

Supplementary

Table S1. Summary of chemicals used

CHEMICALS	FULL NAME	IDENTIFIER SOURCE	FUNCTION TARGETED
AICAR	5-Aminoimidazole-4-carboxamide 1- β -D-ribofuranoside, Acadesine, N1-(β -D-Ribofuranosyl)-5-aminoimidazole-4-carboxamide	AICAR, A9978 \geq 98% (HPLC), Sigma, Product of Canada; Lot # 033M4706V	AMP-activated protein kinase (AMPK) activator (inducer)
KNK437	3-(1,3-Benzodioxol-5-ylmethylene)-2-oxo-1-pyrrolidinecarboxaldehyde	KNK437, SML0964 \geq 98% (HPLC), Sigma, Product of USA; Lot # 024M4622V	Heat shock proteins inhibitor
U0126	1,4-Diamino-2,3-dicyano-1,4-bis(o-aminophenylmercapto)butadiene monoethanolate	U0126 monoethanolate, U120 \geq 98% (HPLC), Sigma, Product of USA; Lot # 032M4603V	Mitogen-activated protein kinase (MAPK)/ERK inhibitor
LPS	Lipopolysaccharides	LPS, L6529 (from <i>Escherichia coli</i> 055:B5), Sigma, Product of Israel; Lot # 121M4024V	Pro-inflammatory cytokines inducer

Table S2. Details of the primer sequence used for qRT-PCR

PRIMER	SEQUENCE (5' – 3')
<i>ACCA</i>	Forward: CACGATGCTCAGTTGTGTCC Reverse: CCATGACAGTGGACTTGACG
<i>FAS</i>	Forward: GAGAAAGCTTGCCAAACAGG Reverse: GAGGGTCTTGCAGGAGACAG
<i>LEPTIN</i>	Forward: AGCTCTCCGCTCAACCTGTA Reverse: CAGCGGGAATCTCTGGATAA
<i>SREBF1</i>	Forward: CATCCACATGGCTCTGAGTG Reverse: CTCATCCACAAAGAAGCGGT
<i>AMPKα</i>	Forward: AGTTATCAGCACACCGACAG Reverse: AGTAATCCACCCCTGAGATG
<i>ERK1</i>	Forward: GCCCTACGTCCAGGAGTACA Reverse: TTA CTCTTGCTGGCGAAC
<i>ATP2A1</i>	Forward: AAGTTGGCGAGGCTACAGAG Reverse: CCTTGGACAGACCACGAACA
<i>SIRT1</i>	Forward: ACAGTTCCAGCCATCTCCATGTCA Reverse: AAGACCCGTGGCACTGAATGATCT
<i>IFN-γ</i>	Forward: GAGAGGCTGGCACATGTTCAA Reverse: CTCTGCACTCTTGCCTGGAAA
<i>IL-1β</i>	Forward: ATCCAAACGGATACGACCAG Reverse: TCGGTGTCTTTCCCTGTCCAT
<i>IL-6</i>	Forward: TCAACTTCTCCAGCGTGATG Reverse: TCTTCCCTCTTTCCCTCTG
<i>TNF-α</i>	Forward: AGGCAATTTCACTTCCAAGG Reverse: AGGTCTTTGATTCAGAGTTGTATCC
<i>HSPA5</i>	Forward: AAGAGGCCGAAGAGAAGGAC Reverse: AGCAGCAGAGCCTCGAAATA
<i>HSP90b1</i>	Forward: ATGGCACCAAGAAGAATGACTT Reverse: GCACCAGCTTTTTACGGATAAC
<i>AKT1</i>	Forward: ACAATGATTACGGTCGTGCG Reverse: TTCTTGAGAAGGCCGAGAG
<i>PGC-1α</i>	Forward: GGCCAGCGAGCCAAACCAA Reverse: TGGCTTTGTGAGGAGCGTGG
<i>BAX</i>	Forward: GATACGGGCAGTGGCAATGA Reverse: ACTCCGGGTCACTTCAGCAT
<i>BCL-2</i>	Forward: CGAGTGTGTGGAGAAGGAGATG Reverse: TGGTTGTCTAGGTAGACGGTCAT
<i>NR3C1</i>	Forward: TCTCCTCCCAACAGCAGGAC Reverse: GTTGCATACAGTCGCAGCC
<i>TP53</i>	Forward: AGTTAAGTGATGTGGTGCCTGCCT Reverse: ATCAGCTTCTTTCCCTGTTTGGGC
<i>VDAC1</i>	Forward: GGAGGIACCAGCTGACCAAAG Reverse: ACAGCCCAGGTAAATGTGCT
<i>UCP1</i>	Forward: AGCCACAGACGTGGTAAAG Reverse: CGGCAGAGTTCCTTTCCAGA
<i>STOML2</i> (NM 201031.1)	Forward: GATGGGCTTCCAGTCTTCCC Reverse: ATTCGGTGAAAGCGTCCCAT
<i>β-ACTIN</i>	Forward: ATGAAGATCCTGACCGAG Reverse: TAGCTCTTCTCCAGGGAG

Table S3-1. Summary of a total of 519 proteins identified by Progenesis QIP and their relative expression ratios.

Accession	Description	Peptide count	Unique peptides	HFD vs. NFD		HAOS vs. HFD	
				p-value	Fold change	p-value	Fold change
A0A0A0MPS0	Si:dkey-222h21.2 OS=Danio rerio GN=si:dkey-222h21.2 PE=4 SV=1	8	1	0.000573804	1.50609578	0.012676344	0.786519766
A0A0B5GNT7	Bone morphogenetic protein 16 OS=Danio rerio GN=bmp16 PE=2 SV=1	3	3	0.949143472	0.961292974	0.177590678	1.138279807
A0A0G2KGN7	Uncharacterized protein OS=Danio rerio PE=4 SV=1	6	1	0.57635515	1.035846533	0.07205454	0.901445177
A0A0G2KGY3	Uncharacterized protein OS=Danio rerio PE=4 SV=1	2	1	0.000951693	0.358426449	0.175675079	1.187607958
A0A0G2KL83	Uncharacterized protein OS=Danio rerio PE=4 SV=1	4	1	0.00024477	3.75694322	0.000993273	0.598377703
A0A0G2KN74	Uncharacterized protein OS=Danio rerio PE=4 SV=1	5	3	0.051160265	1.224985714	0.070461923	0.869709204
A0A0G2KR36	Uncharacterized protein (Fragment) OS=Danio rerio PE=4 SV=1	6	1	0.009928234	2.539025871	0.073515115	0.884535078
A0A0G2KUN8	Uncharacterized protein OS=Danio rerio PE=1 SV=1	5	5	0.078717719	0.036342676	0.084326671	1.459707768
A0A0G2L2K5	Uncharacterized protein OS=Danio rerio GN=LOC564077 PE=1 SV=1	2	2	0.033676479	0.032459075	0.22747149	2.816851436
A0A0G2L6I6	Isocitrate dehydrogenase [NADP] OS=Danio rerio PE=1 SV=1	23	15	3.19E-05	3.135716213	0.000568442	0.662521705
A0A0G2L848	Uncharacterized protein OS=Danio rerio PE=4 SV=1	2	2	0.008647371	11.37864282	0.299260936	1.362313143
A0A0H2UKK8	Pseudouridylyl synthase 7 (putative) OS=Danio rerio GN=pus7 PE=1 SV=1	3	1	0.000110696	2.33956922	0.002659846	0.736527276
A0A0H2UKT2	Utrophin (Fragment) OS=Danio rerio GN=utrn PE=1 SV=1	8	3	0.001040567	0.31106145	0.934495212	0.994075724
A0A0N4STW3	Complement component c3b, tandem duplicate 1 OS=Danio rerio GN=c3b.1 PE=4 SV=1	11	1	0.000638454	2.012500309	0.025260076	0.767601352
A0A0N4SU68	Uncharacterized protein OS=Danio rerio GN=smyhc3 PE=3 SV=1	4	1	0.434974445	1.208796045	0.000232331	0.806417323
A0A0N4SU72	Si:ch73-236c18.6 OS=Danio rerio GN=si:ch73-236c18.6 PE=4 SV=1	6	2	0.037748978	1.200207068	0.09079342	0.863220529
A0A0N4SUF4	Uncharacterized protein OS=Danio rerio GN=smyhc3 PE=3 SV=1	4	1	0.849117642	0.953528753	0.009635236	0.910385255
A0A0R4I9C4	Triosephosphate isomerase OS=Danio rerio GN=tpi1b PE=1 SV=1	16	7	0.191364091	1.090355814	0.565011968	1.028032517
A0A0R4I9I7	Genetic suppressor element 1 OS=Danio rerio GN=gse1 PE=1 SV=1	7	5	0.802543004	0.743690238	0.009495412	0.822810518
A0A0R4IA56	Creatine kinase, muscle b OS=Danio rerio GN=ckmb PE=1 SV=1	68	30	0.131574001	0.870030321	0.232619417	0.950260762
A0A0R4IA89	Si:ch211-203c5.3 OS=Danio rerio GN=si:ch211-203c5.3 PE=4 SV=1	2	1	0.012296732	0.227261713	0.000127025	4.449589252
A0A0R4IAK4	Si:dkey-190j3.4 OS=Danio rerio GN=si:dkey-190j3.4 PE=4 SV=1	7	1	0.010466339	1.229198438	0.062467556	0.881853202
A0A0R4IAK9	Ubiquinol-cytochrome c reductase core protein Ila OS=Danio rerio GN=uqrc2a PE=1 SV=1	3	3	0.001599243	3.331054908	0.49600755	0.935693448
A0A0R4IB01	Si:dkey-165e24.1 OS=Danio rerio GN=si:dkey-165e24.1 PE=4 SV=1	6	1	0.000546698	2.951958048	0.001472405	0.667791213
A0A0R4IBI0	DENN/MADD domain-containing 4B OS=Danio rerio GN=dennd4b PE=1 SV=1	2	1	0.034841313	1.219350649	0.061077566	0.905121938
A0A0R4ICC8	Stomatin (EPB72)-like 2 OS=Danio rerio GN=stoml2 PE=1 SV=1	2	2	0.006202809	16.53599455	0.000557046	0.524276562
A0A0R4ICW1	Si:dkeyp-94b4.1 OS=Danio rerio GN=si:dkeyp-94b4.1 PE=1 SV=1	5	2	0.011425597	1.345551299	0.1069289	0.932738702
A0A0R4IDL5	Si:ch211-232d10.1 OS=Danio rerio GN=si:ch211-232d10.1 PE=4 SV=1	8	1	4.97E-05	2.202386079	0.00053849	0.697950336
A0A0R4IDU6	T-cell lymphoma invasion and metastasis 1b OS=Danio rerio GN=tiam1b PE=4 SV=1	2	1	0.001408037	2.729876609	0.004982947	0.699256879
A0A0R4IDW8	Si:dkey-193i10.4 OS=Danio rerio GN=si:dkey-193i10.4 PE=4 SV=1	3	1	0.029389694	1.301112546	0.011046141	0.798322844
A0A0R4IE10	Elongation factor 1-alpha OS=Danio rerio GN=eef1a111 PE=1 SV=1	28	1	0.0006904	1.469824612	0.005211397	0.867857978
A0A0R4IEU6	Si:ch211-223g7.2 OS=Danio rerio GN=si:ch211-223g7.2 PE=4 SV=1	7	2	0.002321634	1.659133082	0.054603164	0.854804409
A0A0R4IEY9	Si:dkey-16p6.1 OS=Danio rerio GN=si:dkey-16p6.1 PE=4 SV=1	4	2	0.033854539	1.320118454	0.038242921	0.882226864
A0A0R4IFA7	Si:dkey-250k10.4 (Fragment) OS=Danio rerio GN=si:dkey-250k10.4 PE=4 SV=1	6	2	0.141437374	1.298189161	0.637379478	0.975311528
A0A0R4IFD1	Reticulon-4-interacting protein 1 homolog, mitochondrial OS=Danio rerio GN=rtn4ip1	3	1	0.008464273	1.130187317	0.613641035	0.974361893

A0A0R4IFF1	Cytochrome P450, family 2, subfamily AA, polypeptide 7 OS=Danio rerio GN=cyp2aa7 PE=1 SV=1	2	1	0.033087547	0.255297448	0.000999068	1.827403389
A0A0R4IFJ4	Pyruvate carboxylase OS=Danio rerio GN=pcxa PE=1 SV=1	20	8	0.006099167	0.55348172	0.136205049	0.9313224
A0A0R4IFT7	Si:ch211-271g18.1 OS=Danio rerio GN=si:ch211-271g18.1 PE=4 SV=1	4	1	0.225451882	1.12022341	0.067175612	0.868733073
A0A0R4IFW1	Zgc:171445 OS=Danio rerio GN=zgc:171445 PE=1 SV=1	27	6	0.405228133	1.111548162	0.005925258	0.801412568
A0A0R4IGN3	Protein disulfide-isomerase (Fragment) OS=Danio rerio GN=pdia3 PE=1 SV=1	15	9	0.000667044	3.30510559	0.003433813	0.73201314
A0A0R4IGP6	Pyruvate kinase OS=Danio rerio GN=pkma PE=1 SV=1	21	1	0.000480514	1.655927149	0.003110248	0.800841846
A0A0R4IGQ8	Myomesin 1b OS=Danio rerio GN=myom1b PE=1 SV=1	24	16	0.076856744	0.866009184	0.395301645	0.961840661
A0A0R4IHC4	Si:ch211-76m11.3 (Fragment) OS=Danio rerio GN=si:ch211-76m11.3 PE=4 SV=1	4	1	0.000649233	2.976059905	0.001414465	0.661671786
A0A0R4IHH2	Si:ch211-246b8.1 OS=Danio rerio GN=si:ch211-246b8.1 PE=4 SV=1	6	1	0.000677778	2.959686503	0.001362097	0.661866285
A0A0R4IHV1	Pyruvate kinase OS=Danio rerio GN=pkmb PE=1 SV=1	23	16	0.009979593	2.281385885	0.474093043	0.914763094
A0A0R4IHY6	Si:ch211-272n13.3 (Fragment) OS=Danio rerio GN=si:ch211-272n13.3 PE=4 SV=1	3	2	0.881101476	1.037059773	0.856305361	0.996658467
A0A0R4II04	Si:dkey-29j8.1 OS=Danio rerio GN=si:dkey-29j8.1 PE=4 SV=1	10	2	3.22E-05	2.802234343	0.000207298	0.698606849
A0A0R4II73	Solute carrier family 25 (aspartate/glutamate carrier), member 12 (Fragment) OS=Danio rerio GN=slc25a12 PE=1 SV=1	25	19	0.002924111	0.532752194	0.412565942	1.031187714
A0A0R4II89	Catalase OS=Danio rerio GN=cat PE=1 SV=1	12	10	0.002195873	1.286679165	0.748901859	0.982594466
A0A0R4IIH4	FYVE and coiled-coil domain-containing 1a OS=Danio rerio GN=fyco1a PE=1 SV=1	22	13	0.000646066	2.097967893	0.019915594	0.845803384
A0A0R4IHW8	Si:dkey-7114.4 OS=Danio rerio GN=si:dkey-7114.4 PE=4 SV=1	5	1	0.000307368	3.119746855	0.000720046	0.664381746
A0A0R4IU29	Si:dkey-14o6.2 OS=Danio rerio GN=si:dkey-14o6.2 PE=4 SV=1	6	1	0.000444254	2.977983707	0.000921605	0.667119845
A0A0R4IU35	Si:ch211-156l18.7 OS=Danio rerio GN=si:ch211-156l18.7 PE=3 SV=1	9	1	0.008019281	1.748017695	0.42633469	0.963842511
A0A0R4IJS2	Si:ch211-59d8.2 (Fragment) OS=Danio rerio GN=si:ch211-59d8.2 PE=4 SV=1	7	1	0.000156649	2.547390691	0.00123856	0.686383034
A0A0R4IKF0	Apolipoprotein A-Ib OS=Danio rerio GN=apoa1b PE=1 SV=1	25	19	0.087717597	1.156860975	0.714085139	1.017722888
A0A0R4IKI3	Tripartite motif-containing 25 OS=Danio rerio GN=trim25 PE=1 SV=1	3	1	0.517401484	1.041880906	0.154423956	0.911682006
A0A0R4IL11	Leucine-rich repeat (in FLII)-interacting protein 1a OS=Danio rerio GN=lrrfip1a PE=4 SV=1	2	2	0.292804044	0.860574999	0.203062534	1.100195352
A0A0R4IL59	Si:ch211-229110.4 OS=Danio rerio GN=si:ch211-229110.4 PE=4 SV=1	12	3	0.049213538	1.257572789	0.046294574	0.871835039
A0A0R4IL12	Si:dkey-92c21.1 (Fragment) OS=Danio rerio GN=si:dkey-92c21.1 PE=4 SV=1	8	2	0.002077118	1.70014871	0.001861456	0.740799342
A0A0R4ILP1	Calreticulin 3a OS=Danio rerio GN=calr3a PE=1 SV=1	4	3	0.189580456	1.723914122	0.091517218	1.461959472
A0A0R4IMW8	Si:zfos-2131b9.2 (Fragment) OS=Danio rerio GN=si:zfos-2131b9.2 PE=4 SV=1	9	1	0.031911517	0.76216178	0.064518679	1.251256177
A0A0R4IN16	Si:dkey-264f17.2 OS=Danio rerio GN=si:dkey-264f17.2 PE=4 SV=1	4	1	0.000571602	2.941107745	0.001204328	0.654420044
A0A0R4IP07	Elongation factor 1-gamma OS=Danio rerio GN=eef1g PE=1 SV=1	9	4	0.28089306	1.147635557	0.099949582	0.915233801
A0A0R4IP08	Si:dkey-211i20.2 OS=Danio rerio GN=si:dkey-211i20.2 PE=4 SV=1	5	2	0.00026146	2.257682583	0.002443347	0.686619207
A0A0R4IP15	Neogenin 1a OS=Danio rerio GN=neo1a PE=4 SV=1	2	2	0.435245803	1.231107591	0.008623645	1.525629377
A0A0R4IP16	Si:ch211-39d8.1 OS=Danio rerio GN=si:ch211-39d8.1 PE=4 SV=1	5	1	0.00067265	2.967684702	0.001341863	0.65936457
A0A0R4IP53	TAO kinase 1b OS=Danio rerio GN=taok1b PE=4 SV=1	5	2	0.013555091	1.931971083	0.001671098	0.733515064
A0A0R4IPE2	Si:dkey-46g23.5 OS=Danio rerio GN=si:dkey-46g23.5 PE=1 SV=1	28	9	0.004933824	1.243931521	0.0122054	0.849621366
A0A0R4IPH2	Tubulin beta chain OS=Danio rerio GN=tubb4b PE=1 SV=1	33	1	0.149889587	1.039079494	0.208826136	1.047579104
A0A0R4IPK3	Myomesin 2a (Fragment) OS=Danio rerio GN=myom2a PE=1 SV=1	7	1	0.003943091	3.242013334	0.679548058	1.019863249
A0A0R4IQ11	Scinderin-like a OS=Danio rerio GN=scinla PE=1 SV=1	2	1	0.172401143	1.24100496	0.372609387	0.924739212
A0A0R4IQC8	Si:dkeyp-35e5.5 OS=Danio rerio GN=si:dkeyp-35e5.5 PE=4 SV=1	14	2	0.396860241	0.935522208	0.881712265	0.993460878
A0A0R4IQE4	Si:ch211-196f19.1 OS=Danio rerio GN=si:ch211-196f19.1 PE=4 SV=1	6	1	0.005759478	3.209239806	0.006763221	0.752118486
A0A0R4IQI9	Cytoskeleton-associated protein	5	12	0.00023124	3.474135523	0.000589932	0.674213706

	OS=Danio rerio GN=ckap5 PE=1 SV=1								
A0A0R4IQN7	Si:ch211-209j12.6 OS=Danio rerio GN=si:ch211-209j12.6 PE=4 SV=1	2	1	0.283600435	1.10826108	0.083425249	0.88056636		
A0A0R4IR90	Myosin IB OS=Danio rerio GN=myo1b PE=1 SV=1	6	4	0.000478736	5.561367396	0.020287273	1.156373496		
A0A0R4IRB5	General transcription factor IIB OS=Danio rerio GN=gtf2b PE=1 SV=1	3	3	0.009052174	3.67435287	0.298313067	0.772474216		
A0A0R4IRS6	Sideroflexin (Fragment) OS=Danio rerio GN=sfxn5a PE=3 SV=1	2	1	0.002907717	5.000975669	0.861169841	0.958962535		
A0A0R4IRT1	Sodium/potassium-transporting ATPase subunit alpha OS=Danio rerio GN=atp1a1a.1 PE=1 SV=1	29	2	0.001777154	1.23022117	0.076623197	0.915632864		
A0A0R4ISX6	Protein disulfide-isomerase OS=Danio rerio GN=p4hb PE=1 SV=1	18	11	0.000103435	2.384613978	0.002040387	0.745032223		
A0A0R4ITY7	Si:ch211-76m11.8 OS=Danio rerio GN=si:ch211-76m11.8 PE=4 SV=1	6	1	0.000502833	2.335832912	0.002227229	0.691278013		
A0A0R4IU19	Si:ch211-93f2.1 (Fragment) OS=Danio rerio GN=si:ch211-93f2.1 PE=1 SV=1	4	2	0.170218368	0.279393608	0.52265894	1.132953619		
A0A0R4IU65	Creatine kinase, brain a OS=Danio rerio GN=ckba PE=1 SV=1	26	1	0.002042677	1.227689603	0.125405292	0.921351585		
A0A0R4IUB8	Si:dkeyp-5g9.1 OS=Danio rerio GN=si:dkeyp-5g9.1 PE=4 SV=1	4	1	0.013257627	1.336384852	0.069272577	0.877063536		
A0A0R4IUG7	Glutamate dehydrogenase Ia OS=Danio rerio GN=glud1a PE=1 SV=1	14	5	0.476844172	1.026268866	0.235811446	0.942436435		
A0A0R4IUS1	Si:ch211-223g7.6 OS=Danio rerio GN=si:ch211-223g7.6 PE=4 SV=1	9	2	4.48E-05	2.404089047	0.00192935	0.757058554		
A0A0R4IUS8	Si:dkey-29m1.2 OS=Danio rerio GN=si:dkey-29m1.2 PE=4 SV=1	4	1	0.000472949	2.987076736	0.000605749	0.648797149		
A0A0R4IVB0	Heat shock cognate 71 kDa protein OS=Danio rerio GN=hspa8 PE=1 SV=1	33	2	0.000529251	3.621026149	0.017190517	0.63830842		
A0A0R4IVJ6	Si:dkey-121j17.5 OS=Danio rerio GN=si:dkey-121j17.5 PE=4 SV=1	3	1	0.714121815	0.979757271	0.208103537	0.811261768		
A0A0R4IWC6	Annexin OS=Danio rerio GN=anxa1a PE=1 SV=1	6	3	0.018391498	0.57913314	0.971357813	0.996147153		
A0A0R4IWE9	Crystallin, beta A1a OS=Danio rerio GN=eryba1a PE=1 SV=1	2	2	0.912812414	0.925714509	0.000481893	2.030093765		
A0A0R4IX62	Si:dkey-16p6.1 OS=Danio rerio GN=si:dkey-16p6.1 PE=4 SV=1	3	1	0.029288418	1.348250177	0.039841256	0.844955397		
A0A0R4IXC8	Tubulin beta chain OS=Danio rerio GN=tubb6 PE=1 SV=1	12	4	0.174150362	1.053774305	0.481810384	1.033430904		
A0A0R4IXD7	Endothelin-converting enzyme 1 OS=Danio rerio GN=ece1 PE=4 SV=1	3	2	0.180516616	1.599851254	0.428722248	0.810745167		
A0A0R4IY80	Si:dkey-264f17.1 OS=Danio rerio GN=si:dkey-264f17.1 PE=4 SV=1	4	1	0.000529998	2.931677331	0.001608875	0.678124155		
A0A0R4IYS5	Si:ch211-171i17.4 (Fragment) OS=Danio rerio GN=si:ch211-171i17.4 PE=4 SV=1	6	1	0.005026542	2.088669452	0.143548018	0.916257485		
A0A0R4IYW7	Si:dkey-27n6.1 OS=Danio rerio GN=si:dkey-27n6.1 PE=4 SV=1	7	3	0.000449953	2.424390606	0.000402744	0.646618543		
A0A0R4IZD9	Si:ch211-205a14.7 OS=Danio rerio GN=si:ch211-205a14.7 PE=4 SV=1	9	3	0.001624419	1.864324105	0.002292558	0.718291766		
A0A140LGS0	Solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11 OS=Danio rerio GN=slc7a11 PE=4 SV=1	2	1	0.015334591	0.567404071	0.291879208	1.152941414		
A0AUR2	Sarcalumenin OS=Danio rerio GN=srl PE=1 SV=1	9	6	0.048965533	0.664994631	0.043430075	1.129208125		
A0JMD0	Clustered mitochondria protein homolog OS=Danio rerio GN=cluh PE=2 SV=1	2	2	0.598117748	1.104360231	0.303514572	1.17699014		
A0JMP4	Calcium-transporting ATPase OS=Danio rerio GN=atp2a11 PE=1 SV=1	103	37	0.000261172	1.806722341	0.001773418	0.7975854		
A1A600	EF-hand calcium-binding domain-containing protein 4A OS=Danio rerio GN=cracr2b PE=2 SV=2	3	3	0.008567541	6.750042056	0.694275014	1.047446565		
A1A605	Y box binding protein 1 OS=Danio rerio GN=ybx1 PE=1 SV=1	4	3	0.180943626	0.904817611	0.027443825	1.200406512		
A2AR68	Rab GDP dissociation inhibitor OS=Danio rerio GN=gdi1 PE=1 SV=1	9	3	0.959900282	0.9589003	0.283960622	1.041054338		
A2BHA3	Creatine kinase, muscle a OS=Danio rerio GN=ckma PE=1 SV=1	61	25	0.007899446	0.860351254	0.850145211	1.009654519		
A2BIP1	ATPase, Ca ⁺⁺ -transporting, ubiquitous (Fragment) OS=Danio rerio GN=atp2a3 PE=1 SV=1	41	1	0.001621626	1.230373152	0.359660418	0.96887441		
A2CE51	Eukaryotic translation elongation factor 2, -like 2 OS=Danio rerio GN=eef2l2 PE=1 SV=1	23	3	0.657720488	1.054855692	0.105919357	0.935135225		
A2CEI6	Piwi-like protein 2 OS=Danio rerio GN=piwil2 PE=1 SV=2	5	2	0.000439415	3.546206245	0.000230866	0.586373849		
A2CEZ0	Si:dkey-251i10.1 OS=Danio rerio GN=si:dkey-251i10.1 PE=3 SV=1	17	1	0.000782915	1.898164369	0.003858365	0.790045603		
A2CG95	Acyl-CoA dehydrogenase, C-4 to C-12 straight chain OS=Danio rerio GN=acadm PE=1 SV=1	6	4	0.034005982	2.351459983	0.47613394	1.022940531		

A3KPR4	Histone H4 OS=Danio rerio GN=si:dkey-108k21.23 PE=1 SV=1	6	3	0.724320003	1.036447709	0.160529307	0.921989401
A3KPT4	CLIP-associating protein 2 OS=Danio rerio GN=clasp2 PE=1 SV=1	5	3	0.190526229	1.854107592	0.469265966	1.100020533
A4QPA0	Malic enzyme OS=Danio rerio GN=me3 PE=1 SV=1	2	2	0.014824896	3.237519843	0.00152808	0.725823159
A5PMP8	Complement component c3b, tandem duplicate 2 OS=Danio rerio GN=c3b.2 PE=4 SV=1	12	3	0.006965758	1.909691103	0.098437727	0.821529172
A5WUN8	Phospholipid phosphatase-related 5a OS=Danio rerio GN=plppr5a PE=4 SV=1	2	1	0.000415187	2.939760686	0.011540034	0.709279438
A5WUY5	Novel keratin protein (Zgc:110712) OS=Danio rerio GN=DKEY-90G20.1 PE=1 SV=1	9	5	0.648866147	0.93030719	0.0130473	0.859344736
A5WVL5	Fructose-1,6-bisphosphatase 2 OS=Danio rerio GN=fbp2 PE=1 SV=1	3	2	0.077677367	2.411339837	0.009552741	0.729434626
A5WWJ0	Uncharacterized protein OS=Danio rerio GN=cyp46a1.1 PE=1 SV=1	2	1	0.114755124	0.07166919	0.454348313	1.20016594
A8DZ95	Dihydropyrimidinase-like 2b OS=Danio rerio GN=dpysl2b PE=1 SV=1	4	3	0.312336201	0.879986423	0.030298242	1.430093709
A8DZD6	GA-binding protein transcription factor, beta subunit 2b (Fragment) OS=Danio rerio GN=gabpb2b PE=1 SV=1	2	2	0.009762362	4.428223354	0.959225325	0.969460921
A8DZE4	Glucose-6-phosphate isomerase OS=Danio rerio GN=gpib PE=1 SV=1	18	13	6.39E-05	2.032171624	0.013936006	0.834855456
A8E5J9	Ckmt2 protein OS=Danio rerio GN=ckmt2b PE=1 SV=1	21	6	0.000344951	2.295801315	0.091602882	0.916377588
A8E7G6	Peroxiredoxin 3 OS=Danio rerio GN=prdx3 PE=1 SV=1	4	2	0.015531291	2.662168754	0.03389662	0.731842504
A8E7T3	Si:dkey-51d8.2 OS=Danio rerio GN=si:dkey-51d8.2 PE=4 SV=2	3	1	0.000525866	3.14098314	0.001167522	0.65433891
A8KBJ5	Histone H3 OS=Danio rerio GN=zgc:173552 PE=1 SV=1	5	1	0.001181395	895.9162528	0.201017202	1.086954709
A8KBU6	Zgc:158846 OS=Danio rerio GN=zgc:158846 PE=2 SV=1	21	9	0.02200459	1.219548466	0.32929994	0.959520179
A8KBV1	Succinyl-CoA:3-ketoacid-coenzyme A transferase OS=Danio rerio GN=oxct1b PE=1 SV=1	6	3	0.593430737	1.067230288	0.091703155	0.904420687
A8WGC6	ATP synthase subunit beta OS=Danio rerio GN=atp5b PE=1 SV=1	46	38	0.000225829	1.475836163	0.003347051	0.828266287
A9C3Q5	Calcium-transporting ATPase OS=Danio rerio GN=atp2a2a PE=1 SV=1	50	6	0.030906381	1.154867521	0.371092901	0.973965841
B0R068	Sodium/potassium-transporting ATPase subunit alpha OS=Danio rerio GN=atp1a1b PE=1 SV=1	22	4	5.43E-05	2.249021922	0.010596446	0.755836373
B0R1D0	Novel protein (Zgc:63709) OS=Danio rerio GN=psmc4 PE=1 SV=1	4	3	0.247932955	0.930130798	0.307090663	1.046944834
B0S5A9	Golgin A1 OS=Danio rerio GN=golga1 PE=1 SV=1	5	4	0.361295723	0.689680341	0.903479051	1.008892597
B0S5C5	Acetyl-CoA acyltransferase 2 OS=Danio rerio GN=acaa2 PE=1 SV=1	3	1	0.364477936	1.23010375	0.342339701	1.198178336
B0S5Q5	Sodium/potassium-transporting ATPase subunit alpha OS=Danio rerio GN=atp1a2a PE=1 SV=1	19	2	0.000143475	1.948754522	0.075749773	0.883589487
B0S610	Heat shock cognate 70-kd protein,-like OS=Danio rerio GN=hsp70l PE=3 SV=1	21	2	0.549377107	1.036400351	0.06816969	0.930176894
B0S730	Solute carrier family 25 (Mitochondrial carrier adenine nucleotide translocator), member 6 OS=Danio rerio GN=slc25a6 PE=1 SV=1	23	7	0.43118914	1.13493985	0.138683751	0.921673695
B0UXL2	Isocitrate dehydrogenase [NADP] OS=Danio rerio GN=idh1 PE=1 SV=1	2	2	0.14564572	1.274411523	0.345846926	0.935269217
B0UYA3	Crystallin, lambda 1 OS=Danio rerio GN=cryl1 PE=1 SV=1	3	2	0.0659704	0.450439189	0.580482125	0.983315049
B0UYE9	GRIP1-associated protein 1 OS=Danio rerio GN=gripap1 PE=1 SV=1	5	2	0.000270171	1.832902789	0.004123108	0.821671795
B0UYL0	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Danio rerio GN=ndufa10 PE=1 SV=1	2	1	0.168783835	1.276002768	0.335745917	1.186514327
B0UYS0	Keratin 15 OS=Danio rerio GN=krt15 PE=3 SV=1	21	6	0.043179942	0.745722376	0.745224588	1.01263899
B0V1B0	Crystallin, beta B2 (Fragment) OS=Danio rerio GN=crybb2 PE=1 SV=1	5	4	0.486561948	1.202644915	0.336552086	1.054139668
B0V2T6	Dedicator of cytokinesis 8 (Fragment) OS=Danio rerio GN=dock8 PE=1 SV=1	5	2	9.00E-06	3.082634254	0.001575018	0.633627536
B3DFP9	Apolipoprotein A-II OS=Danio rerio GN=apoa2 PE=1 SV=1	9	6	0.006718816	3.185917948	0.000351659	0.695255584
B3DFS9	Myosin, heavy chain 11a, smooth muscle OS=Danio rerio GN=myh11a PE=1 SV=1	8	3	0.077953498	2.408051753	0.283246106	1.062146286
B3DIV6	Acetyltransferase component of pyruvate dehydrogenase complex OS=Danio rerio	3	1	0.011412847	3.825638775	0.600610442	0.797344822

	GN=dlat PE=1 SV=1								
B3DK63	Zgc:194906 OS=Danio rerio	5	3	0.005695477	1.633733301	0.017967392	0.79039822		
B3DKP3	GN=zgc:194906 PE=2 SV=1 O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) OS=Danio rerio GN=ogt.1 PE=1 SV=1	3	1	0.005226977	1.694991562	0.03577641	0.821509008		
B8A478	Zgc:171517 OS=Danio rerio	12	8	0.002195783	2.338037202	0.319735152	0.875864247		
B8A4S2	GN=zgc:171517 PE=1 SV=1 Testis-specific, 10 OS=Danio rerio	5	5	0.001419496	3.047630231	7.75E-06	0.29375047		
B8A516	GN=tsga.10 PE=1 SV=1 Tubulin alpha chain OS=Danio rerio	31	1	0.003589725	1.903390824	0.041976903	0.860635065		
B8A565	GN=tuba.1b PE=1 SV=1 Complement component 9 OS=Danio rerio	9	5	0.986630299	0.966638304	0.190559524	0.927005657		
B8JHU4	GN=c9 PE=1 SV=1 Actinin, alpha 1 OS=Danio rerio GN=actn1	22	6	0.027969668	1.165814642	0.039668349	0.877638815		
B8JI08	PE=1 SV=1 Oxoglutarate (alpha-ketoglutarate) dehydrogenase a (lipoamide) OS=Danio rerio GN=ogdha PE=1 SV=1	5	3	0.220158431	0.834086594	0.583946332	0.981102358		
B8JI18	ATP-binding cassette, sub-family G (WHITE), member 2c OS=Danio rerio	3	1	0.048527678	0.271640636	0.238801045	0.948976652		
B8JH7	GN=abcg2c PE=1 SV=1 ADP-ribosylation factor-like protein 13B OS=Danio rerio GN=arl13b PE=3 SV=1	2	2	0.000205299	5.080242955	0.000237469	0.623410578		
B8JIS1	ATP synthase, H+-transporting, mitochondrial Fo complex, subunit B1 OS=Danio rerio GN=atp5f1 PE=1 SV=1	7	6	0.354307405	0.674884283	0.098082437	1.076263286		
B8JIS5	Glutathione S-transferase mu tandem duplicate 3 OS=Danio rerio GN=gstm.3	4	1	0.092832887	1.241197148	0.181696965	0.920450842		
B8JIS8	PE=1 SV=1 Glutathione S-transferase mu, tandem duplicate 1 OS=Danio rerio GN=gstm.1	6	3	0.001382155	1.686228298	0.002081642	0.800451701		
B8JK95	Elongation of very long chain fatty acids protein 6 OS=Danio rerio GN=elovl6l	2	1	0.792956696	0.986155826	0.057942232	1.32787753		
B8JKN6	PE=3 SV=1 Peptidyl-prolyl cis-trans isomerase OS=Danio rerio GN=ppiaa PE=1 SV=1	7	5	0.620267587	0.889791217	0.531393873	1.032823584		
B8JKS7	Sodium/potassium-transporting ATPase subunit alpha OS=Danio rerio	21	5	0.071558147	1.171042381	0.068899017	0.906991745		
B8JKT0	GN=atp1a1a.4 PE=1 SV=1 Sodium/potassium-transporting ATPase subunit alpha OS=Danio rerio	7	2	0.476359105	0.858737618	0.08363329	1.152870988		
B8JKW4	GN=atp1a1a.3 PE=1 SV=1 Complement component c3a, duplicate 1 OS=Danio rerio GN=c3a.1 PE=1 SV=1	7	6	0.024989822	0.549199164	0.015296062	1.127405032		
B8JL43	Serotransferrin OS=Danio rerio GN=tfa	42	27	0.000719683	1.368793627	0.074048526	0.89551449		
B8JLJ3	PE=1 SV=1 Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide OS=Danio rerio GN=ywhaz	20	11	0.736862725	1.036309106	0.273629701	1.049265708		
B8JLR1	PE=1 SV=1 Programmed cell death 6-interacting protein OS=Danio rerio GN=pcdc6ip	2	1	0.577299863	1.078964379	0.635983761	1.057742535		
D1GJ56	Actinin alpha 3a OS=Danio rerio	20	4	2.04E-06	5.079827332	0.00028357	0.606934621		
D3KYL0	GN=actn3a PE=1 SV=1 Gephyrin a OS=Danio rerio GN=gphna	9	6	0.000764571	2.82267011	0.03940634	0.874122148		
E7EXM8	PE=1 SV=1 DEP domain-containing 5 OS=Danio rerio	5	2	0.017462733	2.289020718	0.189056951	0.922409092		
E7EXT3	GN=depdc5 PE=1 SV=2 Alpha-1,4 glucan phosphorylase OS=Danio rerio GN=pygmb PE=1 SV=1	41	10	0.00122297	1.467861056	0.864714015	1.00493399		
E7EYD0	Myomesin 1a (skelemin) OS=Danio rerio	18	9	1.08E-06	3.561003474	0.000502623	0.671800744		
E7EYE1	GN=myom1a PE=4 SV=1 Myomesin 2a OS=Danio rerio	48	30	0.18674362	1.180493896	0.007538965	0.830922607		
E7EZI7	GN=myom2a PE=1 SV=2 Discs, large homolog 5b (Drosophila), tandem duplicate 1 OS=Danio rerio	5	2	0.00448138	2.178548848	0.004711897	0.795373213		
E7F004	GN=dlg5b.1 PE=4 SV=2 Neogenin 1b OS=Danio rerio GN=neolb	3	3	0.084516017	0.602737286	0.065188611	1.893442758		
E7F0A1	PE=4 SV=2 Profilin OS=Danio rerio GN=pfn1	3	1	0.043582406	0.761969898	0.005800352	0.70789895		
E7F0E8	SV=1 Exportin 1 (CRM1 homolog, yeast) a OS=Danio rerio GN=xpo1a PE=1 SV=2	2	2	0.465502413	0.723837665	0.171320194	1.722326343		
E7F1G8	DEAD (Asp-Glu-Ala-Asp) box helicase 61 OS=Danio rerio GN=ddx61 PE=1 SV=1	3	2	0.19551109	0.440569789	0.175819292	0.820505274		
E7F263	Cingulin a OS=Danio rerio GN=cgna PE=4	3	2	0.016810507	0.544422257	0.001551092	1.894315659		
	SV=1								

E7F354	3-monoxygenase/tryptophan monoxygenase activation protein, gamma polypeptide 2 OS=Danio rerio GN=ywhag2 PE=1 SV=1	5-	11	2	0.995193999	0.974472144	0.003635473	1.2339843
E7F372	RAS p21 protein activator (GTPase-activating protein) 1b OS=Danio rerio GN=rasa1b PE=4 SV=1		3	2	0.001278679	10.32120834	0.026558657	0.389283409
E7F4S5	Uncharacterized protein OS=Danio rerio GN=si:cabz01069012.2 PE=4 SV=2		2	1	0.000980811	2.960429037	0.001721376	0.644973304
E7F6E2	RNA-binding motif protein 12B OS=Danio rerio GN=rhm12b PE=1 SV=2		6	5	0.162467619	1.452487173	0.794756347	1.027479376
E7F6I0	Maestro heat-like repeat family member 1 OS=Danio rerio GN=mroh1 PE=1 SV=1		19	6	0.002332306	2.146737523	0.620701108	0.953557408
E7F8T6	Nicotinamide phosphoribosyltransferase a OS=Danio rerio GN=nampta PE=1 SV=1		3	2	0.078201046	0.782644475	0.064426818	1.245501908
E7F9J5	Multiple C2 domains, transmembrane 2b OS=Danio rerio GN=mctp2b PE=4 SV=2		2	2	0.008031888	0.472234675	0.021054056	1.476415542
E7FAN6	Kinesin family member 20Ba OS=Danio rerio GN=kif20ba PE=1 SV=2		14	4	0.005544956	1.199083612	0.039851393	0.889139095
E7FC32	Tubulin beta chain OS=Danio rerio GN=tubb1 PE=1 SV=1		16	6	0.62703924	0.968578794	0.64085634	0.978619939
E7FCA3	Myomesin 2b (Fragment) OS=Danio rerio GN=myom2b PE=1 SV=2		12	7	4.29E-05	1.963169653	0.027514064	0.878170219
E7FCW1	Uncharacterized protein OS=Danio rerio GN=wu:fk65c09 PE=1 SV=2		9	5	0.796590801	0.860466807	0.451289409	1.035933903
E7FD91	DEAD (Asp-Glu-Ala-Asp) box helicase 6 OS=Danio rerio GN=ddx6 PE=1 SV=2		6	4	0.95711962	0.963116726	0.05823176	0.915809876
E7FE19	2',3'-cyclic nucleotide 3' phosphodiesterase OS=Danio rerio GN=cnp PE=1 SV=1		6	3	0.002509355	1.590010981	0.975349177	0.996143614
E7FEY5	CDC42-binding protein kinase alpha (DMPK-like) b OS=Danio rerio GN=cdc42bpab PE=3 SV=1		8	3	8.71E-05	2.102348989	0.004451788	0.778656558
E7FFI6	Rap guanine nucleotide exchange factor (GEF) 5b OS=Danio rerio GN=rapgef5b PE=4 SV=1		2	1	0.613317966	0.851611892	0.113971616	0.905600268
E7FFZ3	Si:dkey-46g23.2 OS=Danio rerio GN=si:dkey-46g23.2 PE=1 SV=2		29	4	0.529072899	0.752859401	0.001754511	0.779443728
E9QBP3	Actin, beta 1 OS=Danio rerio GN=actb1 PE=1 SV=1		16	1	0.000850946	2.222138039	0.063751028	0.885089259
E9QD79	Clathrin heavy chain OS=Danio rerio GN=cltcb PE=1 SV=2		16	2	0.000126292	2.440877003	0.00582322	0.66258381
E9QDA3	RAB44, member RAS oncogene family OS=Danio rerio GN=rab44 PE=4 SV=1		5	4	0.002917186	1.753529975	0.017584993	0.821827748
E9QDE7	Nicotinamide nucleotide transhydrogenase 2 (Fragment) OS=Danio rerio GN=nnt2 PE=1 SV=1		6	5	0.032809939	0.815637997	0.285902581	0.949876667
E9QDK0	Si:dkey-51d8.1 OS=Danio rerio GN=si:dkey-51d8.1 PE=4 SV=2		8	2	0.000264376	2.234742754	0.001886335	0.688773905
E9QET4	Tight junction protein 1a OS=Danio rerio GN=tjp1a PE=1 SV=2		7	4	0.000407619	3.428040183	0.000951265	0.661670507
E9QFH8	Cold shock domain-containing E1, RNA-binding OS=Danio rerio GN=csde1 PE=1 SV=1		6	2	0.122303117	0.8070169	0.00908474	0.883846921
E9QFR8	Actinin, alpha 2b OS=Danio rerio GN=actn2b PE=1 SV=1		9	1	0.044937318	1.872790092	0.008577528	0.796629391
E9QGT5	Dynein, axonemal, intermediate chain 1, paralog 1 OS=Danio rerio GN=dnai1.1 PE=4 SV=1		2	1	0.9017742	0.964079566	0.164586593	0.898689602
E9QHV8	Si:ch211-258f1.3 OS=Danio rerio GN=si:ch211-258f1.3 PE=4 SV=3		4	1	0.946460421	0.794506251	0.067175926	1.149733762
E9QHZ3	Si:dkey-84o3.7 OS=Danio rerio GN=si:dkey-84o3.7 PE=4 SV=1		2	1	0.058057842	1.857973247	0.044311675	0.901746037
E9QI03	Uncharacterized protein OS=Danio rerio GN=si:dkey-222h21.7 PE=4 SV=2		6	1	0.140147902	0.750954718	0.221781895	0.925983379
E9QIR9	Ribosomal protein L10 (Fragment) OS=Danio rerio GN=rp110 PE=1 SV=1		2	1	0.00506705	615.0098614	0.098306726	1.228448267
E9QJ12	Neural cell adhesion molecule 1b OS=Danio rerio GN=ncam1b PE=1 SV=1		3	1	0.000816436	1.730769678	0.0638642	0.870776165
E9QJ96	14-3-3 protein beta/alpha-A (Fragment) OS=Danio rerio GN=ywhaba PE=1 SV=1		18	1	0.727710257	1.038715536	0.028772744	0.883260935
F1Q4P9	Calcium-transporting ATPase OS=Danio rerio GN=atp2a3 PE=1 SV=2		41	1	0.002850896	1.235080615	0.31187309	0.965615592
F1Q4X3	Si:dkey-222n6.2 (Fragment) OS=Danio rerio GN=si:dkey-222n6.2 PE=1 SV=2		6	2	0.047613916	1.120765116	0.812924217	0.988194039
F1Q555	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial) OS=Danio rerio GN=gpd2 PE=1 SV=1		7	3	0.002280095	1.728431434	0.001437523	0.701060689
F1Q595	SUN domain-containing ossification factor OS=Danio rerio GN=suco PE=4 SV=1		4	3	0.015826908	2.157674781	0.363327841	0.799877191
F1Q5K6	ATP-binding cassette, sub-family B (MDR/TAP), member 10 OS=Danio rerio GN=abcb10 PE=1 SV=1		3	2	0.0023766	4.294165481	0.170940006	0.90619468

F1Q6F0	Phosphorylase kinase, beta OS=Danio rerio GN=phkb PE=1 SV=2	2	2	0.055187606	0.762736557	0.661131281	0.965703128
F1Q6K8	Supervillin a OS=Danio rerio GN=svila PE=4 SV=1	4	2	0.003495901	3.058184624	0.001003787	0.657773193
F1Q6Y6	Remodeling and spacing factor 1b, tandem duplicate 1 OS=Danio rerio GN=rsf1b.1 PE=1 SV=2	13	8	0.0002811	2.099950535	0.010212915	0.826746795
F1Q7L0	Vitellogenin 4 (Fragment) OS=Danio rerio GN=vtg4 PE=1 SV=1	356	8	3.49E-05	3.410229454	0.000825427	0.700593376
F1Q7N8	Calcium-transporting ATPase OS=Danio rerio GN=si:dkey-28b4.8 PE=1 SV=2	29	10	2.23E-05	1.96486752	0.007140528	0.839316158
F1Q883	6-phosphogluconate dehydrogenase, decarboxylating OS=Danio rerio GN=pgd PE=1 SV=1	5	3	0.418171637	1.099052692	0.329415061	0.938271087
F1Q8J4	Acyl-CoA dehydrogenase, very long chain OS=Danio rerio GN=acadvl PE=1 SV=1	10	3	0.000488639	2.82456085	0.050049835	0.735465452
F1Q9F6	LUC7-like 3 pre-mRNA-splicing factor OS=Danio rerio GN=luc7l3 PE=1 SV=1	2	1	0.003183329	2.789638294	0.006779632	1.349541474
F1QA15	Gamma-tubulin complex component OS=Danio rerio GN=tubgcp3 PE=1 SV=2	2	2	0.851716844	1.085005904	0.203536962	0.670234765
F1QAA0	NIF3-like protein 1 OS=Danio rerio GN=nif3l1 PE=1 SV=1	2	2	0.71866128	0.97233595	0.003086938	1.486214922
F1QAJ7	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3b OS=Danio rerio GN=slc25a3b PE=1 SV=1	8	5	0.857632123	1.006361701	0.131099333	0.930531445
F1QBE4	SAMM50 sorting and assembly machinery component OS=Danio rerio GN=samm50 PE=1 SV=1	4	1	0.284235772	0.812809562	0.159821975	0.917327612
F1QC34	Ribophorin II OS=Danio rerio GN=rpn2 PE=1 SV=1	10	6	0.006178187	0.491285115	0.092059286	1.113386814
F1QCD4	Aspartate aminotransferase OS=Danio rerio GN=got2b PE=1 SV=1	15	5	0.417914151	1.053774792	0.28103672	1.063264784
F1QCE3	Peroxiredoxin 5 OS=Danio rerio GN=prdx5 PE=1 SV=1	2	2	0.046733505	0.07177286	0.524287782	1.231694146
F1QCV9	Multivesicular body subunit 12Ba OS=Danio rerio GN=mvb12ba PE=4 SV=2	3	1	0.159916949	0.831800011	0.850718982	0.988705225
F1QDG9	SET and MYND domain-containing 1a OS=Danio rerio GN=smyd1a PE=1 SV=1	6	3	0.000810198	3.190778921	0.078013086	0.724643677
F1QEW2	Si:dkey-183i3.5 OS=Danio rerio GN=si:dkey-183i3.5 PE=1 SV=2	7	2	0.028871795	0.468474583	0.270491496	1.192103304
F1QF00	Phosphoglucomutase 1 OS=Danio rerio GN=pgm1 PE=1 SV=1	27	18	0.14825267	1.144223188	0.339916917	0.958948958
F1QF37	Si:dkey-16p6.1 (Fragment) OS=Danio rerio GN=si:dkey-16p6.1 PE=4 SV=2	5	1	0.019066154	1.378203356	0.035697408	0.841470623
F1QF63	Zgc:165518 OS=Danio rerio GN=zgc:165518 PE=1 SV=1	27	11	0.00759405	2.162591393	7.99E-05	0.662099678
F1QF64	Si:ch211-67f13.8 OS=Danio rerio GN=si:ch211-67f13.8 PE=4 SV=1	2	1	0.000758695	5.27053513	0.01192303	0.598752008
F1QFN1	Uncharacterized protein OS=Danio rerio GN=erc1b PE=1 SV=2	9	5	0.385647381	0.891614133	0.009910677	0.872221412
F1QGH3	Heat shock cognate 70-kd protein, tandem duplicate 1 OS=Danio rerio GN=hsp70.1 PE=3 SV=1	12	1	0.948172386	0.998321136	0.054684682	0.920298988
F1QGK0	Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Danio rerio GN=gpd1b PE=1 SV=1	7	4	0.013668444	1.464256337	0.011607271	0.858679152
F1QGK5	Calcium-binding and coiled-coil domain 2 OS=Danio rerio GN=calcoco2 PE=4 SV=1	2	1	1.11E-06	3.551483107	0.000608321	0.557468217
F1QHA9	Neuropilin OS=Danio rerio GN=nrp1b PE=3 SV=1	2	1	0.005108346	4.810755429	0.00110258	0.722691794
F1QHR0	Apolipoprotein A-IV b, tandem duplicate 1 OS=Danio rerio GN=apoa4b.1 PE=1 SV=1	6	2	0.179473731	0.806140383	0.911351212	1.005012215
F1QIN9	Uncharacterized protein OS=Danio rerio PE=1 SV=2	3	1	0.007450988	0.700124142	0.08586237	1.147476334
F1QJV7	D-dopachrome tautomerase OS=Danio rerio GN=ddt PE=1 SV=1	2	1	0.002512874	0.386304219	0.203909747	1.198840542
F1QK60	Keratin 4 OS=Danio rerio GN=kr4 PE=3 SV=1	42	13	3.09E-05	2.438476495	0.002034582	0.737678951
F1QKE3	Membrane protein, palmitoylated 6a (MAGUK p55 subfamily member 6) OS=Danio rerio GN=mpp6a PE=1 SV=2	8	7	0.168730013	0.512658433	0.000497194	0.681305339
F1QKJ4	FERM and PDZ domain-containing 3 OS=Danio rerio GN=frmpd3 PE=4 SV=2	2	2	0.019291044	0.268156901	0.02057099	1.715297122
F1QKS0	Myosin VB OS=Danio rerio GN=myo5b PE=4 SV=2	5	3	0.005932374	0.689317592	0.398171867	1.046585629
F1QKU5	Glutamine-fructose-6-phosphate transaminase 2 OS=Danio rerio GN=gfpt2 PE=1 SV=1	4	1	0.287727515	0.934000594	0.176519802	1.064254124
F1QMP9	Si:dkey-13n15.2 OS=Danio rerio GN=si:dkey-13n15.2 PE=4 SV=2	3	1	0.140516266	2.817215129	0.696021523	1.022395589
F1QP28	Keratin 96 (Fragment) OS=Danio rerio GN=kr96 PE=3 SV=1	20	1	0.474482778	0.909778179	0.109169401	0.925029838

F1QPL7	Propionyl CoA carboxylase, alpha polypeptide (Fragment) OS=Danio rerio GN=pcca PE=1 SV=1	4	2	0.002550854	1.774975123	0.049402695	0.849080193
F1QPU1	Si:ch211-19719.2 OS=Danio rerio GN=si:ch211-19719.2 PE=4 SV=2	4	2	0.033580483	4.437124033	0.017679559	0.791816953
F1QQ05	Vacuolar protein sorting 8 homolog (S. cerevisiae) OS=Danio rerio GN=vps8 PE=1 SV=1	7	3	2.92E-05	3.581028416	0.002087447	0.710187105
F1QQQ3	Vitellogenin 3, phosphoinositide OS=Danio rerio GN=vtg3 PE=1 SV=2	61	52	0.000802062	2.175718402	0.037680002	0.771786803
F1QQW9	Elongation factor 1-alpha (Fragment) OS=Danio rerio GN=si:dkey-37o8.1 PE=1 SV=1	29	19	0.988164539	0.998374137	0.053343235	0.91438736
F1QR21	Keratin, type 1, gene c5 OS=Danio rerio GN=krt1-c5 PE=3 SV=2	3	1	0.33259069	1.619903949	0.123498986	1.293101471
F1QRM9	Aminopeptidase OS=Danio rerio GN=npepps PE=1 SV=1	4	3	0.277526867	0.91614432	0.586184466	1.029215886
F1QSE1	Ventricular myosin heavy chain-like OS=Danio rerio GN=vmhcl PE=1 SV=1	7	4	0.000397787	2.301580179	0.023709236	0.839980512
F1QTB5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Danio rerio GN=rpn1 PE=1 SV=1	7	4	0.00036825	1.604185244	0.560098602	0.964389726
F1QU55	Betaine--homocysteine S-methyltransferase 1 OS=Danio rerio GN=bhmt PE=1 SV=1	4	4	0.001165318	2.890400148	0.001380166	0.62721277
F1QUE3	Ubiquinol-cytochrome c reductase core protein I OS=Danio rerio GN=uqcr1 PE=1 SV=1	6	6	0.695012967	0.823268506	0.34051902	1.037406943
F1QV15	Vitellogenin 6 (Fragment) OS=Danio rerio GN=vtg6 PE=1 SV=1	335	28	4.10E-05	3.37719704	0.000933787	0.691090927
F1QV31	Keratin 5 OS=Danio rerio GN=krt5 PE=1 SV=1	53	11	1.89E-05	2.37154304	0.003313417	0.779679307
F1QVD5	Si:dkeyp-34c12.1 OS=Danio rerio GN=si:dkeyp-34c12.1 PE=1 SV=1	2	2	0.084707335	1.527221252	0.299845634	1.087654502
F1QXE4	Pentaxin OS=Danio rerio GN=crp PE=1 SV=2	3	2	0.087377556	0.876695959	0.627267004	0.968168037
F1QXF4	THO complex 2 OS=Danio rerio GN=thoc2 PE=4 SV=1	3	1	0.00198962	2.971489375	0.185449987	1.064150954
F1QXV8	Phosphoglycerate kinase OS=Danio rerio GN=pgk1 PE=1 SV=1	18	15	0.170417467	0.625227819	0.01287402	0.883067765
F1QYH7	Glyoxylate reductase/hydroxypyruvate reductase b OS=Danio rerio GN=grhprb PE=1 SV=1	6	4	0.209363612	0.736293313	0.730766289	1.018311884
F1QYX1	Myosin X-like 3 OS=Danio rerio GN=mvo10i3 PE=4 SV=2	5	1	0.003066146	5.809272378	0.378822021	0.950981363
F1QYZ6	Pyruvate carboxylase OS=Danio rerio GN=pcxb PE=1 SV=1	12	1	0.005234743	1.686485653	0.041519891	0.828881075
F1QZL6	Glucose-6-phosphate isomerase OS=Danio rerio GN=gpia PE=1 SV=1	9	7	0.635886018	1.053008303	0.752893793	1.01362829
F1QZU7	Aldehyde dehydrogenase 2 family (mitochondrial), tandem duplicate 2 OS=Danio rerio GN=aldh2.2 PE=1 SV=2	5	2	0.265938969	1.497642197	0.304033889	0.796993653
F1R0A4	Uncharacterized protein OS=Danio rerio GN=vps50 PE=1 SV=1	2	2	0.007731915	0.494171328	0.399885309	1.078532753
F1R2P4	Uncharacterized protein OS=Danio rerio GN=tlr8a PE=3 SV=2	4	2	0.002253785	5.892944035	0.02716397	0.396620104
F1R319	Solute carrier family 25 (mitochondrial carrier, oxoglutarate carrier), member 11 OS=Danio rerio GN=slc25a11 PE=1 SV=1	3	2	0.725639256	0.962794052	0.059259765	0.941375271
F1R343	NUAK family, SNF1-like kinase, 1a OS=Danio rerio GN=nuak1a PE=4 SV=1	3	2	0.000127911	4.679229798	0.000659673	0.587805119
F1R3J4	Si:ch211-220f16.2 OS=Danio rerio GN=si:ch211-220f16.2 PE=1 SV=2	11	4	0.186185159	1.173367189	0.005442682	0.785957071
F1R535	Membrane-associated guanylate kinase, WW and PDZ domain-containing 1a (Fragment) OS=Danio rerio GN=mag1a PE=1 SV=1	2	1	0.072427104	2.465097169	0.972653704	0.959909992
F1R570	Si:dkey-222h21.4 (Fragment) OS=Danio rerio GN=si:dkey-222h21.4 PE=4 SV=3	4	1	0.044266835	1.148353583	0.062508713	0.84919573
F1R5D5	Si:ch211-133j6.3 OS=Danio rerio GN=si:ch211-133j6.3 PE=1 SV=2	3	2	0.095665463	0.718749402	0.330152933	0.945700168
F1R5X0	Alpha-1,4 glucan phosphorylase OS=Danio rerio GN=pygb PE=1 SV=1	34	12	0.566218489	1.080631095	0.001835392	0.776490222
F1R833	Nebulin-related-anchoring protein OS=Danio rerio GN=nrap PE=4 SV=1	3	2	0.054138051	5.071127947	0.005850109	0.65324878
F1R889	Myosin, heavy chain 9a, non-muscle OS=Danio rerio GN=myh9a PE=1 SV=2	6	3	0.062220576	1.881133799	0.363507874	0.951759668
F1R8D7	Synaptotagmin-binding, cytoplasmic RNA-interacting protein,-like OS=Danio rerio GN=syncripl PE=1 SV=1	2	1	0.131088805	0.089498552	0.014462869	1.971811391
F1R8N2	Sb:cb37 (Fragment) OS=Danio rerio GN=sb.cb37 PE=1 SV=2	13	1	0.00156278	1.564194317	0.009303089	0.836281933
F1R8R0	Si:zfos-1897c11.1 OS=Danio rerio	2	1	0.351530723	0.503039816	0.004969176	0.754940881

	GN=si:zfos-1897c11.1 PE=4 SV=3								
F1R8U0	Keratin 94 OS=Danio rerio GN=krt94 PE=1 SV=1	17	2	0.000278318	2.515043775	0.004505759	0.728421329		
F1R966	Clathrin heavy chain OS=Danio rerio GN=cltca PE=1 SV=1	20	6	0.000130195	2.792523788	0.009247555	0.654519779		
F1R9V3	Si:dkey-4p15.3 OS=Danio rerio GN=si:dkey-4p15.3 PE=1 SV=1	23	2	0.009324103	1.614787119	0.156093792	0.852996395		
F1RAV5	Ribosomal protein S6 kinase OS=Danio rerio GN=rps6ka1 PE=1 SV=1	2	1	0.075789225	0.681434544	0.713812019	1.015283911		
F1RBF5	HAUS augmin-like complex, subunit 5 OS=Danio rerio GN=haus5 PE=1 SV=1	2	1	0.527267967	1.153172805	0.250483651	1.150221955		
F1RBS6	Nucleoside diphosphate kinase OS=Danio rerio GN=nme2b.2 PE=1 SV=1	31	10	0.048140497	0.896474966	0.865093237	0.991316756		
F1RCJ3	Regulating synaptic membrane exocytosis 1a OS=Danio rerio GN=rims1a PE=4 SV=2	5	2	2.37E-05	5.958966309	0.000291332	0.586154671		
F1RD80	Cadherin 17, LI cadherin (liver-intestine) OS=Danio rerio GN=cdh17 PE=1 SV=1	3	2	0.013900971	1.876381841	0.001286951	0.717875009		
F1RDA6	NADH dehydrogenase (ubiquinone) Fe-S protein 1 OS=Danio rerio GN=ndufs1 PE=1 SV=1	3	3	0.758555472	0.649675996	0.005702337	0.82353697		
F1RDG4	Si:dkey-222f2.1 OS=Danio rerio GN=si:dkey-222f2.1 PE=1 SV=1	23	8	0.000337306	2.284992204	0.008888176	0.812665351		
F1REE8	Thyroid hormone receptor interactor 11 OS=Danio rerio GN=trip11 PE=1 SV=1	17	11	0.000252502	1.336011537	0.017241312	0.844979675		
F1REK5	Quinoid dihydropteridine reductase b2 OS=Danio rerio GN=qdprb2 PE=1 SV=1	9	4	0.485116261	1.024278959	0.613085542	0.977596291		
F1REP2	Zgc:171426 OS=Danio rerio GN=zgc:171426 PE=1 SV=1	10	3	9.05E-06	2.309818397	0.000255968	0.711967149		
F6NHI0	Glucose-6-phosphate 1-dehydrogenase OS=Danio rerio GN=g6pd PE=1 SV=1	2	1	0.543959964	0.750257633	0.002503958	0.717779369		
F6NI48	Si:ch211-15j1.5 OS=Danio rerio GN=si:ch211-15j1.5 PE=4 SV=1	5	1	0.871819312	1.012463203	0.075985972	0.863495152		
F6NIT0	Zgc:171226 OS=Danio rerio GN=zgc:171226 PE=3 SV=1	2	1	0.06308285	1.425315631	0.911945255	0.98923078		
F6NMG5	Component of oligomeric golgi complex 5 OS=Danio rerio GN=cog5 PE=1 SV=1	2	1	5.39E-05	12.21889161	0.009033012	0.7636104		
F6NXM8	Si:ch211-194e1.7 (Fragment) OS=Danio rerio GN=si:ch211-194e1.7 PE=4 SV=1	2	2	0.08680898	1.636026237	0.014017641	0.865250835		
F6P9S6	Si:ch211-243g18.2 OS=Danio rerio GN=si:ch211-243g18.2 PE=1 SV=1	15	9	0.00076498	1.701551203	0.048825448	0.871578974		
F6P9T1	Kertain 95 OS=Danio rerio GN=krt95 PE=3 SV=1	9	3	0.004845701	2.950107193	0.90712246	1.006948333		
F6PEQ5	Si:dkey-222h21.9 OS=Danio rerio GN=si:dkey-222h21.9 PE=4 SV=1	5	1	0.015172712	1.171919821	0.075776016	0.871372102		
F8W246	Ribosomal protein S13 OS=Danio rerio GN=rps13 PE=1 SV=1	2	2	0.111477199	2.173840162	0.757380557	1.017148825		
F8W2K0	ELKS/RAB6-interacting/CAST family member 1a OS=Danio rerio GN=erc1a PE=1 SV=1	6	1	0.209818532	0.605849369	0.02473767	0.942421251		
F8W2M8	Tripeptidyl peptidase I OS=Danio rerio GN=tp1 PE=1 SV=1	2	2	0.01462111	0.223912505	0.154084794	1.370929888		
F8W371	Ankyrin 3a OS=Danio rerio GN=ank3a PE=1 SV=1	6	3	0.151678724	1.567521596	0.122158225	0.94577349		
F8W446	Heterogeneous nuclear ribonucleoprotein A/Ba (Fragment) OS=Danio rerio GN=hnrnpaba PE=1 SV=1	3	2	0.774297867	0.973609943	0.08133378	1.192583802		
F8W4M7	Aconitate hydratase, mitochondrial (Fragment) OS=Danio rerio GN=aco2 PE=1 SV=2	27	15	0.000393314	1.850923396	0.028786658	0.837318689		
F8W5B8	Alpha-1,4 glucan phosphorylase OS=Danio rerio GN=pygl PE=1 SV=1	31	11	0.027584133	1.32372576	0.068099327	0.864219334		
F8W5U2	Tyrosyl-DNA phosphodiesterase 1 OS=Danio rerio GN=tdp1 PE=1 SV=1	3	3	0.001860906	0.197839773	0.026286954	1.802824219		
G1K2G6	G patch domain-containing 1 OS=Danio rerio GN=gpatch1 PE=1 SV=2	3	1	0.000939253	4.660934982	0.20506481	0.813888341		
H0WEA8	Si:dkey-84h14.2 (Fragment) OS=Danio rerio GN=si:dkey-84h14.2 PE=4 SV=2	7	1	0.000290801	2.789859841	0.003410997	0.717956041		
H0WEN2	Leucine-rich repeat (in FLII)-interacting protein 1a (Fragment) OS=Danio rerio GN=lrrfip1a PE=4 SV=1	2	1	0.029715842	2.977545649	0.198521169	1.091453001		
H0WFD4	Uncharacterized protein OS=Danio rerio GN=si:dkey-156k2.3 PE=4 SV=3	3	1	0.783238902	1.022323429	0.378066632	0.935610622		
H9GX78	Uncharacterized protein OS=Danio rerio PE=4 SV=1	6	1	0.388626689	1.087844372	0.796377843	0.977558658		
H9GXQ9	Protein-methionine sulfoxide oxidase mical3a OS=Danio rerio GN=mical3a PE=4 SV=2	11	6	0.002488226	2.303097656	0.005471979	0.777921433		
I3IT32	Collagen, type XII, alpha 1b (Fragment) OS=Danio rerio GN=coll2a1b PE=1 SV=2	2	1	0.011831418	2.650583961	0.014873335	0.701189841		
K7DY17	Si:ch211-242b18.1 OS=Danio rerio GN=si:ch211-242b18.1 PE=4 SV=1	28	19	9.99E-05	2.679702316	0.004819446	0.712909607		
K7DY31	Si:dkey-4j21.2 OS=Danio rerio	4	1	0.000413771	2.701466535	0.001595887	0.680304916		

	GN=si:dkey-4j21.2 PE=4 SV=1							
M9MM92	Tyrosine-protein kinase OS=Danio rerio GN=zap70 PE=3 SV=1	4	3	0.104801879	1.544431085	0.844646071	0.990190803	
O42363	Apolipoprotein A-I OS=Danio rerio GN=apoa1 PE=2 SV=1	14	9	0.000886217	1.568061479	0.030728783	0.917828881	
O57521	Heat shock protein HSP 90-beta OS=Danio rerio GN=hsp90ab1 PE=1 SV=2	21	12	0.099551029	1.385441544	0.006766393	0.889288343	
O73872	Superoxide dismutase [Cu-Zn] OS=Danio rerio GN=sod1 PE=2 SV=1	2	2	0.455117623	1.169432933	0.286856489	0.945755255	
O93548	Embryonic 1 beta-globin OS=Danio rerio GN=bE1 PE=1 SV=1	11	1	0.000905408	0.609896788	0.021755069	1.163205144	
P17561	Ependymin OS=Danio rerio GN=epd PE=2 SV=2	6	6	0.068479452	1.268006955	0.098785034	0.762229161	
P62084	40S ribosomal protein S7 OS=Danio rerio GN=rps7 PE=2 SV=1	2	2	0.560862717	0.86576301	0.178174209	1.206766011	
P79735	GTP-binding nuclear protein Ran OS=Danio rerio GN=ran PE=2 SV=1	3	3	0.003331054	4.341699615	0.587531664	0.960287833	
Q08BA1	ATP synthase subunit alpha OS=Danio rerio GN=atp5a1 PE=1 SV=1	51	28	2.23E-05	2.181276486	0.000799404	0.703627833	
Q08CD8	Ras homolog-enriched in brain-like 1 OS=Danio rerio GN=rheb11 PE=1 SV=1	2	2	0.075944926	0.022796606	0.179236868	2.221900973	
Q0P466	tRNA wybutosine-synthesizing protein 2 homolog OS=Danio rerio GN=trmt12 PE=2 SV=1	4	1	0.058610354	0.317113021	0.27574067	0.943863889	
Q1ECCX9	Protein disulfide-isomerase A4 OS=Danio rerio GN=pdia4 PE=1 SV=1	2	1	0.000708219	4.31499578	0.000531922	0.556956175	
Q1JPR9	Rho GTPase activating protein 10 OS=Danio rerio GN=arhgap10 PE=1 SV=1	4	4	0.399203046	1.194199325	0.017984457	0.823515109	
Q1L907	Glutathione S-transferase rho OS=Danio rerio GN=gstr PE=1 SV=1	11	8	0.001915003	1.492690723	0.026146309	0.859058252	
Q1LUZ9	Carboxylic ester hydrolase OS=Danio rerio GN=ces3 PE=1 SV=1	8	3	0.002234411	1.699133391	0.061436496	1.189924633	
Q1LWN2	Vitellogenin 1 OS=Danio rerio GN=vtg1 PE=1 SV=1	399	38	1.59E-05	3.294232454	0.000841267	0.686333823	
Q1LXJ1	Keratin 17 OS=Danio rerio GN=krt17 PE=1 SV=1	28	7	0.000423081	1.366923383	0.008894908	0.854517157	
Q1LXJ9	Keratin type 1 c19e OS=Danio rerio GN=krt1c19e PE=1 SV=1	19	4	0.092961514	1.14951272	0.219631878	0.95134913	
Q1LXK0	Keratin, type 1, gene 19d OS=Danio rerio GN=krt1-19d PE=1 SV=1	17	7	0.005046665	1.426343136	0.081090602	0.924176443	
Q1LXN3	InaD-like (Drosophila) OS=Danio rerio GN=inadl PE=4 SV=2	5	2	8.97E-06	2.103936386	0.059210888	0.867757235	
Q1MTC4	Vitellogenin 2 OS=Danio rerio GN=vtg2 PE=1 SV=1	213	65	0.00027527	3.269119548	0.003271108	0.69367795	
Q1MTI4	Triosephosphate isomerase A OS=Danio rerio GN=tpi1a PE=2 SV=1	13	2	0.004000775	1.62617736	0.136489623	0.907595048	
Q1RLR3	Keratin 93 OS=Danio rerio GN=krt93 PE=2 SV=1	17	5	0.255198517	1.117200169	0.334985303	0.96025016	
Q29RA2	Zgc:136908 OS=Danio rerio GN=zgc:136908 PE=1 SV=1	11	4	0.069510978	2.891062299	0.004877762	0.733240743	
Q3B7P7	Ubiquitin A-52 residue ribosomal protein fusion product 1 OS=Danio rerio GN=uba52 PE=2 SV=1	7	4	0.478441465	0.904990986	0.095236813	0.914459918	
Q4QRF4	Histone H3.2 OS=Danio rerio GN=zgc:113984 PE=2 SV=3	5	1	2.21E-05	65.71863619	0.578270201	1.037560574	
Q503C7	Alpha-1,4 glucan phosphorylase OS=Danio rerio GN=pygma PE=1 SV=1	58	23	0.000442198	1.620136932	0.012911882	0.862887175	
Q561S7	UDP-glucuronosyltransferase OS=Danio rerio GN=ugt1ab PE=1 SV=1	3	1	0.533496024	0.899856317	0.963749961	0.982875961	
Q567N5	Ribosomal protein L6 OS=Danio rerio GN=rpl6 PE=1 SV=1	3	2	0.005607365	2.588224695	0.178568022	1.148567592	
Q568L5	Alcohol dehydrogenase [NADP(+)] B OS=Danio rerio GN=akr1a1b PE=2 SV=1	4	3	0.121421886	1.161583208	0.085621973	0.901466965	
Q58EE9	Glial fibrillary acidic protein OS=Danio rerio GN=gfap PE=1 SV=2	11	5	0.001203286	2.018156962	0.270116659	0.930674445	
Q5BKV9	Ribosomal protein L9 OS=Danio rerio GN=rpl9 PE=1 SV=1	5	4	0.04885468	0.692900965	0.78636645	0.961106764	
Q5CZQ1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide 2 OS=Danio rerio GN=ywhae2 PE=1 SV=1	9	1	0.257930039	0.568491311	0.785349353	1.010860985	
Q5MJ86	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Danio rerio GN=gapdh-2 PE=2 SV=1	16	11	1.78E-06	2.57673543	0.005606784	0.801085016	
Q5RGJ8	N-acetylglucosamine-1-phosphotransferase subunits alpha/beta OS=Danio rerio GN=gnptab PE=1 SV=1	2	2	0.004197342	2.710434479	0.507476009	0.881045071	
Q5RH26	ATP synthase subunit gamma OS=Danio rerio GN=atp5c1 PE=1 SV=1	7	5	0.004127752	1.825159293	0.133543003	0.924083204	
Q5RHJ0	Si:ch211-241j12.3 OS=Danio rerio GN=si:ch211-241j12.3 PE=3 SV=2	3	2	0.024524215	3.94575861	0.036042966	0.854548622	
Q5RIC7	Stathmin OS=Danio rerio GN=stmn4 PE=3	2	1	0.001188135	0.661255231	0.405710895	0.955701184	

	SV=1								
Q5RIQ7	Formin 1 OS=Danio rerio GN=fmn1 PE=4 SV=2	2	2	0.402687117	1.201634722	0.428439326	0.950035083		
Q5SNY2	Poly(A) polymerase alpha OS=Danio rerio GN=papola PE=1 SV=1	2	1	0.000122023	4.489148867	0.000164054	0.489142117		
Q5SPJ4	Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1 antiproteinase, antitrypsin), member 1 OS=Danio rerio GN=serpina1 PE=1 SV=1	11	5	0.628168465	1.058732341	0.002194381	1.246818425		
Q5TYP7	EH-domain-containing 3 OS=Danio rerio GN=ehd3 PE=1 SV=1	2	1	0.391282011	1.202696755	0.219424707	1.103338327		
Q5TYR1	RAD51 recombinase OS=Danio rerio GN=rad51 PE=1 SV=1	2	1	0.153500142	1.178537856	0.011899463	0.770037932		
Q5U3A4	Calcium-transporting ATPase OS=Danio rerio GN=atp2a1 PE=1 SV=1	70	12	0.002605095	1.286411498	0.048846239	0.931569922		
Q5XJ10	Glyceraldehyde-3-phosphate dehydrogenase OS=Danio rerio GN=gapdh PE=2 SV=2	32	22	0.054794774	0.86703215	0.311938188	0.960756926		
Q5XTP0	Crystallin, gamma S1 OS=Danio rerio GN=crvgs1 PE=1 SV=1	4	4	0.459525143	0.700707188	0.007118031	1.97866064		
Q5XTP1	Crystallin, gamma S2 OS=Danio rerio GN=crvgs2 PE=1 SV=1	3	2	0.022716022	1.528505551	0.053392285	1.174987682		
Q642H9	40S ribosomal protein S4, X isoform OS=Danio rerio GN=rps4x PE=2 SV=3	3	2	0.506063412	1.091603384	0.067675322	0.897007386		
Q64HD0	Sex hormone binding globulin OS=Danio rerio GN=sbbg PE=1 SV=1	2	1	0.150275314	0.883965254	0.838229702	0.988999959		
Q66HV8	ATP-dependent 6-phosphofructokinase OS=Danio rerio GN=pfkma PE=1 SV=1	4	1	0.011872538	0.570128707	0.283810444	1.146915464		
Q66I73	Myosin light chain, phosphorylatable, fast skeletal muscle b OS=Danio rerio GN=mylpfb PE=1 SV=1	3	1	0.890425838	0.984167102	0.774672638	0.981804305		
Q68EH2	Adenylate kinase isoenzyme 1 OS=Danio rerio GN=ak1 PE=1 SV=1	10	9	0.197177973	1.190986152	0.007252623	0.836058043		
Q6DBY5	Ubiquitin-conjugating enzyme E2 variant 3 OS=Danio rerio GN=uevld PE=2 SV=1	2	1	0.493968909	1.201188819	0.10525065	1.26920274		
Q6DEF9	Socs1 protein OS=Danio rerio GN=socs1a PE=2 SV=1	3	3	0.000153282	1.74175498	0.001072017	0.732649446		
Q6DGE9	Protein unc-45 homolog B OS=Danio rerio GN=unc45b PE=1 SV=2	4	3	0.048775746	0.242608692	0.317355928	0.943932996		
Q6DGJ6	Peroxiredoxin 2 OS=Danio rerio GN=prdx2 PE=1 SV=1	4	3	0.015041887	2.519694365	0.742144404	1.012653426		
Q6DGK2	L-lactate dehydrogenase B-B chain OS=Danio rerio GN=ldhbb PE=2 SV=1	15	2	0.00032094	0.399689205	0.014400265	1.20965268		
Q6DGU9	Glutathione S-transferase kappa OS=Danio rerio GN=gstk1 PE=1 SV=1	3	1	0.424853361	1.104479406	0.05343266	0.870828863		
Q6DHB6	Zgc:92533 OS=Danio rerio GN=krt17 PE=1 SV=1	44	8	0.062984216	1.214792808	0.013113001	0.855104268		
Q6DHQ3	N-acyl-aromatic-L-amino acid amidohydrolase (carboxylate-forming) B OS=Danio rerio GN=acy3.2 PE=2 SV=1	2	2	8.61E-05	10.9440779	3.92E-06	0.296158588		
Q6DHT4	Aldehyde dehydrogenase 6 family, member A1 OS=Danio rerio GN=aldh6a1 PE=1 SV=1	6	2	0.34532968	0.869881252	0.006186083	1.336645139		
Q6DHU3	Keratin 97 OS=Danio rerio GN=krt97 PE=1 SV=1	27	2	0.356962911	0.933684223	0.226070183	0.942164913		
Q6DI20	Dipeptidyl peptidase 3 OS=Danio rerio GN=dpp3 PE=1 SV=1	2	2	0.032126642	0.255059101	0.241323761	1.539700258		
Q6DRF3	Proteasome subunit beta type OS=Danio rerio GN=psmb1 PE=1 SV=1	3	1	9.90E-05	2.766126431	0.000885996	0.645785605		
Q6GMJ1	Carboxylic ester hydrolase (Fragment) OS=Danio rerio GN=ces2 PE=1 SV=1	7	3	0.167230811	1.433387612	0.315486293	0.894631495		
Q6GQM1	Tubulin alpha chain OS=Danio rerio GN=tuba7l PE=1 SV=1	11	1	0.671978926	1.05474097	0.134697369	1.145354454		
Q6GQM9	Eno2 protein OS=Danio rerio GN=eno2 PE=1 SV=1	8	3	0.011200779	3.279434574	0.274809719	0.952770384		
Q6GQN8	Enoyl-[acyl-carrier-protein] reductase, mitochondrial OS=Danio rerio GN=mecr PE=2 SV=2	5	3	0.011368545	1.898315532	0.042966634	0.844334578		
Q6IMW7	Parvalbumin 4 OS=Danio rerio GN=pvalb4 PE=1 SV=1	17	8	0.000446623	0.607436347	0.834774186	1.012157397		
Q6IQ59	Ubiquinol-cytochrome c reductase core protein II OS=Danio rerio GN=uqcr2b PE=1 SV=1	3	1	0.079997023	1.21685169	0.020000873	1.198201564		
Q6NSN5	Adenylosuccinate synthetase isozyme 1 OS=Danio rerio GN=adss1 PE=1 SV=1	3	2	0.050920173	0.760709773	0.484539166	0.937571543		
Q6NUZ3	Synaptotagmin binding, cytoplasmic RNA interacting protein OS=Danio rerio GN=syncrip PE=1 SV=1	5	2	0.000286268	2.144375284	0.033778314	0.763480169		
Q6NW90	Tubulin beta chain OS=Danio rerio GN=tubb5 PE=1 SV=1	32	2	0.000721757	1.355777998	0.231957321	0.948389699		
Q6NWC3	Ribosomal protein S2 OS=Danio rerio GN=rps2 PE=1 SV=1	5	4	0.113217372	0.749983344	0.016889854	0.90199252		

Q6NWF6	Keratin, type II cytoskeletal 8 OS=Danio rerio GN=kr8 PE=1 SV=1	43	12	1.67E-05	2.54798914	0.001088413	0.721917403
Q6NWX8	UDP-glucose pyrophosphorylase 2b OS=Danio rerio GN=ugg2b PE=1 SV=1	3	1	0.965709973	0.912222952	0.097432775	1.125972438
Q6NX10	Solute carrier family 25 (Mitochondrial carrier adenine nucleotide translocator), member 4 OS=Danio rerio GN=slc25a4 PE=1 SV=1	27	3	0.01220005	1.435507039	0.020846048	0.858406862
Q6NXA4	Interleukin enhancer-binding factor 3 homolog OS=Danio rerio GN=ilf3 PE=1 SV=2	3	2	0.009291271	3.558767488	0.149472758	0.762970222
Q6NYL7	Zgc:77517 OS=Danio rerio GN=zgc:77517 PE=1 SV=1	6	4	0.534513336	1.104499231	0.161978633	1.058342345
Q6NYQ7	Nicotinamide nucleotide transhydrogenase OS=Danio rerio GN=nnt PE=1 SV=1	2	2	0.084671063	0.655836931	0.450243504	1.091069851
Q6P043	Fructose-bisphosphate aldolase OS=Danio rerio GN=aldoab PE=1 SV=1	18	2	0.001889276	0.696657793	0.323700554	1.034199847
Q6P0S5	Alcohol dehydrogenase 8a OS=Danio rerio GN=adh8a PE=1 SV=1	10	4	0.037159345	1.204682752	0.360334972	1.037303527
Q6P0V8	Annexin OS=Danio rerio GN=anxa5b PE=1 SV=1	5	2	0.00239324	1.841766346	0.000856687	1.535362373
Q6P102	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide like OS=Danio rerio GN=ywhab1 PE=1 SV=1	15	2	8.30E-05	3.088446428	0.013732356	0.633035476
Q6P315	Hedgehog acyltransferase-like, a OS=Danio rerio GN=hhatla PE=1 SV=1	2	2	0.487603858	1.08094147	0.027219981	1.368225659
Q6P3J5	Eukaryotic translation elongation factor 2 OS=Danio rerio GN=eef2b PE=1 SV=1	46	21	0.617241849	1.044111467	0.004688825	0.874011294
Q6P3L3	Heat shock protein 5 OS=Danio rerio GN=hspa5 PE=1 SV=1	29	16	0.004809494	1.423471119	0.000920424	0.722940828
Q6P3L9	Glutamate dehydrogenase 1 OS=Danio rerio GN=glud1b PE=1 SV=1	17	4	0.0054552	1.358315599	0.038103887	0.85847811
Q6P6E0	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g OS=Danio rerio GN=atp5l PE=1 SV=1	6	3	0.502669866	1.095189074	0.359074391	0.914132059
Q6P972	Tubulin alpha chain OS=Danio rerio GN=tuba2 PE=1 SV=1	26	3	0.63187919	1.034477171	0.123484543	1.101961078
Q6PC12	Enolase 1, (Alpha) OS=Danio rerio GN=eno1a PE=1 SV=1	21	5	0.000956947	1.465270638	0.931186577	0.997430406
Q6PC47	Solute carrier family 25 (Mitochondrial carrier phosphate carrier), member 3, like OS=Danio rerio GN=slc25a3a PE=1 SV=1	10	4	0.734147428	1.024980636	0.774537959	1.010094435
Q6PC77	ATP synthase subunit d, mitochondrial OS=Danio rerio GN=atp5h PE=1 SV=1	2	1	0.834148656	0.941716683	0.439910337	0.959296498
Q6PC89	Enolase 1b, (alpha) OS=Danio rerio GN=eno1b PE=1 SV=1	14	3	0.000736843	0.316969587	0.030394439	1.326495731
Q6PC95	Tubulin alpha chain OS=Danio rerio GN=tuba8l2 PE=1 SV=1	21	1	0.008665903	1.442646149	0.412852426	0.940270256
Q6PE34	Tubulin beta chain OS=Danio rerio GN=zgc:65894 PE=1 SV=1	35	4	2.52E-05	1.642671465	0.004714427	0.793002432
Q6PGX4	Heat shock cognate 70 OS=Danio rerio GN=hsc70 PE=1 SV=1	33	8	0.001166546	1.930866685	0.003172162	0.79633885
Q6PHG2	Hemopexin OS=Danio rerio GN=hpx PE=2 SV=2	19	16	0.480012877	0.961955337	0.015768529	1.215893396
Q6PHI8	Tkt protein OS=Danio rerio GN=ktb PE=1 SV=1	15	10	0.035016242	1.905200849	0.281839399	0.929054864
Q6PI20	Histone H3.3 OS=Danio rerio GN=h3f3a PE=2 SV=3	5	1	5.48E-05	307.7699803	0.40573497	1.055086732
Q6Q417	Ribosomal protein L7 OS=Danio rerio GN=rpl7 PE=1 SV=1	4	3	0.043543676	1.412928732	0.023665297	0.81022902
Q6TA36	BHLH transcription factor OS=Danio rerio GN=her12 PE=2 SV=1	2	2	0.041254372	1.315908091	0.020279212	1.32991885
Q6TGS5	Tubulin alpha chain OS=Danio rerio GN=tuba4l PE=1 SV=1	22	4	0.000246171	1.662643764	0.096750009	0.899541961
Q6TH14	Enolase 1, (Alpha) OS=Danio rerio GN=eno3 PE=1 SV=1	35	21	0.829466967	1.008674895	0.16647633	1.063822051
Q6TLG8	Ribosomal protein S3 OS=Danio rerio GN=rps3 PE=1 SV=1	10	7	0.041976876	1.356495128	0.110245965	0.918875075
Q6TNP9	Tubulin alpha chain OS=Danio rerio GN=tuba8l1 PE=1 SV=1	16	1	0.014492869	1.486224275	0.691464209	1.022698421
Q6TNT9	Rab GDP dissociation inhibitor OS=Danio rerio GN=gdi2 PE=1 SV=1	18	9	0.007346892	2.335548811	0.122973884	0.932489381
Q6VN46	Myoglobin OS=Danio rerio GN=mb PE=2 SV=3	10	5	0.000462043	1.628264339	0.008027651	0.85505371
Q6XG62	Protein S100 OS=Danio rerio GN=icn PE=1 SV=1	3	3	0.004031089	0.163766183	0.036139212	1.575012564
Q6ZM12	Novel beta globin OS=Danio rerio GN=hbba2 PE=1 SV=1	8	6	0.040020967	1.416727158	0.014924708	0.886614451
Q6ZM13	Novel alpha globin OS=Danio rerio GN=hbba2 PE=1 SV=1	13	3	5.80E-05	0.465095913	0.000441012	1.207822528
Q6ZM17	Novel protein similar to zebrafish	45	5	7.41E-06	0.460171999	0.000258752	1.25647928

	hemoglobin alpha-adult 1 (Hbaa1) OS=Danio rerio GN=si:ch2111-5k11.8 PE=1 SV=1							
Q6ZM23	Cytochrome c oxidase subunit VIc OS=Danio rerio GN=cox6c PE=1 SV=1	2	1	0.003961247	1.351776783	0.013314829	0.752366111	
Q6ZM60	Calcium-transporting ATPase OS=Danio rerio GN=atp2a2b PE=1 SV=1	40	1	0.005641305	1.159655981	0.401607733	0.972472816	
Q7SX99	Fumarate hydratase, mitochondrial OS=Danio rerio GN=fh PE=2 SV=1	7	6	0.037361195	1.58239353	0.070824596	0.820598128	
Q7SXL4	Nucleoside diphosphate kinase OS=Danio rerio GN=nme2b.2 PE=1 SV=1	40	15	0.000465017	0.780408592	0.646814983	1.014292204	
Q7SY23	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Danio rerio GN=aldh4a1 PE=2 SV=1	3	2	0.033408118	2.112568654	0.027486384	0.677544297	
Q7SYK1	Queuine tRNA-ribosyltransferase catalytic subunit 1 OS=Danio rerio GN=qtrt1 PE=2 SV=1	2	1	0.763081001	0.824304569	0.55539784	1.046618315	
Q7SYK7	Aspartate aminotransferase OS=Danio rerio GN=got2a PE=1 SV=1	18	8	0.001046727	1.968483559	0.108719458	0.883920458	
Q7SZ53	Pentaxin OS=Danio rerio GN=crp2 PE=1 SV=2	3	2	0.000930702	1.854680968	0.000376177	0.776761375	
Q7SZE3	Lethal(2) giant larvae protein homolog 2 OS=Danio rerio GN=llgl2 PE=1 SV=1	4	2	0.000695894	0.736385844	0.948867283	1.006095344	
Q7SZR0	Ddc protein OS=Danio rerio GN=ddc PE=1 SV=1	3	3	0.020101337	0.144098439	0.032551381	4.787868304	
Q7T1B0	Embryonic globin beta e2 OS=Danio rerio GN=hbb2 PE=1 SV=1	11	3	0.000452193	0.534999	0.04179889	1.1690983	
Q7T2F5	N-ethylmaleimide sensitive fusion protein attachment protein alpha OS=Danio rerio GN=napab PE=1 SV=1	2	2	5.11E-05	4.8882624	0.455381939	1.049078419	
Q7T334	Malate dehydrogenase OS=Danio rerio GN=mdh2 PE=1 SV=1	14	8	0.036567782	0.762327144	0.137132661	0.928045753	
Q7T356	14-3-3 protein beta/alpha-B OS=Danio rerio GN=ywhabb PE=2 SV=1	19	4	0.238838357	1.160901676	0.020392197	0.903207992	
Q7T368	Pyruvate dehydrogenase (Lipoamide) beta OS=Danio rerio GN=pdhb PE=1 SV=1	7	6	0.045313969	0.76189183	0.276234156	0.95191175	
Q7T3F0	Tropomyosin 4 OS=Danio rerio GN=tpm4a PE=1 SV=1	3	1	0.009592566	1.335803656	0.048366582	0.894023442	
Q7T3G2	Tyrosine 3-monooxygenase/tryptophan 5- monooxygenase activation protein, eta polypeptide OS=Danio rerio GN=ywhah PE=1 SV=1	13	3	0.899340584	0.988757415	0.00139212	1.284262315	
Q7T3G4	Phosphoglycerate mutase OS=Danio rerio GN=pgam2 PE=1 SV=1	11	6	0.00038169	2.170889844	0.006192602	0.770744461	
Q7T3L3	Chaperone protein GP96 OS=Danio rerio GN=hsp90b1 PE=1 SV=1	13	8	0.001391568	3.305438598	0.002044765	0.735525656	
Q7ZT36	Parvalbumin 3 OS=Danio rerio GN=pvalb3 PE=1 SV=1	12	8	0.006817267	0.672119903	0.066035671	1.101378708	
Q7ZTS4	Keratin, type I cytoskeletal 18 OS=Danio rerio GN=krt18 PE=1 SV=2	19	11	2.03E-05	3.26388007	0.003286336	0.756125109	
Q7ZU29	Nuclear pore complex protein Nup93 OS=Danio rerio GN=dye PE=2 SV=1	8	4	0.459062112	1.03009115	0.047580449	0.933407712	
Q7ZU67	Eukaryotic translation initiation factor 4A, isoform 1B OS=Danio rerio GN=eif4a1b PE=1 SV=1	11	2	0.227574017	0.65442866	0.735128071	0.95017535	
Q7ZU99	Transitional endoplasmic reticulum ATPase OS=Danio rerio GN=vcp PE=1 SV=1	30	17	0.0289591	1.229715687	0.038371729	0.900296615	
Q7ZUN7	Ckmt1 protein OS=Danio rerio GN=ckmt1 PE=1 SV=1	20	8	0.001208424	1.643904151	0.079783653	0.933624614	
Q7ZUU6	Creatine kinase, mitochondrial 2a (sarcomeric) OS=Danio rerio GN=ckmt2a PE=1 SV=1	20	7	0.002039721	1.628136352	0.007625887	0.827220552	
Q7ZUW8	Aspartate aminotransferase OS=Danio rerio GN=got1 PE=1 SV=1	17	11	0.005589907	1.765474858	0.012043001	0.844907924	
Q7ZUY3	Histone H2AX OS=Danio rerio GN=h2afx PE=2 SV=3	2	1	0.233909708	1.269225548	0.469038363	1.048182492	
Q7ZVA4	Protein S100 OS=Danio rerio GN=s100a10b PE=1 SV=1	4	3	0.000996651	2.088735985	0.007302372	0.780612535	
Q7ZVF9	Actin, cytoplasmic 2 OS=Danio rerio GN=actb PE=2 SV=2	36	9	0.002470083	1.712344375	0.24896615	0.940627629	
Q7ZVG7	Fgg protein OS=Danio rerio GN=fgg PE=1 SV=1	4	3	0.56787325	1.075015322	0.547699375	0.968892814	
Q7ZVT2	Pyruvate kinase OS=Danio rerio GN=pkma PE=1 SV=1	20	3	0.001108756	1.637411383	0.002602224	0.776421782	
Q7ZVY5	Citrate synthase, mitochondrial OS=Danio rerio GN=cs PE=2 SV=1	12	11	0.043500631	1.312489542	0.002828696	0.716682754	
Q7ZW20	Tyrosine 3-monooxygenase/tryptophan 5- monooxygenase activation protein, epsilon polypeptide 1 OS=Danio rerio GN=ywhae1 PE=1 SV=1	12	1	0.431116026	0.690056218	0.765816694	0.98925404	
Q7ZW40	USO1 homolog, vesicle docking protein (Yeast) OS=Danio rerio GN=uso1 PE=1	3	2	0.356105973	0.640638835	0.21154732	0.694248255	

	SV=1								
Q7ZW95	Ribosomal protein L4 OS=Danio rerio GN=rpl4 PE=1 SV=1	14	9	0.001476417	1.406239911	0.067528361	0.894300004		
Q7ZZJ7	Anion exchange protein OS=Danio rerio GN=slc4a1a PE=1 SV=1	2	2	0.146884806	0.633084969	0.012166048	1.368059006		
Q801E6	Malate dehydrogenase OS=Danio rerio GN=mdh1aa PE=1 SV=1	19	17	0.457147532	0.954860496	0.823817394	1.008702306		
Q802C9	Eukaryotic translation initiation factor 4A, isoform 1A OS=Danio rerio GN=eif4a1a PE=1 SV=1	14	3	0.002089353	0.528449291	0.526224925	0.966639905		
Q803B0	Heat shock 60 protein 1 OS=Danio rerio GN=hspd1 PE=1 SV=1	2	2	0.746750995	0.058035417	0.085444651	0.672808708		
Q803F6	40S ribosomal protein SA OS=Danio rerio GN=rpsa PE=2 SV=1	5	3	0.485437275	0.830585074	0.0231706	1.149603615		
Q803M8	Tryptophan 3-monooxygenase/tryptophan 5- monooxygenase activation protein, zeta polypeptide OS=Danio rerio GN=ywhaqb PE=1 SV=1	16	5	0.433659007	0.784702891	0.565415948	1.021437987		
Q803Q7	Fructose-bisphosphate aldolase OS=Danio rerio GN=aldoaa PE=1 SV=1	27	7	0.013343892	0.777211552	0.522558017	1.023772263		
Q803T5	Adenosylhomocysteinase OS=Danio rerio GN=ahcy PE=1 SV=1	7	3	1.37E-05	1.992484208	0.003709031	0.737210021		
Q804W0	Parvalbumin 1 OS=Danio rerio GN=pvalb1 PE=1 SV=1	11	4	0.000716416	0.646484405	0.085245968	1.099127326		
Q8AW60	Isovaleryl Coenzyme A dehydrogenase OS=Danio rerio GN=ivd PE=1 SV=1	3	2	0.00285605	0.849289474	0.902100131	1.007703349		
Q8AWD0	Vdac2 protein OS=Danio rerio GN=vdac2 PE=1 SV=1	3	2	0.100355191	1.38694548	0.119130658	1.090345241		
Q8AX99	Actinin alpha 3b OS=Danio rerio GN=actn3b PE=1 SV=1	22	8	8.57E-05	1.680810707	0.000796265	0.742072385		
Q8AY63	Brain-subtype creatine kinase OS=Danio rerio GN=ckbb PE=1 SV=1	30	6	0.001485078	1.190315142	0.136028562	0.936202908		
Q8JFV8	Synaptic vesicle membrane protein VAT-1 homolog OS=Danio rerio GN=vat1 PE=2 SV=1	8	4	0.05525548	1.41637277	0.852947551	0.991573707		
Q8JH70	Fructose-bisphosphate aldolase C-B OS=Danio rerio GN=aldocb PE=2 SV=1	3	1	0.002676081	3.396060841	0.00270008	0.740703067		
Q8JH71	Fructose-bisphosphate aldolase B OS=Danio rerio GN=aldob PE=2 SV=1	9	6	0.000122922	5.335342999	0.000139104	0.630349272		
Q8JH10	Solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 OS=Danio rerio GN=slc25a5 PE=1 SV=1	33	9	0.056476183	1.311956789	0.00291862	0.761877229		
Q8JH16	Mediator of RNA polymerase II transcription subunit 29 OS=Danio rerio GN=med29 PE=2 SV=1	2	2	0.956299825	0.118313139	0.040468852	1.622792557		
Q90473	Heat shock cognate 71 kDa protein OS=Danio rerio GN=hspa8 PE=2 SV=1	25	1	0.000842911	4.380213574	0.015218121	0.615946824		
Q90485	Hemoglobin subunit beta-2 OS=Danio rerio GN=ba2 PE=1 SV=3	41	4	0.036539788	0.732176418	0.426863398	1.029037151		
Q90486	Hemoglobin subunit beta-1 OS=Danio rerio GN=ba1 PE=1 SV=3	48	1	0.002865321	0.600961956	0.013049543	1.139159769		
Q90487	Hemoglobin subunit alpha OS=Danio rerio GN=hbaa1 PE=2 SV=3	47	5	1.13E-05	0.471267363	0.000315173	1.237555166		
Q92005	Elongation factor 1-alpha OS=Danio rerio GN=eef1a PE=2 SV=1	30	4	0.002422058	1.444134069	0.007622427	0.884738699		
Q92051	Carbonic anhydrase OS=Danio rerio GN=cahz PE=1 SV=2	3	2	0.003361774	1.952762788	0.017725083	0.793681719		
Q9DDL2	MALT paracaspase 2 OS=Danio rerio GN=malt2 PE=2 SV=1	2	1	0.004248765	1.374726939	0.02537021	0.846090153		
Q9DDU5	Glutathione S-transferase pi OS=Danio rerio GN=gstp1 PE=1 SV=1	8	4	0.03582769	1.309854269	0.033715465	0.810021626		
Q9DEU2	Sodium/potassium-transporting ATPase subunit alpha OS=Danio rerio GN=atp1a3b PE=1 SV=1	21	5	0.000221054	1.687816366	0.02404873	0.8811652		
Q9DGL6	Sodium/potassium-transporting ATPase subunit alpha OS=Danio rerio GN=atp1a1a.1 PE=1 SV=1	31	3	2.62E-05	2.179936638	0.007343664	0.754756538		
Q918V0	Parvalbumin-2 OS=Danio rerio GN=pvalb2 PE=3 SV=3	20	8	0.016809747	0.74125975	0.125002754	1.089624509		
Q9MIY7	Cytochrome c oxidase subunit 2 OS=Danio rerio GN=mt-co2 PE=3 SV=1	3	3	0.003893551	0.456196025	0.098868091	1.339585377		
Q9PV90	60S acidic ribosomal protein P0 OS=Danio rerio GN=rplp0 PE=2 SV=1	8	5	0.124454547	1.080411113	0.031121378	0.895086324		
Q9PVK4	L-lactate dehydrogenase B-A chain OS=Danio rerio GN=ldhba PE=2 SV=4	20	6	0.290124116	0.953519231	0.765468509	0.990627098		
Q9PVK5	L-lactate dehydrogenase A chain OS=Danio rerio GN=ldha PE=2 SV=3	19	9	0.277978412	0.940642274	0.685581846	1.015625756		
R4GE02	Uncharacterized protein OS=Danio rerio GN=si:ch211-113a14.11 PE=1 SV=1	4	1	4.40E-05	3.775215033	0.060600852	0.827631396		
R4GED5	Si:ch73-168d20.1 OS=Danio rerio GN=si:ch73-168d20.1 PE=4 SV=1	10	4	9.34E-05	1.533189618	0.000991853	0.706120978		

R4GEU2	Si:dkey-4p15.3 (Fragment) OS=Danio rerio GN=si:dkey-4p15.3 PE=1 SV=6	6	1	0.008491427	2.103925359	0.159899966	0.755753925
R4GF04	Si:dkey-187i8.2 OS=Danio rerio GN=si:dkey-187i8.2 PE=4 SV=1	9	6	3.09E-05	5.487848542	0.00041039	0.629119817
U3JAX6	Si:dkey-61p9.9 OS=Danio rerio GN=si:dkey-61p9.9 PE=4 SV=1	5	4	0.857466237	1.008162861	0.000900608	0.90503395
X1WBJ0	Tripartite motif-containing 65 OS=Danio rerio GN=trim65 PE=4 SV=1	2	1	0.420522825	0.784366998	0.602987771	1.087271191
X1WBT0	Si:dkey-105h12.2 OS=Danio rerio GN=si:dkey-105h12.2 PE=1 SV=1	13	2	0.201135369	1.051969833	0.976834372	1.001967576
X1WC44	Si:ch211-212c13.8 (Fragment) OS=Danio rerio GN=si:ch211-212c13.8 PE=1 SV=1	18	3	0.001105132	1.341858328	0.45057968	0.968204158
X1WEB9	Dedicator of cytokinesis 9b OS=Danio rerio GN=dock9b PE=1 SV=1	14	11	0.00043563	1.909749743	0.0024002	0.753136649
X1WGM2	Si:ch211-181d7.1 (Fragment) OS=Danio rerio GN=si:ch211-181d7.1 PE=4 SV=1	7	2	0.00053201	3.434483294	0.001665965	0.748754086
X1WHD9	Immunoglobulin-like and fibronectin type III domain-containing 1, tandem duplicate 1 OS=Danio rerio GN=igfn1.1 PE=1 SV=2	13	8	0.101426228	1.157952388	0.537350829	0.970822191

Table S3-2. Comparative proteins significantly changed with HFD and AOS supplemented (ratios of HFD/NFD and HAOS/HFD after 35 days feeding period). with upregulated proteins having expressions ≥ 1.2 , red;

downregulated proteins having expressions ≤ 0.83 , green. Cut-off: Anova $p < 0.05$, peptide count ≥ 2 , unique peptide ≥ 1 .

UniProt Accession No.	Symbols	Protein name	HFD/NFD Fold Change	HAOS/HFD Fold Change
A0A0R4ICC8	STOML2	stomatatin (EPB72)-like 2	16.54	0.52
F6NMG5	COG5	component of oligomeric golgi complex 5	12.22	0.76
Q6DHFQ3	ACY3.2	aspartoacylase (aminocyclase) 3, tandem duplicate 2	10.94	0.30
E7F372	RASA1B	RAS p21 protein activator (GTPase activating protein) 1b	10.32	0.39
F1RCJ3	RIMS1A	regulating synaptic membrane exocytosis 1a	5.96	0.59
F1R2P4	TLR8A	toll-like receptor 8a	5.89	0.40
R4GF04	SI:DKEY- 187I8.2	si:dkey-187i8.2	5.49	0.63
Q8JH71	ALDOB	aldolase b, fructose-bisphosphate	5.34	0.63
F1QF64	SI:CH211- 67F13.8	si:ch211-67f13.8	5.27	0.60
B8JIH7	ARL13B	ADP-ribosylation factor-like 13b	5.08	0.62
D1GJ56	ACTN3A	actinin alpha 3a	5.08	0.61
F1QHA9	NRP1B	neuropilin 1b	4.81	0.72
F1R343	NUAK1A	NUAK family, SNF1-like kinase, 1a	4.68	0.59
Q5SNY2	PAPOLA	poly(A) polymerase alpha	4.49	0.49
F1QPU1	SI:CH211- 197L9.2	si:ch211-197l9.2	4.44	0.79
Q90473	HSPA8	Heat shock cognate 71 kDa protein	4.38	0.62
Q1ECX9	PDIA4	protein disulfide isomerase family A, member 4	4.31	0.56
A0A0G2KL83	-	Uncharacterized protein	3.76	0.60
A0A0R4IVB0	HSPA8	heat shock protein 8-like	3.62	0.64
F1QQ05	VPS8	vacuolar protein sorting 8 homolog (S. cerevisiae)	3.58	0.71
E7EYD0	MYOM1A	myomesin 1a (skelemin)	3.56	0.67
F1QGK5	CALCOCO2	calcium binding and coiled-coil domain 2	3.55	0.56
A2CEI6	PIWIL2	piwi-like RNA-mediated gene silencing 2	3.55	0.59
A0A0R4IQ19	CKAP5	cytoskeleton associated protein 5	3.47	0.67
X1WGM2	SI:CH211- 181D7.1	si:ch211-181d7.1	3.43	0.75
E9QET4	TJPIA	tight junction protein 1a	3.43	0.66
F1Q7L0	VTG4	vitellogenin 4	3.41	0.70
Q8JH70	ALDOCB	aldolase C, fructose-bisphosphate, b	3.40	0.74
F1QV15	VTG6	vitellogenin 6	3.38	0.69
Q7T3L3	HSP90B1	heat shock protein 90, beta (grp94), member 1	3.31	0.74
A0A0R4IGN3	PDIA3	protein disulfide isomerase family A, member 3	3.31	0.73
Q1LWN2	VTG1	vitellogenin 1	3.29	0.69
Q1MTC4	VTG2	vitellogenin 2	3.27	0.69
Q7ZTS4	KRT18	keratin 18	3.26	0.76
A4QPA0	ME3	malic enzyme 3, NADP(+)-dependent, mitochondrial	3.24	0.73
A0A0R4IQE4	SI:CH211- 196F19.1	si:ch211-196f19.1	3.21	0.75
B3DFP9	APOA2	apolipoprotein A-II	3.19	0.70
A8E7T3	SI:DKEY- 51D8.2	si:dkey-51d8.2	3.14	0.65
A0A0G2L6I6	NADP	Isocitrate dehydrogenase	3.14	0.66
A0A0R4IIW8	SI:DKEY- 71L4.4	si:dkey-71l4.4	3.12	0.66
Q6P102	YWHABL	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide like	3.09	0.63
B0V2T6	DOCK8	dedicator of cytokinesis 8	3.08	0.63
F1Q6K8	SVILA	supervillin a	3.06	0.66
B8A4S2	TSGA10	testis specific, 10	3.05	0.29
A0A0R4IUS8	SI:DKEY- 29M1.2	si:dkey-29m1.2	2.99	0.65

A0A0R4IJ29	SI:DKEY-14O6.2	si:dkey-14o6.2	2.98	0.67
A0A0R4IHC4	SI:CH211-76M11.3	si:ch211-76m11.3	2.98	0.66
A0A0R4IP16	SI:CH211-39D8.1	si:ch211-39d8.1	2.97	0.66
E7F4S5	LOC103910258	protein NLRC3-like	2.96	0.64
A0A0R4IHI2	SI:CH211-246B8.1	si:ch211-246b8.1	2.96	0.66
A0A0R4IB01	SI:DKEY-165E24.1	si:dkey-165e24.1	2.95	0.67
A0A0R4IN16	SI:DKEY-264F17.2	si:dkey-264f17.2	2.94	0.65
A5WUN8	PLPPR5A	phospholipid phosphatase related 5a	2.94	0.71
A0A0R4IY80	SI:DKEY-264F17.1	si:dkey-264f17.1	2.93	0.68
F1QU55	BHMT	betaine-homocysteine methyltransferase	2.89	0.63
A0A0R4II04	SI:DKEY-29J8.1	si:dkey-29j8.1	2.80	0.70
F1R966	CLTCA	clathrin, heavy chain a (Hc)	2.79	0.65
H0WEA8	SI:DKEY-84H14.2	si:dkey-84h14.2	2.79	0.72
Q6DRF3	PSMB1	proteasome subunit beta 1	2.77	0.65
A0A0R4IDU6	TIAM1B	T-cell lymphoma invasion and metastasis 1b	2.73	0.70
K7DY31	SI:DKEY-4J21.2	si:dkey-4j21.2	2.70	0.68
K7DY17	SI:CH211-242B18.1	si:ch211-242b18.1	2.68	0.71
A8E7G6	PRDX3	peroxiredoxin 3	2.66	0.73
I3IT32	COL12A1B	collagen, type XII, alpha 1b	2.65	0.70
Q5MJ86	GAPDHS	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	2.58	0.80
Q6NWF6	KRT8	keratin 8	2.55	0.72
A0A0R4IJS2	SI:CH211-59D8.2	si:ch211-59d8.2	2.55	0.69
F1R8U0	KRT94	keratin 94	2.52	0.73
E9QD79	CLTCB	clathrin, heavy chain b (Hc)	2.44	0.66
F1QK60	KRT4	keratin 4	2.44	0.74
A0A0R4IYW7	SI:DKEY-27N6.1	si:dkey-27n6.1	2.42	0.65
A0A0R4IUS1	SI:CH211-223G7.6	si:ch211-223g7.6	2.40	0.76
A0A0R4ISX6	P4HB	prolyl 4-hydroxylase, beta polypeptide	2.38	0.75
F1QV31	KRT5	keratin 5	2.37	0.78
A0A0H2UKK8	PUS7	pseudouridylylase 7 (putative)	2.34	0.74
A0A0R4ITY7	SI:CH211-76M11.8	si:ch211-76m11.8	2.34	0.69
F1REP2	ZGC:171426	zgc:171426	2.31	0.71
H9GXQ9	MICAL3A	microtubule-associated monooxygenase, calponin and LIM domain containing 3a	2.30	0.78
F1RDG4	SI:DKEY-222F2.1	si:dkey-222f2.1	2.28	0.81
A0A0R4IP08	SI:DKEY-211I20.2	si:dkey-211i20.2	2.26	0.69
B0R068	ATP1A1B	ATPase, Na ⁺ /K ⁺ transporting, alpha 1b polypeptide	2.25	0.76
E9QDK0	SI:DKEY-51D8.1	si:dkey-51d8.1	2.23	0.69
A0A0R4IDL5	SI:CH211-232D10.1	si:ch211-232d10.1	2.20	0.70
Q08BA1	ATP5A1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	2.18	0.70
Q9DGL6	ATP1A1A.1	ATPase, Na ⁺ /K ⁺ transporting, alpha 1a polypeptide, tandem duplicate 1	2.18	0.75
E7EZI7	DLG5B.1	discs, large homolog 5b (Drosophila), tandem duplicate 1	2.18	0.80

F1QQQ3	VTG3	vitellogenin 3, phosvitinless	2.18	0.77
Q7T3G4	PGAM2	phosphoglycerate mutase 2 (muscle)	2.17	0.77
F1QF63	ZGC:165518	zgc:165518	2.16	0.66
Q6NUZ3	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	2.14	0.76
Q7SY23	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	2.11	0.68
E7FEY5	SI:CH211-89P3.3	si:ch211-89p3.3	2.10	0.78
F1Q6Y6	RSF1B.1	remodeling and spacing factor 1b, tandem duplicate 1	2.10	0.83
Q7ZVA4	S100A10B	S100 calcium binding protein A10b	2.09	0.78
A0A0N4STW3	C3B	complement component c3b, tandem duplicate 1	2.01	0.77
Q803T5	AHCY	adenosylhomocysteinase	1.99	0.74
Q92051	CAHZ	carbonic anhydrase	1.95	0.79
A0A0R4IP53	TAOK1B	TAO kinase 1b	1.93	0.73
Q6PGX4	HSC70	heat shock cognate 70	1.93	0.80
X1WEB9	DOCK9B	dedicator of cytokinesis 9b	1.91	0.75
A2CEZ0	SI:DKEY-251I10.1	si:dkey-251i10.1	1.90	0.79
F1RD80	CDH17	cadherin 17, LI cadherin (liver-intestine)	1.88	0.72
E9QFR8	ACTN2B	actinin, alpha 2b	1.87	0.80
A0A0R4IZD9	SI:CH211-205A14.7	si:ch211-205a14.7	1.86	0.72
Q7SZ53	CRP2	C-reactive protein 2	1.85	0.78
B0UYE9	GRIPAP1	GRIP1 associated protein 1	1.83	0.82
A0JMP4	ATP2A1	ATPase, Ca ⁺⁺ transporting, cardiac muscle, fast twitch 1 like	1.81	0.80
E9QDA3	RAB44	Rab44, member ras oncogene family	1.75	0.82
Q6DEF9	SOCS1A	Suppressor of cytokine signaling 1a	1.74	0.73
F1Q555	GPD2	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	1.73	0.70
A0A0R4IL12	SI:DKEY-92C21.	Si:dkey-92c21.1	1.70	0.74
B3DKP3	OGT.1	O-linked n-acetylglucosamine (glcnac) transferase, tandem duplicate 1	1.69	0.82
F1QYZ6	PCXB	Pyruvate carboxylase b	1.69	0.83
B8JIS8	GSTM.1	Glutathione s-transferase mu, tandem duplicate 1	1.69	0.80
Q8AX99	ACTN3B	Actinin alpha 3b	1.68	0.74
A0A0R4IGP6	PKMA	Pyruvate kinase, muscle, a	1.66	0.80
Q6PE34	ZGC:65894	Zgc:65894	1.64	0.79
Q7ZVT2	PKMA	Pyruvate kinase, muscle, a	1.64	0.78
B3DK63	ZGC:194906	Zgc:194906	1.63	0.79
Q7ZUU6	CKMT2A	Creatine kinase, mitochondrial 2a (sarcomeric)	1.63	0.83
R4GED5	SI:CH73-168D20.1	Si:ch73-168d20.1	1.53	0.71
A0A0A0MPS0	SI:DKEY-222H21.2	Si:dkey-222h21.2	1.51	0.79
A8WGC6	ATP5B	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, beta polypeptide	1.48	0.83
Q6P3L3	HSPA5	heat shock protein 5	1.42	0.72
Q6Q417	RPL7	ribosomal protein L7	1.41	0.81
Q6ZM23	COX6C	cytochrome c oxidase subunit VIc	1.35	0.75
Q7ZVY5	CS	citrate synthase	1.31	0.72
Q9DDU5	GSTP1	glutathione S-transferase pi 1	1.31	0.81
A0A0R4IDW8	SI:DKEY-193I10.4	si:dkey-193i10.4	1.30	0.80
Q6XG62	ICN	Ictacalcin(icn)	0.16	1.58
F8W5U2	TDP1	Tyrosyl-DNA phosphodiesterase 1	0.20	1.80
A0A0R4IA89	SI:CH211-203C5.3	Si:ch211-203c5.3	0.23	4.45
A0A0R4IFF1	CYP2AA7	Cytochrome P450, family 2, subfamily AA, polypeptide 7	0.26	1.83
F1QKJ4	FRMPD3	FERM and PDZ domain-containing 3	0.27	1.72
Q6PC89	ENO1B	Enolase 1b, (alpha)	0.32	1.33
Q6DGK2	LDHBB	L-lactate dehydrogenase B-B chain	0.40	1.21
Q6ZM17	SI:CH211-5K11.8	Novel protein similar to zebrafish hemoglobin alpha-adult 1 (Hbaa1)	0.46	1.26
Q6ZM13	SI:CH211-	Novel alpha globin	0.47	1.21

	5K11.6			
Q7SZR0	DDC	Dopa decarboxylase(ddc) protein	0.47	4.79
Q90487	HBAA1	Hemoglobin subunit alpha	0.47	1.24
E7F9J5	MCTP2B	Multiple C2 domains, transmembrane 2b	0.47	1.48
E7F263	CGNA	Cingulin a	0.54	1.89
F1Q9F6	LUC7L3	LUC7-like 3 pre-mRNA-splicing factor	2.79	1.35
Q6P0V8	ANXA5B	Annexin	1.84	1.54
Q6TA36	HER12	BHLH transcription factor	1.32	1.33
E7F0A1	PFN1	Profilin	0.76	0.71

Table S4. Biological functional profiling of proteins regulated by HFD and AOS supplementation in zebrafish using Ingenuity Pathway Analysis (IPA).

Category	Functional Annotation	p-value	Activation z-score	Molecules
Cancer, Gastrointestinal Disease, Hepatic System Disease, Organismal Injury and Abnormalities	Hepatitis B virus-related hepatocellular carcinoma	1.43E-10	--	ALDH4A1, ALDOB, ANXA5, BHMT, HSP90B1, HSPA5, HSPA8
	Hepatitis C virus-related hepatocellular carcinoma	1.26E-06	--	ANXA5, HSP90B1, HSPA5, HSPA8
	Gastroesophageal adenocarcinoma	1.96E-06	--	ALDOB, BHMT, GSTP1, HSP90B1, NUAK1, PKM, TUBB4A
	Esophageal adenocarcinoma	3.73E-06	--	ALDOB, BHMT, GSTP1, HSP90B1, NUAK1, TUBB4A
	Liver cancer	2.16E-05	--	ALDH4A1, ALDOB, ANXA5, ATP5F1A, BHMT, CDH17, GSTP1, HSP90B1, HSPA5, HSPA8, PKM, PSMB1, SOCS1, TUBB4A
	Liver carcinoma	3.09E-05	--	ALDH4A1, ALDOB, ANXA5, BHMT, CDH17, HSP90B1, HSPA5, HSPA8, PKM, PSMB1, SOCS1, TUBB4A
	Hepatic steatosis	5.84E-05	0.068	ATP5F1A, DDC, GSTP1, PC, PKM, S100A10, S100A4
Cancer, Organismal Injury and Abnormalities	Malignant solid tumor	2.79E-09	-1.673	AHCY, ALDH4A1, ALDOB, ALDOC, ANXA5, ATP1A1, ATP2A1, ATP5F1A, ATP5F1B, BHMT, CALCOCO2, CDH17, CGN, CKAP5, DOCK8, GSTM3, GSTP1, HSP90B1, HSPA5, HSPA8, KRT15, KRT18, KRT8, NUAK1, OGT, P4HB, PC, PDIA3, PIWIL2, PKM, PSMB1, RPL7, RSF1, S100A10, S100A4, SOCS1, SYNCRIP, TDP1, TIAM1, TJP1, TLR8, TUBB4A, YWHAZ
	Cancer	1.16E-08	0.398	AHCY, ALDH4A1, ALDOB, ALDOC, ANXA5, ATP1A1, ATP2A1, ATP5F1A, ATP5F1B, BHMT, CALCOCO2, CDH17, CGN, CKAP5, DDC, DOCK8, GSTM3, GSTP1, HSP90B1, HSPA5, HSPA8, KRT15, KRT18, KRT8, NUAK1, OGT, P4HB, PC, PDIA3, PIWIL2, PKM, PSMB1, RPL7, RSF1, S100A10, S100A4, SOCS1, SYNCRIP, TDP1, TIAM1, TJP1, TLR8, TUBB4A, YWHAZ
	Solid tumor	1.39E-08	-1.319	AHCY, ALDH4A1, ALDOB, ALDOC, ANXA5, ATP1A1, ATP2A1, ATP5F1A, ATP5F1B, BHMT, CALCOCO2, CDH17, CGN, CKAP5, DOCK8, GSTM3, GSTP1, HSP90B1, HSPA5, HSPA8, KRT15,

Inflammatory Response and Apoptosis				KRT18, KRT8, NUAK1, OGT, P4HB, PC, PDIA3, PIWIL2, PKM, PSMB1, RPL7, RSF1, S100A10, S100A4, SOCS1, SYNCRIP, TDP1, TIAM1, TJP1, TLR8, TUBB4A, YWHAZ
	Tumorigenesis of tissue	7.29E-08	-1.01	Actn3, ALDH4A1, ALDOB, ALDOC, ANXA5, ATP1A1, ATP2A1, ATP5F1B, BHMT, CALCOCO2, CDH17, CLTC, DOCK8, GSTP1, HSP90B1, HSPA5, HSPA8, KRT18, NUAK1, P4HB, PC, PDIA3, PKM, PSMB1, RPL7, RSF1, S100A10, S100A4, SOCS1, SYNCRIP, TIAM1, TUBB4A, YWHAZ
	Inflammation of organ	2.01E-05	0.242	AHCY, ANXA5, ATP1A1, CA13, GSTP1, HSP90B1, HSPA5, KRT15, KRT8, P4HB, PDIA3, PKM, PSMB1, S100A10, S100A4, SOCS1, TLR8, TUBB4A
	Necrosis	2.34E-05	1.485	ANXA5, ATP1A1, ATP2A1, ATP5F1A, CKAP5, CLTC, CS, DOCK8, GSTP1, HSP90B1, HSPA5, HSPA8, KRT18, KRT8, NUAK1, OGT, P4HB, PDIA3, PKM, PRDX3, PSMB1, RPL7, S100A10, S100A4, SOCS1, SVIL, TIAM1, YWHAZ
	Cell viability	4.01E-05	-2.601	ANXA5, CKAP5, DOCK8, GSTP1, HBZ, HSP90B1, HSPA5, NUAK1, OGT, P4HB, PDIA3, PIWIL2, PKM, RSF1, S100A4, SOCS1, SVIL, TUBB4A, YWHAZ
	Chronic inflammatory disorder	0.00038	--	BHMT, CA13, HSP90B1, HSPA5, HSPA8, LDHB, P4HB, PDIA3, PKM, PSMB1, S100A10, S100A4, SOCS1
	Apoptosis	0.000443	0.268	ANXA5, ATP1A1, ATP2A1, CKAP5, CLTC, CS, GSTP1, HSPA5, HSPA8, KRT18, KRT8, NUAK1, OGT, P4HB, PDIA3, PKM, PRDX3, PSMB1, S100A10, S100A4, SOCS1, TIAM1, YWHAZ
	Inflammation of body cavity	0.000702	0.537	ANXA5, GSTP1, HSP90B1, HSPA5, KRT8, P4HB, PDIA3, PKM, S100A4, SOCS1, TLR8
	Inflammation of absolute anatomical region	0.00148	0.199	ANXA5, CA13, GSTP1, HSP90B1, HSPA5, KRT8, P4HB, PDIA3, PKM, S100A4, SOCS1, TLR8

Table S5. The top canonical pathways profiling of significant proteins ($p < 0.05$) regulated by HFD and AOS supplementation in zebrafish using Ingenuity Pathway Analysis (IPA).

Ingenuity Canonical Pathways	-log(p-value)	Ratio	Molecules
Glycolysis I	7.69	0.192	ALDOB, PKM, PGAM2, GAPDHS, ALDOC
Gluconeogenesis I	7.69	0.192	ALDOB, ME3, PGAM2, GAPDHS, ALDOC
Unfolded protein response	4.47	0.0714	HSPA8, HSP90B1, P4HB, HSPA5
Mitochondrial Dysfunction	3.61	0.0292	PRDX3, ATP5F1B, Cox6c, GPD2, ATP5F1A
Aldosterone Signaling in Epithelial Cells	3.58	0.0287	HSPA8, HSP90B1, PDIA3, HSPA5, AHCY
Sertoli Cell-Sertoli Cell Junction Signaling	3.48	0.0273	TJP1, ACTN2, CGN, Actn3, TUBB4A
Sucrose Degradation V (Mammalian)	3.43	0.222	ALDOB, ALDOC
Calcium Transport I	3.33	0.2	ANXA5, ATP2A1
Glucocorticoid Receptor Signaling	3.02	0.0173	HSPA8, HSP90B1, KRT8, KRT18, HSPA5, KRT15
Aryl Hydrocarbon Receptor Signaling	2.92	0.0282	ALDH4A1, HSP90B1, GSTM3, GSTP1
Huntington's Disease Signaling	2.85	0.0198	HSPA8, ATP5F1B, ATP5F1A, CLTC, HSPA5
Remodeling of Epithelial Adherens Junctions	2.82	0.0435	ACTN2, Actn3, TUBB4A
Endoplasmic Reticulum Stress Pathway	2.67	0.0952	HSP90B1, HSPA5
Germ Cell-Sertoli Cell Junction Signaling	2.54	0.0222	TJP1, ACTN2, Actn3, TUBB4A

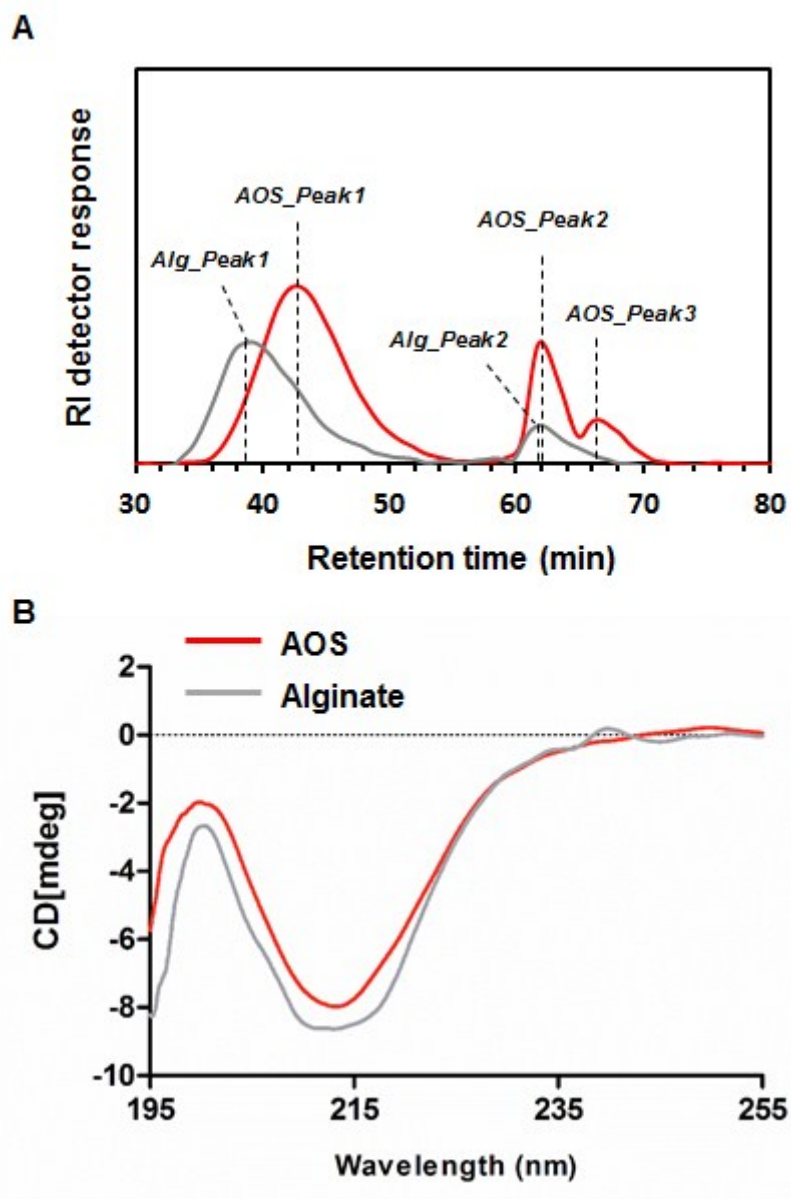


Figure S1. Characterization of depolymerized alginate oligosaccharide (AOS, red) in comparison with sodium alginate (Alg, grey) by gel filtration chromatograph GFC (A) and Circular dichroism (B).

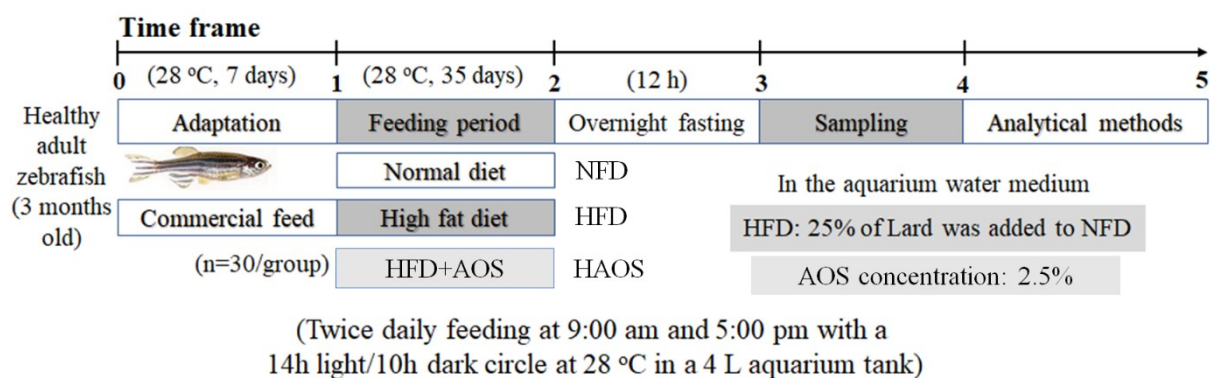


Figure S2. Outline of the HFD and AOS supplemented feeding protocol.

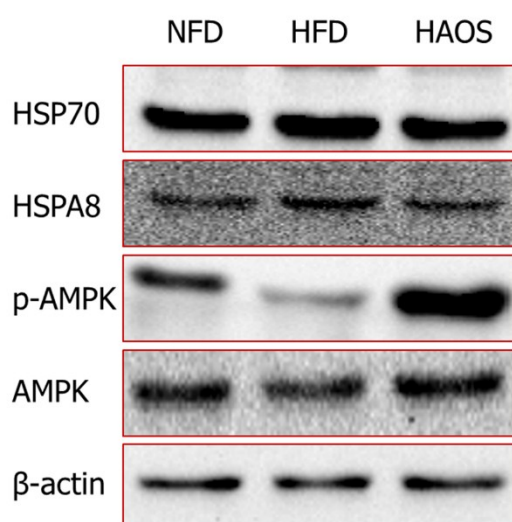


Figure S3. The western blotting analysis of protein in adult zebrafish of normal feeding diet (NFD), high-fat diet (HFD) and a high-fat diet supplemented AOS (HAOS) groups after feeding period (5 weeks). Proteins extracted from all treatment groups were quantified using a Pierce BSA Protein Assay Kit (23209; Thermo Scientific). Equal amounts of total proteins (20- μ g/well) were separated by 12% SDS-PAGE (Bio-Rad Laboratories) and transferred onto PVDF membranes (Immobilon Transfer Membrane, Millipore) at 4°C overnight. The membranes were blocked with 5% skim milk (BIOPURE, Seoul, Korea) in Tris-buffered saline with Tween-20 (TBS-T) for 1-h at room temperature (RT), washed thrice with TBS-T (5-min each), and incubated with primary antibodies against β -actin, heat shock protein (HSP)70, HSPA8, and p-AMPK and AMPK α (were freshly prepared in the blocking solution at concentration of 1:1,000, details are given in Table S6) at 4°C overnight. Then, the relevant conjugated secondary antibodies (1:10,000, Table S6) were used for incubation the membranes at RT, 1-h. Finally, the blots were detected using the Chemi-Doc systems.

Table S6. Details of antibodies used for western blotting

ANTIBODIES	SOURCE/SUPPLIER	IDENTIFIER
β -Actin	Cell signaling	β -Actin Antibody #4967L; 1:1,000
HSPA8	Cell signaling	HSPA8 (D12F2) Rabbit mAb #8444; 1:1,000
HSP70	Cell signaling	HSP70 (D69) Antibody #4872S; 1:1,000
AMPK α	Cell signaling	AMPK-alpha Rabbit Antibody #2532S; 1:1,000
p-AMPK α	Cell signaling	Phospho-AMPK-alpha (Thr172) Rabbit Antibody #2531; 1:1,000
Conjugated antibody	(Dako)	Anti-rabbit secondary antibodies (Ref. no. P0448; Lot: 00094764; polyclonal goat-anti rabbit immunoglobulins/HRP; 1:10,000

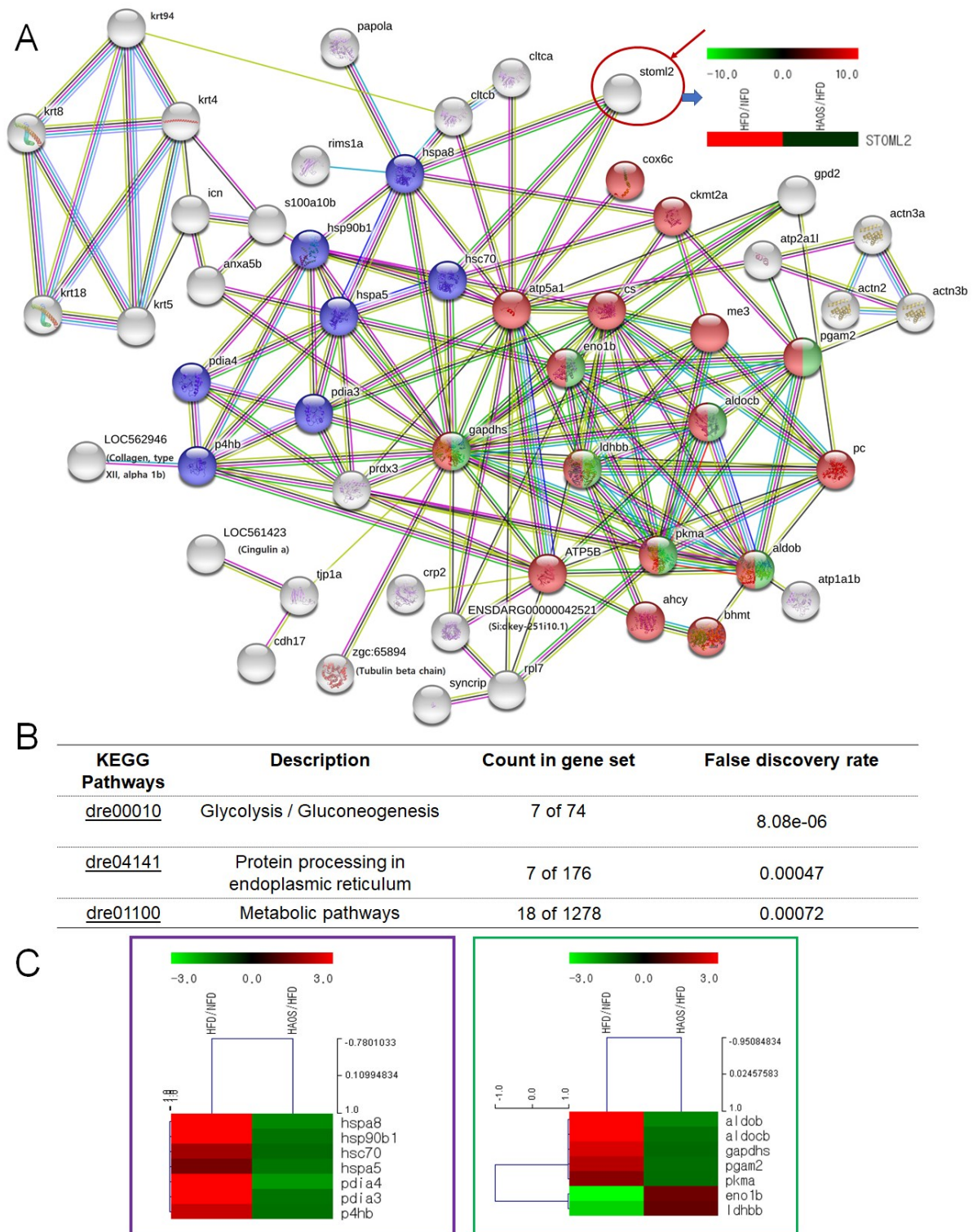


Figure S4. The network relationship analyzed by using a web-based search of the STRING database (<https://string-db.org/>, accessed on 15/02/2019). (A) Interaction network of 51 proteins that highly interacted together and differentially regulated between HFD and AOS treatment ($p < 0.05$); STOML2 was predicted as a bridge factor between immune system (ER, nodes in blue) and metabolism (metabolic pathways, nodes in red) in zebrafish with HFD; (B) KEGG Pathways analysis and (C), A hierarchical heatmap of significant identified proteins of metabolism and immune systems. Ratios are shown as Log₂ fold change, with upregulated proteins having expressions > 0.0 , red; downregulated proteins having expressions < 0.0 , green; Anova $p < 0.05$.

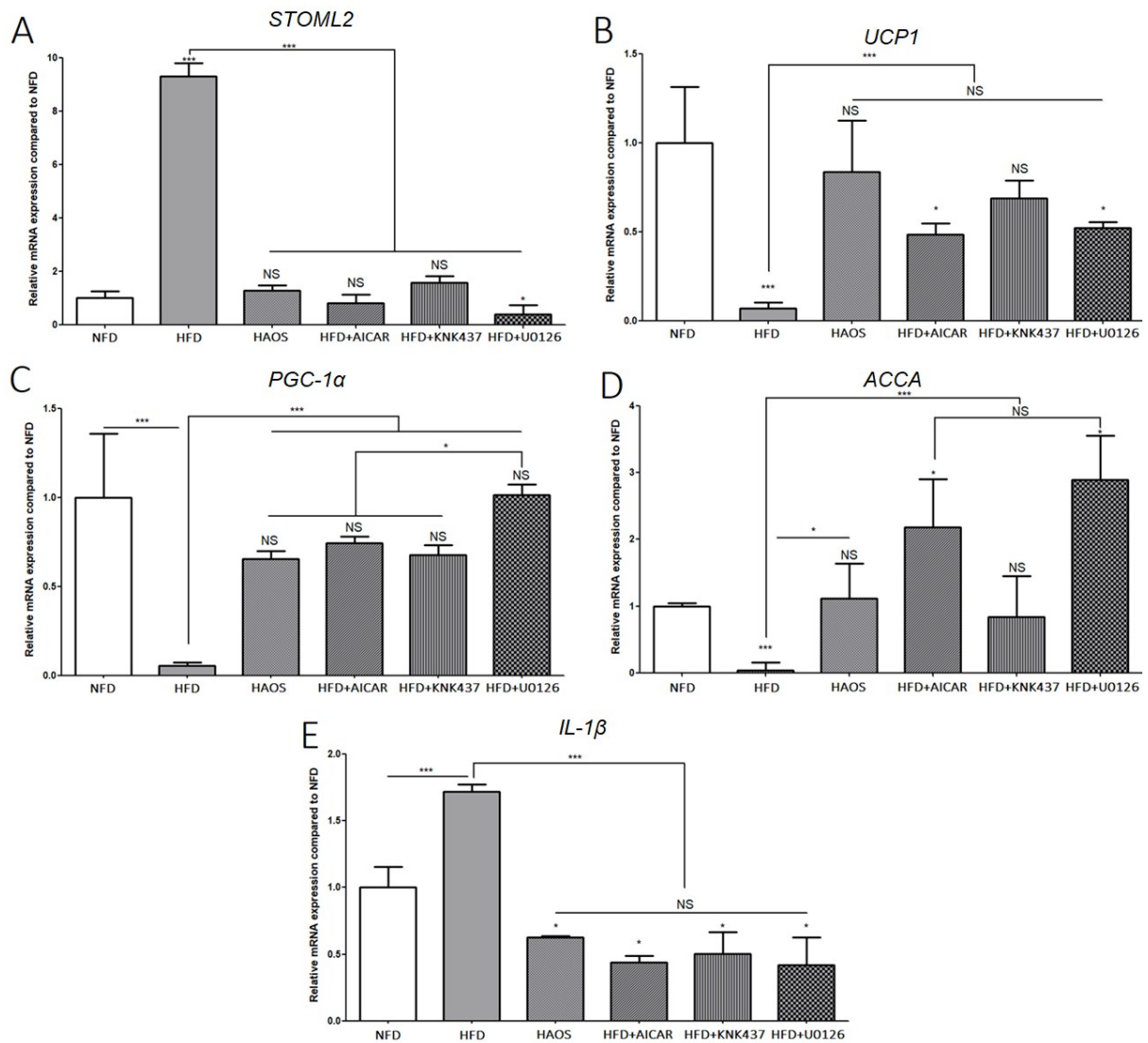


Figure S5. Relative mRNA expression levels of *STOML2* (A), *UCP1* (B), *PGC-1α* (C), *ACCA* (D) and *IL-1β* (E) in adult zebrafish of normal feeding diet (NFD) and high-fat diet (HFD) under different treatments. Results are means \pm SD of 3 - 4 replication. Asterisks and letters above bars indicate the level of significant difference from the groups determined using Student's t-test analysis (NS, not significance, * $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$).