATUS</i> )	0.164073293
PROTEIN OF UNKNOWN FUNCTION	0.163405256
C3 COMPLEMENT C3 (FRAGMENT) ( <i>ONCORHYNCHUS MYKISS</i> )	0.158777821
ITIH3 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 ( <i>MUS MUSCULUS</i> )	0.156855282

Table 4: List of all differentially expressed genes in 6 dph larvae between ambient (~503 $\mu$ atm) and high (~1179  $\mu$ atm)  $p\text{CO}_2$

Gene (gene name in uniprot/swissprot)	Involved in	$\log_2$ Fold Change	$L_2$ FC SE	p-value	p adjusted (FDR=BH)
<b>MEP1B Meprin A subunit beta (Homo sapiens)</b>	Hydrolase, Metalloprotease, Protease, Inflammatory response	-0.38	0.08	1.45E-06	0.01373
<b>Ugt2a2 UDP-glucuronosyltransferase 2A2 (Mus musculus)</b>	Glycosyltransferase, Transferase	-0.34	0.07	8.66E-07	0.01373
<b>ANKRD6 Ankyrin repeat domain-containing protein 6 (Homo sapiens)</b>	Positive JNK cascade regulation, Wnt Pathway	-0.39	0.08	1.81E-06	0.01373

Table 5: List of all differentially expressed genes in 13 dph larvae between ambient (~503 $\mu$ atm) and high (~1179  $\mu$ atm)

Gene (gene name in uniprot/swissprot)	Involved in	log <sub>2</sub> Fold Change	L <sub>2</sub> FC SE	p-value	p adjusted (FDR=BH)
<b>ANXA5 Annexin A5 (Macaca fascicularis)</b>	Blood coagulation, Calcium ion binding	0.91	0.11	3.11E-17	7.10E-13
<b>Protein of unknown function</b>		0.54	0.11	3.87E-07	0.00441
<b>blm Bloom syndrome protein homolog (Xenopus laevis)</b>	DNA-binding, DNA replication	-0.48	0.10	8.18E-07	0.00622
<b>zpld1 Zona pellucida-like domain-containing protein 1 (X. laevis)</b>	Membrane component	0.49	0.10	3.45E-06	0.01310
<b>C1QL4 Complement C1q-like protein 4 (Homo sapiens)</b>	Identical protein binding, negative regulation fat cell differentiation and fibroblast proliferation	0.51	0.11	2.95E-06	0.01310
<b>CILP2 Cartilage intermediate layer protein 2 (Homo sapiens)</b>	Extra cellular matrix	0.45	0.10	2.82E-06	0.01310
<b>Nol6 Nucleolar protein 6 (Mus musculus)</b>	RNA-binding, RNA transport	-0.51	0.11	4.40E-06	0.01434
<b>KIAA1586 Uncharacterized protein KIAA1586 (Homo sapiens)</b>	Ligase activity	-0.48	0.11	1.25E-05	0.03057
<b>col27a1b Collagen alpha-1(XXVII) chain B (Danio rerio)</b>	Calcification of cartilage, bone development	0.42	0.10	1.60E-05	0.03057

<b>GATM Glycine amidinotransferase, mitochondrial (Gallus gallus)</b>	amidinotransferase activity	-0.42	0.10	1.69E-05	0.03057
<b>NR4A3 Nuclear receptor subfamily 4 group A member 3 (Homo sapiens)</b>	DNA binding, Transcript regulation	-0.48	0.11	1.45E-05	0.03057
<b>Irg1 Cis-aconitate decarboxylase (Mus musculus)</b>	Antimicrobial, Inflammatory response	-0.43	0.10	1.88E-05	0.03057
<b>Protein of unknown function</b>		-0.49	0.11	1.24E-05	0.03057
<b>comA Comitín (Dictyostelium discoideum)</b>	Actin-binding	-0.46	0.11	1.81E-05	0.03057
<b>SPR Sepiapterin reductase (Homo sapiens)</b>	Oxidoreductase	-0.39	0.09	2.69E-05	0.04090
<b>Trypsin I-P1 (Gallus gallus)</b>	Hydrolase, Protease, Digestion	0.46	0.11	2.97E-05	0.04235

Table 6: List of all differentially expressed genes with L2FC  $\leq -1/\geq 1$  in 36 dph larvae between ambient ( $\sim 503 \mu\text{atm}$ ) and high ( $\sim 1179 \mu\text{atm}$ )

Gene (gene name in uniprot/swissprot)		log <sub>2</sub> Fold Change	L <sub>2</sub> FC SE	p-value	p adjusted (FDR=BH)
<b>Fosb Protein fosB (Mus musculus)</b>	DNA binding	-2.29	0.18	1.22E-37	2.35E-33
<b>Klf4 Krueppel-like factor 4 (M. musculus)</b>	DNA binding, Transcription regulation	-1.79	0.18	1.26E-23	8.13E-20
<b>ATF3 Cyclic AMP-dependent transcription factor ATF-3 (Homo sapiens)</b>	DNA binding, Transcription regulation	-1.68	0.17	2.05E-23	9.87E-20
<b>Ptchd3 Patched domain-containing protein 3 (M. musculus)</b>	Membrane component	-1.54	0.22	6.74E-12	9.28E-09
<b>lin28a Protein lin-28 homolog A (Danio rerio)</b>	RNA binding, gene silencing	-1.33	0.20	1.49E-11	1.92E-08
<b>AREG Amphiregulin (Homo sapiens)</b>	Growth factor	-1.33	0.15	2.37E-19	7.63E-16
<b>KLF2 Krueppel-like factor 2 (Homo sapiens)</b>	DNA binding, Transcription regulation	-1.30	0.11	2.98E-34	2.87E-30
<b>phlda2 Pleckstrin homology-like domain family A member 2 (Salmo salar)</b>	Membrane component	-1.18	0.12	2.55E-22	9.84E-19
<b>Fosl1 Fos-related antigen 1 (Rattus norvegicus)</b>	DNA binding	-1.18	0.21	4.24E-08	2.21E-05
<b>Trim39 E3 ubiquitin-protein ligase TRIM39 (M.s musculus)</b>	Identical protein binding, Transferase	-1.17	0.22	6.95E-08	3.11E-05
<b>Protein of unknown function</b>		-1.13	0.17	3.55E-11	4.03E-08
<b>PTGER4 Prostaglandin E2 receptor EP4 subtype (Homo sapiens)</b>	Numerous functions	-1.08	0.22	1.46E-06	0.00032
<b>Sgms2 Phosphatidylcholine:ceramide cholinephosphotransferase 2 (R. norvegicus)</b>	Membrane component	-1.03	0.15	4.30E-12	6.92E-09

<b>Myosin heavy chain. fast skeletal muscle (Cyprinus carpio)</b>	Actin binding muscle protein	1.00	0.22	6.23E-06	0.00101
<b>Protein of unknown function</b>		1.01	0.22	6.53E-06	0.00103
<b>ADPRH [Protein ADP-ribosylarginine] hydrolase (Homo sapiens)</b>	Cellular protein modification	1.01	0.21	1.53E-06	0.00033
<b>insig1 Insulin-induced gene 1 protein (Xenopus tropicalis)</b>	Lipid and Cholesterol metabolism	1.04	0.20	3.68E-07	0.00011
<b>ENTPD5 Ectonucleoside triphosphate diphosphohydrolase 5 (Gallus gallus)</b>	Cell growth and proliferation	1.06	0.22	1.01E-06	0.00025
<b>Protein of unknown function</b>		1.06	0.22	2.29E-06	0.00045

Table 7: List of differentially expressed candidate genes related to acid-base regulation and stress response in 36 dph larvae between ambient (~503  $\mu\text{atm}$ ) and high  $p\text{CO}_2$  treatment (~1179  $\mu\text{atm}$ ).

Name	Group	Source reference	Annotation name (uniprot/swissprot)	log2 FoldChange	p value	padj
A3 SLC family 26 (SLC26A3)	Acid-Base	Micheal et al., 2015	Slc26a3 Chloride anion exchanger ( <i>Rattus norvegicus</i> )	-0,3846619	0,02075377	0,13462717
A3 SLC family 26 (SLC26A3)	Acid-Base	Micheal et al., 2015	Slc26a3 Chloride anion exchanger ( <i>Rattus norvegicus</i> )	0,0600537	0,73268794	0,87740277
A6 SLC family 26 (SLC26A6)	Acid-Base	Micheal et al., 2015	Slc26a6 Solute carrier family 26 member 6 ( <i>Mus musculus</i> )	-0,1109202	0,41296842	0,67135219
A6 SLC family 26 (SLC26A6)	Acid-Base	Micheal et al., 2015	Slc26a6 Solute carrier family 26 member 6 ( <i>Mus musculus</i> )	-0,4247676	0,00640451	0,06972912
A6 SLC family 26 (SLC26A6)	Acid-Base	Micheal et al., 2015	Slc26a6 Solute carrier family 26 member 6 ( <i>Mus musculus</i> )	-0,1963062	0,22446881	0,49480152



AE1 SLC4a1 (HCO <sub>3</sub> transporter)	Acid-Base	Heuer&Grossell, 2014	slc4a1 Band 3 anion exchange protein ( <i>Oncorhynchus mykiss</i> )	0,08014627	0,60939462	0,81080286	
AE2 SLC4a2 (HCO <sub>3</sub> transporter)	Acid-Base	Heuer&Grossell, 2014	SLC4A2 Anion exchange protein 2 ( <i>Homo sapiens</i> )	0,11318606	0,15677774	0,40898133	
AE2 SLC4a2 (HCO <sub>3</sub> transporter)	Acid-Base	Heuer&Grossell, 2014	SLC4A2 Anion exchange protein 2 ( <i>Homo sapiens</i> )	-0,1728193	0,04767664	0,21370794	
CA (carbonic anhydras)	Acid-Base	Heuer&Grossell, 2014	ca1 Carbonic anhydrase 1 ( <i>Chionodraco hamatus</i> )	0,26481502	0,05228608	0,22502006	
CA (carbonic anhydras)	Acid-Base	Heuer&Grossell, 2014	CA14 Carbonic anhydrase 14 ( <i>Homo sapiens</i> )	0,00280535	0,97561354	0,99014811	
CA (carbonic anhydras)	Acid-Base	Heuer&Grossell, 2014	CA4 Carbonic anhydrase 4 ( <i>Homo sapiens</i> )	-0,2938201	0,04929332	0,21780218	
CA (carbonic anhydras)	Acid-Base	Heuer&Grossell, 2014	CA4 Carbonic anhydrase 4 ( <i>Homo sapiens</i> )	0,24796459	0,12511754	0,36278252	
CA (carbonic anhydras)	Acid-Base	Heuer&Grossell, 2014	Ca4 Carbonic anhydrase 4 ( <i>Rattus norvegicus</i> )	-0,5427883	1,6746E-05	0,00192171	*
CA (carbonic anhydras)	Acid-Base	Heuer&Grossell, 2014	CA5B Carbonic anhydrase 5B, mitochondrial ( <i>Homo sapiens</i> )	-0,0567403	0,75825013	0,89093809	
CA (carbonic anhydras)	Acid-Base	Heuer&Grossell, 2014	CA6 Carbonic anhydrase 6 ( <i>Homo sapiens</i> )	0,11641642	0,1739237	0,43248743	
CA (carbonic anhydras)	Acid-Base	Heuer&Grossell, 2014	CA7 Carbonic anhydrase 7 ( <i>Homo sapiens</i> )	-0,2156911	0,22043977	0,4897843	
CA (carbonic anhydras)	Acid-Base	Heuer&Grossell, 2014	cahz Carbonic anhydrase ( <i>Danio rerio</i> )	-0,0867529	0,57359484	0,78705972	
CA (carbonic anhydras)	Acid-Base	Heuer&Grossell, 2014	CA12 Carbonic anhydrase 12 ( <i>Homo sapiens</i> )	-0,0285542	0,89257103	NA	
NBC1 (Na/HCO <sub>3</sub> cotransporter 1) SLC4A4	Acid-Base	Heuer&Grossell, 2014	Slc4a4 Electrogenic sodium bicarbonate cotransporter 1 ( <i>Mus musculus</i> )	-0,0477387	0,81337672	0,91725253	
NBC1 (Na/HCO <sub>3</sub> cotransporter 1) SLC4A4	Acid-Base	Heuer&Grossell, 2014	SLC4A4 Electrogenic sodium bicarbonate cotransporter 1 ( <i>Oryctolagus cuniculus</i> )	-0,0728577	0,1597365	0,41313037	
NHE1 (Na/H exchanger)SLC9A1	Acid-Base	Heuer&Grossell, 2014	SLC9A1 Sodium/hydrogen exchanger 1 ( <i>Oryctolagus cuniculus</i> )	-0,0757678	0,64436079	0,83123418	

NHE2 (Na/H exchanger) SLC9 member 2	Acid-Base	Heuer&Grossell, 2014	SLC9A2 Sodium/hydrogen exchanger 2 ( <i>Oryctolagus cuniculus</i> )	0,0485859	0,70673443	0,86437437
NHE2 (Na/H exchanger) SLC9 member 2	Acid-Base	Heuer&Grossell, 2014	Slc9a2 Sodium/hydrogen exchanger 2 ( <i>Rattus norvegicus</i> )	-0,0892483	0,66849604	NA
NHE3 (Na/H exchanger) SLC9A3	Acid-Base	Heuer&Grossell, 2014	SLC9A3 Sodium/hydrogen exchanger 3 ( <i>Didelphis virginiana</i> )	-0,0820974	0,68420678	0,85405131
NHE3 (Na/H exchanger) SLC9A3	Acid-Base	Heuer&Grossell, 2014	Slc9a3 Sodium/hydrogen exchanger 3 ( <i>Rattus norvegicus</i> )	-0,1747312	0,23027821	0,50164221
NKA Na/K ATPase	Acid-Base	Heuer&Grossell, 2014	ATP1A1 Sodium/potassium-transporting ATPase subunit alpha-1 ( <i>Bos taurus</i> )	0,15435617	0,04064224	0,19608152
NKA Na/K ATPase	Acid-Base	Heuer&Grossell, 2014	ATP1A1 Sodium/potassium-transporting ATPase subunit alpha-1 ( <i>Bos taurus</i> )	-0,0531942	0,69609749	0,86064667
NKA Na/K ATPase	Acid-Base	Heuer&Grossell, 2014	ATP1A1 Sodium/potassium-transporting ATPase subunit alpha-1 ( <i>Pongo abelii</i> )	-0,0438916	0,64592473	0,83222417
NKA Na/K ATPase	Acid-Base	Heuer&Grossell, 2014	ATP1A2 Sodium/potassium-transporting ATPase subunit alpha-2 ( <i>Sus scrofa</i> )	-0,108302	0,52712569	0,75748779
NKA Na/K ATPase	Acid-Base	Heuer&Grossell, 2014	atp1a3 Sodium/potassium-transporting ATPase subunit alpha-3 ( <i>Oreochromis mossambicus</i> )	0,23089579	0,00888909	0,08414143
NKA Na/K ATPase	Acid-Base	Heuer&Grossell, 2014	ATP1B2 Sodium/potassium-transporting ATPase subunit beta-2 ( <i>Homo sapiens</i> )	0,14173092	0,17917111	0,43954238
NKA Na/K ATPase	Acid-Base	Heuer&Grossell, 2014	ATP1B2 Sodium/potassium-transporting ATPase subunit beta-2 ( <i>Homo sapiens</i> )	0,02628338	0,84745887	0,93270306
NKA Na/K ATPase	Acid-Base	Heuer&Grossell, 2014	atp1b3 Sodium/potassium-transporting ATPase subunit beta-3 ( <i>Xenopus laevis</i> )	0,05616159	0,50566192	0,74405862
NKCC1 (Na/K/Cl cotransporter)SLC12A2	Acid-Base	Heuer&Grossell, 2014	SLC12A2 Solute carrier family 12 member 2 ( <i>Homo sapiens</i> )	0,03271988	0,63205002	0,8247795
NKCC1 (Na/K/Cl cotransporter)SLC12A2	Acid-Base	Heuer&Grossell, 2014	Slc12a2 Solute carrier family 12 member 2 ( <i>Mus</i> )	0,1074674	0,48685514	0,72845016

*musculus*)

NKCC1 (Na/K/Cl cotransporter)SLC12A2	Acid-Base	Heuer&Grossell, 2014	Slc12a2 Solute carrier family 12 member 2 ( <i>Mus musculus</i> )	0,11312732	0,33450782	0,60434602	
RH transporter	Acid-Base-related	Heuer&Grossell, 2014	Similar to RHAG Ammonium transporter Rh type A ( <i>Homo sapiens</i> )	0,14296829	0,05392902	0,2284024	
RH transporter	Acid-Base-related	Heuer&Grossell, 2014	Similar to Rhag Ammonium transporter Rh type A ( <i>Mus musculus</i> )	-0,5249972	0,00758553	0,0765662	
RH transporter	Acid-Base-related	Heuer&Grossell, 2014	Similar to rhbg Ammonium transporter Rh type B ( <i>Takifugu rubripes</i> )	0,4042237	0,00174209	0,03315483	*
RH transporter	Acid-Base-related	Heuer&Grossell, 2014	Similar to rhbg Ammonium transporter Rh type B ( <i>Xenopus tropicalis</i> )	0,04694015	0,82553266	0,92258096	
RH transporter	Acid-Base-related	Heuer&Grossell, 2014	Similar to rhbg-a Ammonium transporter Rh type B-A ( <i>Xenopus laevis</i> )	0,06444727	0,43681513	0,68998518	
RH transporter	Acid-Base-related	Heuer&Grossell, 2014	Similar to rhcg Ammonium transporter Rh type C ( <i>Tetraodon nigroviridis</i> )	-0,128581	0,52099571	0,75394883	
RH transporter	Acid-Base-related	Heuer&Grossell, 2014	Similar to rhcg2 Ammonium transporter Rh type C 2 ( <i>Takifugu rubripes</i> )	-0,3687006	0,00047045	0,01599065	*
6 phosphogluconate dehydrogenase	Stress	Kültz, 2005	PGD 6-phosphogluconate dehydrogenase, decarboxylating ( <i>Homo sapiens</i> )	0,09998854	0,58764526	0,79727045	
Aldehyde dehydrogenase	Stress	Kültz, 2005	ALDH16A1 Aldehyde dehydrogenase family 16 member A1 ( <i>Bos taurus</i> )	0,04050142	0,61711186	0,81583347	
Aldehyde dehydrogenase	Stress	Kültz, 2005	ALDH1A3 Aldehyde dehydrogenase family 1 member A3 ( <i>Homo sapiens</i> )	0,390955	0,00111631	0,0262097	*
Aldehyde dehydrogenase	Stress	Kültz, 2005	ALDH2 Aldehyde dehydrogenase, mitochondrial ( <i>Mesocricetus auratus</i> )	0,09585625	0,41507678	0,67302483	
Aldehyde dehydrogenase	Stress	Kültz, 2005	ALDH3A2 Fatty aldehyde dehydrogenase ( <i>Macaca fascicularis</i> )	-0,0484776	0,7329881	0,87744661	

Aldehyde dehydrogenase	Stress	Kültz, 2005	ALDH3A2 Fatty aldehyde dehydrogenase ( <i>Macaca fascicularis</i> )	0,0053013	0,94620884	0,97812119	
Aldehyde dehydrogenase	Stress	Kültz, 2005	Aldh6a1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial ( <i>Mus musculus</i> )	0,15815337	0,2964247	0,5679305	
Aldehyde dehydrogenase	Stress	Kültz, 2005	Aldh6a1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial ( <i>Mus musculus</i> )	0,00319833	0,98000719	0,99178785	
Aldehyde dehydrogenase	Stress	Kültz, 2005	Aldh6a1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial ( <i>Rattus norvegicus</i> )	0,21835788	0,02559703	0,15171187	
Aldehyde dehydrogenase	Stress	Kültz, 2005	ALDH7A1 Alpha-aminoadipic semialdehyde dehydrogenase ( <i>Bos taurus</i> )	0,13771501	0,35701142	0,62392812	
Aldehyde dehydrogenase	Stress	Kültz, 2005	aldh8a1 Aldehyde dehydrogenase family 8 member A1 ( <i>Danio rerio</i> )	-0,1634678	0,33560169	0,60575461	
Aldehyde dehydrogenase	Stress	Kültz, 2005	aldh9A1 Betaine aldehyde dehydrogenase ( <i>Gadus morhua subsp. callarias</i> )	0,2732407	0,10537731	0,33055144	
Aldehyde dehydrogenase	Stress	Kültz, 2005	aldh9a1b Aldehyde dehydrogenase family 9 member A1-B ( <i>Danio rerio</i> )	0,16217874	0,14447711	0,3923615	
Aldehyde reductase	Stress	Kültz, 2005	AKR1B10 Aldo-keto reductase family 1 member B10 ( <i>Homo sapiens</i> )	0,22983971	0,00351227	0,04882458	*
Aldehyde reductase	Stress	Kültz, 2005	Akr7a2 Aflatoxin B1 aldehyde reductase member 2 ( <i>Rattus norvegicus</i> )	0,05875718	0,64148548	0,82945664	
Aminobutyrate aminotransferase	Stress	Kültz, 2005	ABAT 4-aminobutyrate aminotransferase, mitochondrial ( <i>Homo sapiens</i> )	-0,1419473	0,06935656	0,26368077	
Aromatic amino acid aminotransferase	Stress	Kültz, 2005	very diverse, not included in analysis	no data	no data	no data	
Ca <sup>2+</sup> /Mg <sup>2+</sup> -transporting ATPase	Stress	Kültz, 2005	ATP2C1 Calcium-transporting ATPase type 2C member 1 ( <i>Homo sapiens</i> )	-0,1908614	0,15400883	0,40555311	

Citrate synthase (Krebs cycle)	Stress	Kültz, 2005	ACLY ATP-citrate synthase ( <i>Homo sapiens</i> )	0,17301081	0,02634519	0,15349318
Citrate synthase (Krebs cycle)	Stress	Kültz, 2005	Acly ATP-citrate synthase ( <i>Mus musculus</i> )	0,15680517	0,23542998	0,50730124
Citrate synthase (Krebs cycle)	Stress	Kültz, 2005	cs Citrate synthase, mitochondrial ( <i>Thunnus obesus</i> )	0,17901739	0,11636408	0,34942572
DnaJ/HSP40	Stress	Kültz, 2005	DNAJA1 DnaJ homolog subfamily A member 1 ( <i>Bos taurus</i> )	-0,0357413	0,71843904	0,87019995
DnaJ/HSP40	Stress	Kültz, 2005	DNAJA2 DnaJ homolog subfamily A member 2 ( <i>Bos taurus</i> )	0,18150822	0,07017261	0,2650064
DnaJ/HSP40	Stress	Kültz, 2005	DNAJA2 DnaJ homolog subfamily A member 2 ( <i>Bos taurus</i> )	0,04247645	0,60364992	0,80765127
DnaJ/HSP40	Stress	Kültz, 2005	DNAJA3 DnaJ homolog subfamily A member 3, mitochondrial ( <i>Homo sapiens</i> )	0,06949067	0,31794881	0,58841395
DnaJ/HSP40	Stress	Kültz, 2005	Dnaja3 DnaJ homolog subfamily A member 3, mitochondrial ( <i>Mus musculus</i> )	-0,0043983	0,94553563	0,97784473
DnaJ/HSP40	Stress	Kültz, 2005	Dnaja4 DnaJ homolog subfamily A member 4 ( <i>Mus musculus</i> )	0,44972268	0,02314699	0,14302908
DnaJ/HSP40	Stress	Kültz, 2005	DNAJB1 DnaJ homolog subfamily B member 1 ( <i>Bos taurus</i> )	-0,2479703	0,05783629	0,23653499
DnaJ/HSP40	Stress	Kültz, 2005	DNAJB1 DnaJ homolog subfamily B member 1 ( <i>Bos taurus</i> )	-0,1639037	0,24544656	0,51735593
DnaJ/HSP40	Stress	Kültz, 2005	Dnajb11 DnaJ homolog subfamily B member 11 ( <i>Mus musculus</i> )	0,2431193	0,2151039	0,48421306
DnaJ/HSP40	Stress	Kültz, 2005	DNAJB12 DnaJ homolog subfamily B member 12 ( <i>Homo sapiens</i> )	0,02549595	0,85990797	0,93826281
DnaJ/HSP40	Stress	Kültz, 2005	Dnajb12 DnaJ homolog subfamily B member 12 ( <i>Mus musculus</i> )	-0,134784	0,26770777	0,54082974

DnaJ/HSP40	Stress	Kültz, 2005	Dnajb14 DnaJ homolog subfamily B member 14 ( <i>Mus musculus</i> )	0,00635806	0,9297732	0,97106798
DnaJ/HSP40	Stress	Kültz, 2005	DNAJB4 DnaJ homolog subfamily B member 4 ( <i>Bos taurus</i> )	-0,1594646	0,08142115	0,28783044
DnaJ/HSP40	Stress	Kültz, 2005	Dnajb5 DnaJ homolog subfamily B member 5 ( <i>Mus musculus</i> )	-0,0069921	0,95523642	0,98183108
DnaJ/HSP40	Stress	Kültz, 2005	DNAJB6 DnaJ homolog subfamily B member 6 ( <i>Macaca fascicularis</i> )	0,00145631	0,98694081	0,99501831
DnaJ/HSP40	Stress	Kültz, 2005	dnajb6-b DnaJ homolog subfamily B member 6-B ( <i>Xenopus laevis</i> )	0,61006077	0,0011255	0,02633305 *
DnaJ/HSP40	Stress	Kültz, 2005	DNAJB9 DnaJ homolog subfamily B member 9 ( <i>Homo sapiens</i> )	0,1460925	0,22877974	0,50034814
DnaJ/HSP40	Stress	Kültz, 2005	Dnajb13 DnaJ homolog subfamily B member 13 ( <i>Mus musculus</i> )	0,13460262	0,5279619	NA
DnaJ/HSP40	Stress	Kültz, 2005	Dnajb9 DnaJ homolog subfamily B member 9 ( <i>Rattus norvegicus</i> )	-0,0628816	0,6748741	0,84927531
DnaJ/HSP40	Stress	Kültz, 2005	Dnajc1 DnaJ homolog subfamily C member 1 ( <i>Mus musculus</i> )	0,00585137	0,97450812	0,98975567
DnaJ/HSP40	Stress	Kültz, 2005	dnajc10 DnaJ homolog subfamily C member 10 ( <i>Xenopus laevis</i> )	0,10610631	0,39034194	0,6516064
DnaJ/HSP40	Stress	Kültz, 2005	DNAJC11 DnaJ homolog subfamily C member 11 ( <i>Homo sapiens</i> )	0,08536099	0,38471985	0,64692664
DnaJ/HSP40	Stress	Kültz, 2005	Dnajc11 DnaJ homolog subfamily C member 11 ( <i>Mus musculus</i> )	0,21920236	0,07662637	0,27862688
DnaJ/HSP40	Stress	Kültz, 2005	DNAJC13 DnaJ homolog subfamily C member 13 ( <i>Homo sapiens</i> )	-0,0483966	0,65775407	0,83848613
DnaJ/HSP40	Stress	Kültz, 2005	Dnajc14 DnaJ homolog subfamily C member 14	-0,052349	0,62853723	0,82337224

(*Mus musculus*)

DnaJ/HSP40	Stress	Kültz, 2005	DNAJC16 DnaJ homolog subfamily C member 16 ( <i>Gallus gallus</i> )	-0,029718	0,70630494	0,86434373
DnaJ/HSP40	Stress	Kültz, 2005	DNAJC16 DnaJ homolog subfamily C member 16 ( <i>Homo sapiens</i> )	0,03739141	0,65876462	0,83899293
DnaJ/HSP40	Stress	Kültz, 2005	DNAJC17 DnaJ homolog subfamily C member 17 ( <i>Homo sapiens</i> )	0,1120517	0,2702668	0,54394755
DnaJ/HSP40	Stress	Kültz, 2005	DNAJC18 DnaJ homolog subfamily C member 18 ( <i>Bos taurus</i> )	0,03481691	0,6672229	0,84444235
DnaJ/HSP40	Stress	Kültz, 2005	dnajc2 DnaJ homolog subfamily C member 2 ( <i>Danio rerio</i> )	0,37292936	0,02894158	0,16243513
DnaJ/HSP40	Stress	Kültz, 2005	dnajc21 DnaJ homolog subfamily C member 21 ( <i>Danio rerio</i> )	0,25408699	0,10812931	0,33538748
DnaJ/HSP40	Stress	Kültz, 2005	dnajc22 DnaJ homolog subfamily C member 22 ( <i>Xenopus tropicalis</i> )	-0,2994548	0,048528	0,21606727
DnaJ/HSP40	Stress	Kültz, 2005	DNAJC24 DnaJ homolog subfamily C member 24 ( <i>Homo sapiens</i> )	0,02187165	0,88806147	0,95089903
DnaJ/HSP40	Stress	Kültz, 2005	dnajc25 DnaJ homolog subfamily C member 25 ( <i>Xenopus tropicalis</i> )	0,23227578	0,17185702	0,42934732
DnaJ/HSP40	Stress	Kültz, 2005	dnajc27 DnaJ homolog subfamily C member 27 ( <i>Danio rerio</i> )	-0,1849614	0,01809832	0,12456891
DnaJ/HSP40	Stress	Kültz, 2005	DNAJC3 DnaJ homolog subfamily C member 3 ( <i>Homo sapiens</i> )	0,2276701	0,05541614	0,2312985
DnaJ/HSP40	Stress	Kültz, 2005	DNAJC30 DnaJ homolog subfamily C member 30 ( <i>Homo sapiens</i> )	-0,1752619	0,10543791	0,33064352
DnaJ/HSP40	Stress	Kültz, 2005	DNAJC30 DnaJ homolog subfamily C member 30 ( <i>Homo sapiens</i> )	0,25257003	0,23328839	0,50494743

DnaJ/HSP40	Stress	Kültz, 2005	Dnajc4 DnaJ homolog subfamily C member 4 ( <i>Mus musculus</i> )	0,2751197	0,00702109	0,07344488	
DnaJ/HSP40	Stress	Kültz, 2005	Dnajc5 DnaJ homolog subfamily C member 5 ( <i>Rattus norvegicus</i> )	0,07265772	0,5117175	0,74747086	
DnaJ/HSP40	Stress	Kültz, 2005	dnajc5 DnaJ homolog subfamily C member 5 ( <i>Torpedo californica</i> )	0,4114178	0,00539704	0,06240544	
DnaJ/HSP40	Stress	Kültz, 2005	dnajc5 DnaJ homolog subfamily C member 5 ( <i>Torpedo californica</i> )	-0,2375847	0,20527141	0,47204225	
DnaJ/HSP40	Stress	Kültz, 2005	dnajc5 DnaJ homolog subfamily C member 5 ( <i>Xenopus laevis</i> )	0,14448282	0,02209352	0,13920085	
DnaJ/HSP40	Stress	Kültz, 2005	DNAJC6 Putative tyrosine-protein phosphatase auxilin ( <i>Bos taurus</i> )	0,01673022	0,8637702	0,93995569	
DnaJ/HSP40	Stress	Kültz, 2005	DNAJC8 DnaJ homolog subfamily C member 8 ( <i>Homo sapiens</i> )	0,1616395	0,06614509	0,25662629	
DnaJ/HSP40	Stress	Kültz, 2005	Dnajc9 DnaJ homolog subfamily C member 9 ( <i>Mus musculus</i> )	0,53052605	0,00115683	0,02674162	*
Enolase (glycolysis)	Stress	Kültz, 2005	eno4 Enolase-like protein ENO4 ( <i>Danio rerio</i> )	0,14440751	0,50943685	NA	
Enolase (glycolysis)	Stress	Kültz, 2005	ENO1 Alpha-enolase ( <i>Gallus gallus</i> )	0,2826528	0,0178996	0,12386554	
Enolase (glycolysis)	Stress	Kültz, 2005	ENO2 Gamma-enolase ( <i>Homo sapiens</i> )	0,14702294	0,03028003	0,16626849	
Enolase (glycolysis)	Stress	Kültz, 2005	ENO2 Gamma-enolase ( <i>Homo sapiens</i> )	0,04704805	0,65764808	0,83848613	
Enolase (glycolysis)	Stress	Kültz, 2005	ENO3 Beta-enolase ( <i>Salmo salar</i> )	0,50747962	0,00045652	0,01580124	*
FtsH/proteasome-regulatory subunit	Stress	Kültz, 2005	Yme1l1 ATP-dependent zinc metalloprotease YME1L1 ( <i>Mus musculus</i> )	0,36519981	0,00715933	0,07424671	
FtsH/proteasome-regulatory subunit	Stress	Kültz, 2005	Yme1l1 ATP-dependent zinc metalloprotease YME1L1 ( <i>Rattus norvegicus</i> )	-0,1728105	0,09635154	0,31473423	



Glutathione reductase	Stress	Kültz, 2005	Gsr Glutathione reductase, mitochondrial ( <i>Mus musculus</i> )	-0,1045629	0,10245657	0,32597357	
Glycerol-3-phosphate dehydrogenase	Stress	Kültz, 2005	gpd1 Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic ( <i>Takifugu rubripes</i> )	0,84857478	2,3651E-07	8,1306E-05	*
Glycerol-3-phosphate dehydrogenase	Stress	Kültz, 2005	gpd1 Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic ( <i>Takifugu rubripes</i> )	-0,289349	0,07302165	0,27108681	
Glycerol-3-phosphate dehydrogenase	Stress	Kültz, 2005	gpd1l Glycerol-3-phosphate dehydrogenase 1-like protein ( <i>Danio rerio</i> )	0,3146587	0,05072033	0,22143051	
Glycerol-3-phosphate dehydrogenase	Stress	Kültz, 2005	gpd1l Glycerol-3-phosphate dehydrogenase 1-like protein ( <i>Xenopus tropicalis</i> )	0,07080786	0,51509394	0,74950492	
Glycerol-3-phosphate dehydrogenase	Stress	Kültz, 2005	GPD2 Glycerol-3-phosphate dehydrogenase, mitochondrial ( <i>Homo sapiens</i> )	-0,1643592	0,2797175	0,55213205	
GrpE	Stress	Kültz, 2005	GRPEL1 GrpE protein homolog 1, mitochondrial ( <i>Bos taurus</i> )	0,06325665	0,53424353	0,76214896	
Hsp 47	Stress	Abdel-Gawad & Khalil, 2013	SERPINH1 Serpin H1 ( <i>Gallus gallus</i> )	0,72302959	1,4035E-05	0,00170173	*
Hsp 47	Stress	Abdel-Gawad & Khalil, 2013	SERPINH1 Serpin H1 ( <i>Gallus gallus</i> )	-0,0936289	0,30818958	0,57860825	
HSP60	Stress	Kültz, 2005	HSPD1 60 kDa heat shock protein, mitochondrial ( <i>Gallus gallus</i> )	0,32446635	0,08534515	0,29511123	
HSP70	stress	Kültz, 2005	Heat shock 70 kDa protein 1 ( <i>Oryzias latipes</i> )	0,75200875	0,00043952	0,0154065	*
HSP70	stress	Kültz, 2005	Heat shock 70 kDa protein 1 ( <i>Oryzias latipes</i> )	0,51146259	0,01921057	0,12848486	
HSP70	stress	Kültz, 2005	Heat shock 70 kDa protein 1 ( <i>Oryzias latipes</i> )	-0,2190849	0,2116296	0,48045302	
HSP70	stress	Kültz, 2005	Heat shock 70 kDa protein 1 ( <i>Oryzias latipes</i> )	0,19838258	0,3485764	0,61651539	
HSP70	stress	Kültz, 2005	Heat shock 70 kDa protein 1 ( <i>Oryzias latipes</i> )	-0,0440985	0,80789728	0,91452048	
Hydroxyacylglutathione hydrolase	Stress	Kültz, 2005	hagh Hydroxyacylglutathione hydrolase, mitochondrial ( <i>Danio rerio</i> )	0,02300864	0,8347145	0,92593186	

Inositol monophosphataseb	Stress	Kültz, 2005	IMPA1 Inositol monophosphatase 1 ( <i>Bos taurus</i> )	0,05184595	0,74797155	0,88554062
Inositol monophosphataseb	Stress	Kültz, 2005	IMPA1 Inositol monophosphatase 1 ( <i>Homo sapiens</i> )	0,18523506	0,11343719	0,34470888
Inositol monophosphataseb	Stress	Kültz, 2005	impad1 Inositol monophosphatase 3 ( <i>Danio rerio</i> )	0,12119763	0,34025252	0,60959877
Isocitrate dehydrogenase	Stress	Kültz, 2005	IDH1 Isocitrate dehydrogenase [NADP] cytoplasmic ( <i>Bos taurus</i> )	0,28400279	0,10216866	0,32573221
Isocitrate dehydrogenase	Stress	Kültz, 2005	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial ( <i>Bos taurus</i> )	0,09239702	0,6126502	0,81285845
Isocitrate dehydrogenase	Stress	Kültz, 2005	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial (Fragment) ( <i>Sus scrofa</i> )	0,41259168	0,02310097	0,14288211
Isocitrate dehydrogenase	Stress	Kültz, 2005	ldh3a Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial ( <i>Mus musculus</i> )	0,22716399	0,03054447	0,16701441
Isocitrate dehydrogenase	Stress	Kültz, 2005	ldh3a Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial ( <i>Mus musculus</i> )	0,21198584	0,11574912	0,34829518
Isocitrate dehydrogenase	Stress	Kültz, 2005	IDH3B Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial ( <i>Macaca fascicularis</i> )	0,20792493	0,07551283	0,27619271
Isocitrate dehydrogenase	Stress	Kültz, 2005	ldh3g Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial ( <i>Mus musculus</i> )	0,09609688	0,13468964	0,37731496
Isocitrate dehydrogenase	Stress	Kültz, 2005	IDH3G Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial ( <i>Bos taurus</i> )	0,24112538	0,00857829	0,08256659
Lon protease/protease La	Stress	Kültz, 2005	Lonp1 Lon protease homolog, mitochondrial ( <i>Rattus norvegicus</i> )	0,23151518	0,07473851	0,27475204
Lon protease/protease La	Stress	Kültz, 2005	lonp2 Lon protease homolog 2, peroxisomal ( <i>Danio rerio</i> )	-0,1610909	0,14909542	0,39905742
Long-chain fatty acid ABC transporter	Stress	Kültz, 2005	SLC27A1 Long-chain fatty acid transport protein 1 ( <i>Homo sapiens</i> )	0,22987098	0,04734361	0,21305296

Long-chain fatty acid ABC transporter	Stress	Kültz, 2005	SLC27A4 Long-chain fatty acid transport protein 4 ( <i>Homo sapiens</i> )	-0,302294	0,03880116	0,19024607	
Long-chain fatty acid ABC transporter	Stress	Kültz, 2005	SLC27A6 Long-chain fatty acid transport protein 6 ( <i>Homo sapiens</i> )	-0,2187064	0,03966388	0,19274368	
Long-chain fatty acid ABC transporter	Stress	Kültz, 2005	SLC27A6 Long-chain fatty acid transport protein 6 ( <i>Homo sapiens</i> )	0,10965643	0,33765059	0,60784251	
Long-chain-fatty-acid CoA ligase	Stress	Kültz, 2005	ACSBG2 Long-chain-fatty-acid--CoA ligase ACSBG2 ( <i>Gallus gallus</i> )	0,26324513	0,01828256	0,12507792	
Long-chain-fatty-acid CoA ligase	Stress	Kültz, 2005	acsbg2 Long-chain-fatty-acid--CoA ligase ACSBG2 ( <i>Xenopus laevis</i> )	-0,1774469	0,3071425	0,57747223	
Long-chain-fatty-acid CoA ligase	Stress	Kültz, 2005	ACSL1 Long-chain-fatty-acid--CoA ligase 1 ( <i>Cavia porcellus</i> )	0,24714912	0,11213524	0,342445	
Long-chain-fatty-acid CoA ligase	Stress	Kültz, 2005	ACSL1 Long-chain-fatty-acid--CoA ligase 1 ( <i>Cavia porcellus</i> )	-0,137843	0,12322295	0,35977816	
Long-chain-fatty-acid CoA ligase	Stress	Kültz, 2005	Acs1 Long-chain-fatty-acid--CoA ligase 1 ( <i>Rattus norvegicus</i> )	0,24586071	0,09865126	0,31905681	
Long-chain-fatty-acid CoA ligase	Stress	Kültz, 2005	ACSL3 Long-chain-fatty-acid--CoA ligase 3 ( <i>Homo sapiens</i> )	0,24283601	0,08858378	0,30141313	
Long-chain-fatty-acid CoA ligase	Stress	Kültz, 2005	ACSL3 Long-chain-fatty-acid--CoA ligase 3 ( <i>Homo sapiens</i> )	0,22061061	0,11238775	0,34294451	
Long-chain-fatty-acid CoA ligase	Stress	Kültz, 2005	Acs15 Long-chain-fatty-acid--CoA ligase 5 ( <i>Rattus norvegicus</i> )	-0,1850102	0,14385297	0,39110723	
Long-chain-fatty-acid CoA ligase	Stress	Kültz, 2005	Acs16 Long-chain-fatty-acid--CoA ligase 6 ( <i>Rattus norvegicus</i> )	0,49570693	0,00098853	0,02456686	*
MsrA/PMSR	Stress	Kültz, 2005	MSRA Mitochondrial peptide methionine sulfoxide reductase ( <i>Homo sapiens</i> )	-0,0915487	0,28799847	0,55982612	
MutL/MLH	Stress	Kültz, 2005	Mlh1 DNA mismatch repair protein Mlh1 ( <i>Mus</i> )	0,04082803	0,64902527	0,83361481	

*musculus*)

MutS/MSH	Stress	Kültz, 2005	MSH4 MutS protein homolog 4 ( <i>Homo sapiens</i> )	0	1	NA	
MutS/MSH	Stress	Kültz, 2005	MSH5 MutS protein homolog 5 ( <i>Homo sapiens</i> )	-0,1970061	0,34243713	NA	
MutS/MSH	Stress	Kültz, 2005	MSH5 MutS protein homolog 5 ( <i>Homo sapiens</i> )	0,03753203	0,7546332	NA	
MutS/MSH	Stress	Kültz, 2005	MSH2 DNA mismatch repair protein Msh2 ( <i>Chlorocebus aethiops</i> )	0,51151545	0,00377669	0,05088112	
MutS/MSH	Stress	Kültz, 2005	MSH3 DNA mismatch repair protein Msh3 ( <i>Homo sapiens</i> )	-0,0995816	0,16765154	0,42405589	
MutS/MSH	Stress	Kültz, 2005	MSH4 MutS protein homolog 4 ( <i>Homo sapiens</i> )	0,38453742	0,00064716	0,01906865	*
Nucleoside diphosphate kinase	Stress	Kültz, 2005	NME1-2 Nucleoside diphosphate kinase A 2 ( <i>Bos taurus</i> )	0,59847051	2,2563E-05	0,00232397	*
Nucleoside diphosphate kinase	Stress	Kültz, 2005	NME2 Nucleoside diphosphate kinase B ( <i>Sus scrofa</i> )	0,2197657	0,05337044	0,22736444	
Nucleoside diphosphate kinase	Stress	Kültz, 2005	Nme4 Nucleoside diphosphate kinase, mitochondrial ( <i>Mus musculus</i> )	-0,0970111	0,50750571	0,74496106	
Nucleoside diphosphate kinase	Stress	Kültz, 2005	NME5 Nucleoside diphosphate kinase homolog 5 ( <i>Homo sapiens</i> )	-0,0996001	0,56199909	0,78106877	
Nucleoside diphosphate kinase	Stress	Kültz, 2005	nme6 Nucleoside diphosphate kinase 6 ( <i>Danio rerio</i> )	0,34354491	0,0176642	0,1228972	
Nucleoside diphosphate kinase	Stress	Kültz, 2005	Nme7 Nucleoside diphosphate kinase 7 ( <i>Mus musculus</i> )	-0,0870626	0,38070009	0,64347861	
Peroxiredoxin	Stress	Kültz, 2005	Peroxiredoxin ( <i>Cynops pyrrhogaster</i> )	0,28317077	0,04578585	0,20928344	
Peroxiredoxin	Stress	Kültz, 2005	PRDX1 Peroxiredoxin-1 ( <i>Myotis lucifugus</i> )	0,10261875	0,50591659	0,74416442	
Peroxiredoxin	Stress	Kültz, 2005	PRDX5 Peroxiredoxin-5, mitochondrial ( <i>Homo sapiens</i> )	0,27819123	0,03948861	0,19217809	

Peroxiredoxin	Stress	Kültz, 2005	PRDX6 Peroxiredoxin-6 ( <i>Gallus gallus</i> )	0,11702803	0,37874032	0,64157233
Peroxiredoxin	Stress	Kültz, 2005	PRDX6 Peroxiredoxin-6 ( <i>Gallus gallus</i> )	0,12437383	0,52598911	0,75686903
Petidyl-prolyl isomerase	Stress	Kültz, 2005	PIN1 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 ( <i>Homo sapiens</i> )	0,06150119	0,45205853	0,70167428
Phosphoglucomutase	Stress	Kültz, 2005	PGM1 Phosphoglucomutase-1 ( <i>Macaca fascicularis</i> )	0,4641161	0,02358025	0,14505539
Phosphoglucomutase	Stress	Kültz, 2005	Pgm1 Phosphoglucomutase-1 ( <i>Mus musculus</i> )	0,41084113	0,00744629	0,0760366
Phosphoglucomutase	Stress	Kültz, 2005	PGM2 Phosphoglucomutase-2 ( <i>Homo sapiens</i> )	-0,1766138	0,03182217	0,17084366
Proline oxidase	Stress	Kültz, 2005	PRODH Proline dehydrogenase 1, mitochondrial ( <i>Bos taurus</i> )	-0,2054665	0,19667464	0,46188242
Proline oxidase	Stress	Kültz, 2005	Prodh Proline dehydrogenase 1, mitochondrial ( <i>Mus musculus</i> )	0,2348219	0,21772139	0,48739556
Proline oxidase	Stress	Kültz, 2005	prodh2 Probable proline dehydrogenase 2 ( <i>Xenopus laevis</i> )	0,02217484	0,90136449	0,95641945
Proline oxidase	Stress	Kültz, 2005	prodh2 Probable proline dehydrogenase 2 ( <i>Xenopus laevis</i> )	0,01047238	0,91384906	0,96273749
Protease II/prolyl endopetidase	Stress	Kültz, 2005	FAP Prolyl endopeptidase FAP ( <i>Bos taurus</i> )	0,51949238	0,01403818	0,10899804
Protease II/prolyl endopetidase	Stress	Kültz, 2005	Prep Prolyl endopeptidase ( <i>Mus musculus</i> )	0,34268662	0,00210075	0,03675176 *
Putative oxidoreductase YIM4	Stress	Kültz, 2005	glyr1 Putative oxidoreductase GLYR1 ( <i>Danio rerio</i> )	-0,0486269	0,53659593	0,76352741
Quinone oxidoreductase	Stress	Kültz, 2005	MT-ND1 NADH-ubiquinone oxidoreductase chain 1 ( <i>Gadus morhua</i> )	0,22931012	0,02899064	0,16249258
Quinone oxidoreductase	Stress	Kültz, 2005	NDUFS1 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial ( <i>Homo sapiens</i> )	-0,4328279	0,02529622	0,15093629
Quinone oxidoreductase	Stress	Kültz, 2005	NDUFS1 NADH-ubiquinone oxidoreductase 75	0,10646753	0,3734363	0,63740402

kDa subunit, mitochondrial (*Pongo pygmaeus*)

Quinone oxidoreductase	Stress	Kültz, 2005	TP53I3 Quinone oxidoreductase PIG3 ( <i>Homo sapiens</i> )	0,21148297	0,17237532	0,43013509
RecA/Rad51	Stress	Kültz, 2005	RAD51 DNA repair protein RAD51 homolog 1 ( <i>Homo sapiens</i> )	0,59041721	0,00675341	0,07213101
RecA/Rad51	Stress	Kültz, 2005	RAD51B DNA repair protein RAD51 homolog 2 ( <i>Homo sapiens</i> )	0,01210745	0,91109003	0,96114389
RecA/Rad51	Stress	Kültz, 2005	Rad51c DNA repair protein RAD51 homolog 3 ( <i>Mus musculus</i> )	0,26207945	0,13633057	0,38013967
RecA/Rad51	Stress	Kültz, 2005	Rad51d DNA repair protein RAD51 homolog 4 ( <i>Mus musculus</i> )	-0,1042373	0,26461028	0,53697381
Ribosomal RNA methyltransferase	Stress	Kültz, 2005	Emg1 Ribosomal RNA small subunit methyltransferase NEP1 ( <i>Mus musculus</i> )	0,28353456	0,0360367	0,1825891
Ribosomal RNA methyltransferase	Stress	Kültz, 2005	Ftsj2 rRNA methyltransferase 2, mitochondrial ( <i>Mus musculus</i> )	0,2641028	0,05587136	0,2322432
Ribosomal RNA methyltransferase	Stress	Kültz, 2005	Nop2 Probable 28S rRNA (cytosine-C(5))-methyltransferase ( <i>Mus musculus</i> )	0,20879802	0,16526881	0,42078939
Ribosomal RNA methyltransferase	Stress	Kültz, 2005	nsun4 5-methylcytosine rRNA methyltransferase NSUN4 ( <i>Xenopus laevis</i> )	0,29807049	0,03100567	0,16857255
Ribosomal RNA methyltransferase	Stress	Kültz, 2005	NSUN5 Probable 28S rRNA (cytosine-C(5))-methyltransferase ( <i>Homo sapiens</i> )	0,1810732	0,03156768	0,17028353
Ribosomal RNA methyltransferase	Stress	Kültz, 2005	RNMTL1 rRNA methyltransferase 3, mitochondrial ( <i>Homo sapiens</i> )	0,19448019	0,04187058	0,19926315
Ribosomal RNA methyltransferase	Stress	Kültz, 2005	Wbscr22 Probable 18S rRNA (guanine-N(7))-methyltransferase ( <i>Mus musculus</i> )	0,1145616	0,28732639	0,55936237
SelB	Stress	Kültz, 2005	EEFSEC Selenocysteine-specific elongation factor ( <i>Homo sapiens</i> )	0,15193804	0,21309646	0,48202354

Serine protease	Stress	Kültz, 2005	F56F10.1 Putative serine protease F56F10.1 ( <i>Caenorhabditis elegans</i> )	-0,2348553	0,20272516	0,46896309	
Serine protease	Stress	Kültz, 2005	Htra1 Serine protease HTRA1 ( <i>Rattus norvegicus</i> )	0,27358533	0,20814437	0,47607253	
Serine protease	Stress	Kültz, 2005	htra1a Serine protease HTRA1A ( <i>Danio rerio</i> )	0,49455987	3,2877E-05	0,00309192	*
Serine protease	Stress	Kültz, 2005	htra1a Serine protease HTRA1A ( <i>Danio rerio</i> )	0,26790745	0,14365531	0,3907442	
Serine protease	Stress	Kültz, 2005	HTRA2 Serine protease HTRA2, mitochondrial ( <i>Bos taurus</i> )	0,03796473	0,58841845	0,79770662	
Serine protease	Stress	Kültz, 2005	HTRA3 Serine protease HTRA3 ( <i>Homo sapiens</i> )	0,62953631	0,0013168	0,02878293	*
Serine protease	Stress	Kültz, 2005	Htra3 Serine protease HTRA3 ( <i>Rattus norvegicus</i> )	0,0573185	0,53513815	0,76254132	
Serine protease	Stress	Kültz, 2005	Prss16 Thymus-specific serine protease ( <i>Mus musculus</i> )	-0,1445216	0,40008456	0,66015322	
Serine protease	Stress	Kültz, 2005	Prss23 Serine protease 23 ( <i>Rattus norvegicus</i> )	0,25774794	0,20917566	0,47752487	
Serine protease	Stress	Kültz, 2005	PRSS27 Serine protease 27 ( <i>Homo sapiens</i> )	-0,3783159	0,05058709	0,22114934	
Serine protease	Stress	Kültz, 2005	PRSS27 Serine protease 27 ( <i>Homo sapiens</i> )	-0,2235663	0,31336512	0,58417651	
Serine protease	Stress	Kültz, 2005	PRSS27 Serine protease 27 ( <i>Homo sapiens</i> )	-0,1689149	0,35045715	0,61835298	
Serine protease	Stress	Kültz, 2005	Prss27 Serine protease 27 ( <i>Rattus norvegicus</i> )	-0,4477272	0,01058158	0,09291189	
Serine protease	Stress	Kültz, 2005	Prss27 Serine protease 27 ( <i>Rattus norvegicus</i> )	-0,3882908	0,02738613	0,15679384	
Serine protease	Stress	Kültz, 2005	Prss27 Serine protease 27 ( <i>Rattus norvegicus</i> )	-0,1124598	0,28200636	0,55447837	
Serine protease	Stress	Kültz, 2005	htra1b Serine protease HTRA1B ( <i>Danio rerio</i> )	0,33267545	0,13864094	NA	
Serine protease	Stress	Kültz, 2005	Prss57 Serine protease 57 ( <i>Mus musculus</i> )	-0,0636853	0,77297281	NA	
Serine protease	Stress	Kültz, 2005	PRSS35 Inactive serine protease 35 ( <i>Homo</i>	0,34689785	0,08343624	0,29165477	

*sapiens*)

Succinate-semialdehyde dehydrogenase	Stress	Kültz, 2005	Aldh5a1 Succinate-semialdehyde dehydrogenase, mitochondrial ( <i>Rattus norvegicus</i> )	0,28853965	0,1201571	0,35523826
Superoxide dismutase	Stress	Kültz, 2005	SOD2 Superoxide dismutase [Mn], mitochondrial ( <i>Bos taurus</i> )	0,11683525	0,08559427	0,29567674
Superoxide dismutase	Stress	Kültz, 2005	SOD3 Extracellular superoxide dismutase [Cu-Zn] ( <i>Homo sapiens</i> )	0,07964429	0,70538519	0,8639253
Thioredoxin	Stress	Kültz, 2005	Txn1l1 Thioredoxin-like protein 1 ( <i>Mus musculus</i> )	0,04447477	0,78270101	0,90273778
Thioredoxin	Stress	Kültz, 2005	TXNRD1 Thioredoxin reductase 1, cytoplasmic ( <i>Sus scrofa</i> )	-0,0512619	0,75458975	0,88933462
Thioredoxin	Stress	Kültz, 2005	Txnrd2 Thioredoxin reductase 2, mitochondrial ( <i>Mus musculus</i> )	-0,0142916	0,86703013	0,94149238
Thioredoxin	Stress	Kültz, 2005	TXNRD3 Thioredoxin reductase 3 ( <i>Homo sapiens</i> )	-0,0301976	0,72375005	0,87277156
Topoisomerase I/III	Stress	Kültz, 2005	TOP1 DNA topoisomerase 1 ( <i>Chlorocebus aethiops</i> )	0,05236843	0,78277204	0,90273778
Topoisomerase I/III	Stress	Kültz, 2005	TOP1 DNA topoisomerase 1 ( <i>Homo sapiens</i> )	0,24329612	0,06667777	0,25778282
Topoisomerase I/III	Stress	Kültz, 2005	top1 DNA topoisomerase 1 ( <i>Xenopus laevis</i> )	0,10503409	0,16905713	0,42582499
Topoisomerase I/III	Stress	Kültz, 2005	TOP3B DNA topoisomerase 3-beta-1 ( <i>Homo sapiens</i> )	0,16576543	0,21566015	0,48509066



Table 8 Supplementary information and References to Figure 4

Reference Nr in Figure 4	Species	Stressor	time	tissue	mRNA/ Protein	Reference	HSP70	
1	<i>Solea senegalensis</i>	pCO <sub>2</sub>	1 month	pooled whole larvae	Protein	Pimentel et al., 2015	1.4849861	
1	<i>Solea senegalensis</i>	pCO <sub>2</sub>	1 month	pooled whole larvae	Protein	Pimentel et al., 2015	2.1364074	*
2	<i>Carassius carassius</i>	hypoxia	7 day	brain	mRNA	Stenslokken et al., 2010	0.9610716	
2	<i>Carassius carassius</i>	hypoxia	7 day	heart	mRNA	Stenslokken et al., 2010	1.6777697	*
2	<i>Carassius carassius</i>	hypoxia	7 day	brain	mRNA	Stenslokken et al., 2010	11.9058795	*
3	<i>Paralichthys olivaceus</i>	salinity	2 weeks	liver	mRNA	Choi, 2010	29.3750244	*
3	<i>Paralichthys olivaceus</i>	salinity	2 weeks	liver	mRNA	Choi, 2010	53.3750634	*
3	<i>Paralichthys olivaceus</i>	salinity	2 weeks	liver	mRNA	Choi, 2010	55.8750634	*
4	<i>Mylio macrocephalus</i>	salinity	8 month	liver	Protein	Deane et al., 2002	1.8479852	*
4	<i>Mylio macrocephalus</i>	salinity	8 month	liver	Protein	Deane et al., 2002	0.4994684	
4	<i>Mylio macrocephalus</i>	salinity	8 month	liver	Protein	Deane et al., 2002	1.6354201	*
5	<i>Sparus sarba</i>	salinity	1 month	liver	mRNA	Deane and Woo, 2004	0.9412418	
5	<i>Sparus sarba</i>	salinity	1 month	liver	mRNA	Deane and Woo, 2004	1.1841484	
5	<i>Sparus sarba</i>	salinity	1 month	liver	mRNA	Deane and Woo, 2004	1.0051117	
5	<i>Sparus sarba</i>	salinity	1 month	kidney	mRNA	Deane and Woo, 2004	1.0950025	
5	<i>Sparus sarba</i>	salinity	1 month	kidney	mRNA	Deane and Woo, 2004	0.9226692	
5	<i>Sparus sarba</i>	salinity	1 month	kidney	mRNA	Deane and Woo, 2004	0.8055263	
5	<i>Sparus sarba</i>	salinity	1 month	gill	mRNA	Deane and Woo, 2004	1.6199978	
5	<i>Sparus sarba</i>	salinity	1 month	gill	mRNA	Deane and Woo, 2004	0.3400002	*
5	<i>Sparus sarba</i>	salinity	1 month	gill	mRNA	Deane and Woo, 2004	0.3266668	*
7	<i>Paralichthys olivaceus</i>	salinity	48h	whole larvae	mRNA	Wu et al., 2017	1.3661964	
7	<i>Paralichthys olivaceus</i>	salinity	48h	whole larvae	mRNA	Wu et al., 2017	1.5563394	
3	<i>Paralichthys olivaceus</i>	temperature	2 weeks	liver	mRNA	Choi, 2010	49.6489394	*
3	<i>Paralichthys olivaceus</i>	temperature	2 weeks	liver	mRNA	Choi, 2010	46.3822024	*
1	<i>Solea senegalensis</i>	temperature	1 month	pooled whole	Protein	Pimentel et al., 2015	1.0679184	
1	<i>Solea senegalensis</i>	temperature	1 month	pooled whole	Protein	Pimentel et al., 2015	1.7344358	*
8	<i>Melanotaenia duboulayi</i>	temperature	14 days	liver	mRNA	Smith et al., 2013	9.9000000	*
This study	<i>Gadus morhua</i>	pCO <sub>2</sub>	36 days	whole larvae	mRNA		1.6800000	*

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