

Transcriptomic Analysis of Early Stages of Intestinal Regeneration in *Holothuria glaberrima*

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Table S1. Results of transcriptome assessment with BUSCO

Parameter	BUSCO result
Core genes queried	978
Complete core genes detected	99.1%
Complete single copy core genes	27.2%
Complete duplicated core genes	71.9%
Fragmented core genes detected	0.4%
Missing core genes	0.5%

Table S2. Transcriptome length statistics and composition assessments with gVolante

Parameter	Result
Number of sequences	491 436
Total length (nt)	408 930 895
Longest sequence (nt)	34 610
Shortest sequence (nt)	200
Mean sequence length (nt)	832
N50 sequence length (nt)	1 691

Table S3. RNA-seq data read statistic values

Accession (SRA)	Sample	Quantity of reads		Mapped reads
		Before Filtering	After Filtering	
SRR12564573	NormalA	89 424 588.00	88 112 720.00	94.18%
SRR12564572	NormalB	74 105 862.00	72 983 434.00	93.79%
SRR12564570	NormalC	60 626 094.00	59 767 896.00	91.55%

SRR12564564	Day1A	32 499 910.00	31 721 976.00	90.67%
SRR12564563	Day1B	35 164 514.00	34 237 960.00	91.37%
SRR12564571	Day1C	43 519 280.00	42 179 220.00	91.53%
SRR12564567	Day3A	64 094 536.00	62 995 792.00	90.26%
SRR12564566	Day3B	71 654 462.00	70 158 078.00	91.07%
SRR12564565	Day3C	71 259 560.00	70 418 332.00	90.75%
SRR12564569	Day3D*	107 688 184.00	106 083 898.00	-
SRR12564568	Day3E*	108 372 334.00	106 767 522.00	-

*Samples used for the assembly but not for differential expression analysis

Table S4. Genes and primers used for RT-qPCR

Gene	Primers
VBP	F: AGGTCAAAATGTCCGGCCTCTGT R: TCACGCTGGCGGTGTCAAACCT
FoxA	F: ACGGCGAAGGTAGCATCCGTTT R: ATGGCAATCCAGCAAGCGCCAA
Wnt6	F: CCTGCAATAATCCGGTGAGT R: CGCGAATGTAAATGTCATGG
Sox4	F: CGCTCTCCATTTTCAGAGGAC R: GTCTTTCTGCCTCCTCAACG
Tap26	F: TGCCTGAGCTTTCTGTTCTT R: CCCTCAAAGAATGGTGGAAA
NADH	F: CAATGGTTGTTGCTGGAGTCTTT R: CGCAGAAGTAGCCGCGAATAT
Tenascin-N	F: CGTTGAAATACCGTCCATCC R: AACGAAGGATACGCTGGAGA

Table S5. Mean Ct values obtained from RT-qPCR

Gene	Stage	Ct Mean	Ct SD
VBP	Normal	28.636	1.268
	Day 1	28.263	0.640
	Day 3	27.958	0.738
FoxA	Normal	23.611	0.371
	Day 1	27.643	3.124
	Day 3	27.824	3.201
Wnt6	Normal	28.607	1.399

	Day 1	25.253	1.965
	Day 3	27.842	3.703
	Normal	26.038	0.784
Sox4	Day 1	25.424	1.143
	Day 3	29.242	1.014
Tap26	Normal	27.634	1.319
	Day 1	26.727	0.483
	Day 3	29.512	1.311
NADH	Normal	18.843	0.271
	Day 1	20.829	0.355
	Day 3	22.583	0.341
Tenascin	Normal	21.025	3.217
	Day 3	30.992	1.519

Table S6. Comparison of expressed transcripts in RNA-seq with previous studies

Gene	RNA-seq		RT-PCR/qPCR	Northern Blot/In situ
	Day 1 (Log2FC)	Day 3 (Log2FC)	Day 3	Days 2-3
Myc	2.72 ↑	2.05 ↑	↑	NA
β-catenin	0.88	0.46 ^{NS}	↓ ^{NS}	NA
Melanotransferrin	3.55 ↑	3.7 ↑	↑	NA
Serum amyloid A protein	2.39 ↑	3.2 ↑	NA	↑
WNT9	2.69 ↑	2.88 ↑	NA	↑
BMP	3.53 ↑	3.31 ↑	NA	↑
survivin	-0.90 ^{NS}	-0.31 ^{NS}	↓ ^{NS}	-

↑: Upregulated; ↓: Downregulated; -: No significant change; NS: Not significant (Pvalue > 0.05)

Table S7. Comparison of expressed transcripts in RNA-seq with microarray study

Gene	RNA-seq	Microarray
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	Day 1 (Log2FC)	Day 3 (Log2FC)	Day 3
Tensc-R	3.26↑	2.03 ^{NS}	↑
Actin-1	6.12↑	7.47↑	↑
Actin-2	1.71↑	1.56↑	↑
Collagen alfa-1	-1.54↓	-0.67 ^{NS}	↑
Laminin alpha1	-3.67↓	-2.79↓	↑
Stromelysin-3 (MMP-11)	-4.16↓	-2.65↓	↑
Hox9	1.03↑	-0.83 ^{NS}	↑
Krueppel like	-1.09↓	0.12 ^{NS}	↓
Gelsolin	-0.79 ^{NS}	-2.69↓	↓

↑: Upregulated; ↓: Downregulated; -: No significant change; NS: Not significant (Pvalue > 0.05)

Table S8. Differentially expressed transcripts between day 3 vs 1 comparison

ID	Description	Log2FC	Adjusted p-value
Transcript_223195	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	2.13	3.58E-02
Transcript_298217	4-aminobutyrate aminotransferase, mitochondrial	2.98	2.81E-05
Transcript_334800	40S ribosomal protein S15	6.73	1.89E-04
Transcript_254071	actin, cytoskeletal 3B actin, cytoskeletal 3	3.00	1.19E-02
Transcript_432551	actin, muscle	3.65	5.45E-03
Transcript_383802	adenylyltransferase and sulfurtransferase MOCS3-like	3.21	3.38E-02
Transcript_308851	alcohol dehydrogenase class-3	2.33	1.59E-02
Transcript_425811	calreticulin	2.45	9.78E-08
Transcript_298293	collagen alpha-1(XII) chain tenascin-X	2.08	7.99E-05
Transcript_196327	creatine kinase, flagellar	5.16	4.69E-02
Transcript_380459	cryptochrome-2	2.03	3.75E-03
Transcript_226806	cytochrome P450 3A24	2.25	1.83E-02
Transcript_262552	cytochrome P450 3A9	4.03	3.31E-02
Transcript_175314	cytochrome P450 4V2	2.00	4.85E-02
Transcript_172290	cytosol aminopeptidase	2.21	1.97E-05

Transcript_184414	dehydrogenase/reductase SDR family member 7	2.25	1.39E-03
Transcript_175770	deleted in malignant brain tumors 1 protein	2.65	2.63E-02
Transcript_461577	deoxyribodipyrimidine photo-lyase	2.68	2.66E-03
Transcript_432963	DNA replication licensing factor mcm5	2.57	4.81E-07
Transcript_359454	dynein light chain LC6, flagellar outer arm	2.35	6.25E-04
Transcript_347359	ectonucleotide pyrophosphatase/phosphodiesterase family member 7-like	3.16	4.27E-03
Transcript_273238	epidermal growth factor-like protein 7	2.49	1.23E-05
Transcript_276903	ERI1 exoribonuclease 2	2.86	3.80E-03
Transcript_365063	extracellular transglutaminase	2.62	5.99E-09
Transcript_350713	fibrillin-1	2.08	9.82E-03
Transcript_356914	ficolin-2-like	3.74	1.04E-02
Transcript_179574	ficolin-2-like	3.05	3.76E-02
Transcript_221519	formin-J	2.02	1.31E-04
Transcript_358088	fucose mutarotase	2.46	1.86E-08
Transcript_351559	G patch domain-containing protein 3	4.02	5.91E-03
Transcript_185057	GDH/6PGL endoplasmic bifunctional protein hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	2.07	2.55E-06
Transcript_402303	GTP 3',8-cyclase, mitochondrial cyclic pyranopterin monophosphate synthase, mitochondrial molybdenum cofactor biosynthesis protein 1	2.32	8.19E-03
Transcript_438891	H2.0-like homeobox protein Homeobox domain-containing protein	3.45	1.75E-11
Transcript_251717	hairy/enhancer-of-split related with YRPW motif protein 1	3.17	2.39E-02
Transcript_456276	heparan sulfate glucosamine 3-O-sulfotransferase 1	3.31	1.15E-02
Transcript_438353	homeobox protein EMX1	3.86	8.19E-03
Transcript_290553	isoamyl acetate-hydrolyzing esterase 1 homolog	2.80	5.95E-05
Transcript_409717	isochorismatase domain-containing protein 2 isochorismatase domain-containing protein 2, mitochondrial	2.95	4.66E-03
Transcript_258900	KRP170	2.69	1.74E-02
Transcript_189831	L-gulonolactone oxidase	2.45	6.22E-03
Transcript_297492	laminin subunit alpha-2 laminin subunit alpha-1	2.21	1.74E-05
Transcript_305145	LOW QUALITY PROTEIN: DNA replication licensing factor mcm2	2.94	6.14E-07
Transcript_381204	LOW QUALITY PROTEIN: transcription factor Sox-10	3.54	6.83E-09
Transcript_285150	LOW QUALITY PROTEIN: zygotic DNA replication licensing factor mcm6-B	2.29	2.08E-07
Transcript_294196	low-density lipoprotein receptor-related protein 1	2.14	2.64E-04
Transcript_328691	MAM and LDL-receptor class A domain-containing protein 1	2.14	7.82E-04
Transcript_257273	methylsterol monooxygenase 1	3.02	3.79E-03

Transcript_324570	microfibril-associated glycoprotein 4 tenascin-N	2.48	3.32E-02
Transcript_263515	polycystic kidney disease protein 1-like 2	2.32	1.61E-02
Transcript_269460	probable D-lactate dehydrogenase, mitochondrial lactate dehydrogenase D	3.55	2.01E-02
Transcript_236563	protein FAM166B-like	17.42	4.96E-04
Transcript_437843	protein lin-52 homolog	2.10	2.16E-03
Transcript_375637	protein Wnt-6	2.25	2.75E-03
Transcript_197666	putative aminopeptidase W07G4.4	2.06	2.59E-04
Transcript_311247	putative hydroxypyruvate isomerase	2.52	5.99E-04
Transcript_443748	pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2 pyridine nucleotide-disulphide oxidoreductase domain 2	2.41	1.73E-02
Transcript_297199	ryncolin-1-like	5.18	3.37E-02
Transcript_406209	sulfite oxidase	3.85	2.99E-07
Transcript_54760	testis-specific serine/threonine-protein kinase 4-like	5.30	3.42E-02
Transcript_251414	transcription factor Sp5	2.40	4.19E-03
Transcript_384474	transmembrane protein KIAA1109	2.08	1.48E-05
Transcript_266841	tuftelin	2.47	1.33E-02
Transcript_368226	ubiquitin	6.29	1.18E-03
Transcript_270219	ubiquitin-40S ribosomal protein S27a	6.47	4.00E-04
Transcript_437026	uncharacterized protein K02A2.6-like	3.43	2.72E-05
Transcript_190019	uncharacterized protein K02A2.6- like Reverse transcriptase domain- containing protein	2.32	1.79E-02
Transcript_291904	uncharacterized protein LOC105438010 Glycoside hydrolase family 31 domain containing protein	2.14	3.79E-04
Transcript_283678	uncharacterized protein LOC583353 neurotrypsin	4.75	9.63E-03
Transcript_26623	uncharacterized protein LOC592324	7.59	2.53E-06
Transcript_442525	uncharacterized protein LOC753842 Protease inhibitor I35 (TIMP) domain containing protein	2.01	2.72E-04
Transcript_270528	uncharacterized protein LOC757055 glyoxylate/hydroxypyruvate reductase A HPR2	2.01	7.71E-05
Transcript_263687	valacyclovir hydrolase-like	2.34	1.86E-03
Transcript_428635	zygotic DNA replication licensing factor mcm3	2.64	3.93E-04
Transcript_167684			
Transcript_294311	-	-3.44	2.27E-02
Transcript_251847	-	-2.32	7.18E-05
Transcript_254514	-	-2.01	2.89E-02
Transcript_395263	14-3-3 family protein artA 14-3-3 protein 3	-5.90	2.83E-03
Transcript_285870	26S proteasome non-ATPase regulatory subunit 5	-3.03	1.24E-09

Transcript_42693	26S proteasome regulatory subunit 6A-B 26S protease regulatory subunit 6A-B 26S protease regulatory subunit 6A-like	-2.16	6.22E-06
Transcript_48454	40S ribosomal protein S13	-3.47	4.95E-02
Transcript_345624	40S ribosomal protein S16	-3.43	4.17E-02
Transcript_399286	40S ribosomal protein S9	-4.03	1.07E-03
Transcript_382713	60S ribosomal protein L10a	-2.42	9.80E-03
Transcript_6160	60S ribosomal protein L19	-3.63	1.40E-03
Transcript_1415	60S ribosomal protein L27a	-3.01	1.48E-02
Transcript_110850	60S ribosomal protein L3	-4.01	1.67E-05
Transcript_274172	60S ribosomal protein L3	-3.54	3.44E-03
Transcript_242646	60S ribosomal protein L31	-3.19	2.25E-02
Transcript_258108	60S ribosomal protein L8	-4.33	5.37E-05
Transcript_438569	acetylcholine receptor subunit beta gamma-aminobutyric acid receptor subunit gamma-2	-2.21	8.54E-03
Transcript_310621	acid-sensing ion channel 1A	-4.52	9.37E-03
Transcript_388716	actin CyI, cytoplasmic	-4.82	1.87E-02
Transcript_305867	actin CyI, cytoplasmic	-2.41	1.99E-02
Transcript_198859	actin-5C	-2.66	1.48E-02
Transcript_407345	actin, muscle	-2.21	2.99E-07
Transcript_225582	adenylate cyclase type 3	-2.06	2.98E-03
Transcript_360808	ADP-ribosylation factor	-2.02	9.73E-04
Transcript_197796	alpha-1 collagen	-3.43	3.20E-11
Transcript_198232	alpha-1 collagen	-2.61	2.61E-08
Transcript_396043	alpha-1 collagen	-2.18	6.97E-05
Transcript_345429	alpha-amylase 4N	-2.34	2.95E-03
Transcript_410512	alpha-crystallin B chain	-2.94	1.49E-03
Transcript_430725	alpha-crystallin B chain	-2.03	1.93E-05
Transcript_195199	angiopoietin-4-like	-2.43	9.40E-03
Transcript_211686	arylsulfatase	-4.17	1.71E-03
Transcript_234345	barH-like 2 homeobox protein	-3.23	7.50E-05
Transcript_374682	bromodomain-containing protein 4-like dentin sialophosphoprotein	-2.12	6.69E-03
Transcript_203368	calcitonin gene-related peptide type 1 receptor	-2.32	5.00E-05
Transcript_82280	calcium-activated chloride channel regulator 1 epithelial chloride channel protein	-2.04	4.83E-06
Transcript_454815	calmodulin	-3.16	1.16E-02
Transcript_346536	calmodulin	-2.13	5.15E-06
Transcript_60050	cAMP-dependent protein kinase catalytic subunit 1 catalytic subunit of cAMP-dependent histone kinase	-2.62	7.18E-05
Transcript_7357	cardioacceleratory peptide receptor-like	-2.28	2.73E-02
Transcript_387252	cathepsin Z	-8.84	1.47E-08
Transcript_443599	cholecystokinin receptor type A	-2.23	1.66E-02
Transcript_198131	cyclin-dependent kinase 20-like	-2.29	2.97E-05

Transcript_338163	cysteine and glycine-rich protein 1 cysteine and glycine-rich protein 2	-2.87	2.40E-16
Transcript_53888	cytochrome P450 27C1 25-hydroxyvitamin D-1 alpha hydroxylase, mitochondrial probable cytochrome P450 49a1	-2.45	2.73E-03
Transcript_179647	D(1) dopamine receptor	-2.15	1.15E-02
Transcript_213703	deleted in malignant brain tumors 1 protein	-3.53	2.76E-03
Transcript_321418	deleted in malignant brain tumors 1 protein	-2.73	2.76E-03
Transcript_74981	disintegrin and metalloproteinase domain-containing protein 23-like disintegrin and metalloproteinase domain-containing protein 12	-2.32	8.72E-03
Transcript_455894	DNA-directed RNA polymerases I, II, and III subunit RPABC3	-2.59	9.85E-03
Transcript_44175	E-selectin-like	-2.09	6.66E-03
Transcript_412294	E3 ubiquitin-protein ligase TRIM56-like	-4.42	3.14E-02
Transcript_366986	fibrinogen C domain-containing protein 1	-2.20	3.17E-02
Transcript_298990	ficolin-1-like	-4.27	5.65E-06
Transcript_366365	ficolin-1-like	-2.21	1.60E-02
Transcript_259611	ficolin-2	-2.54	1.29E-02
Transcript_435128	formin-J	-2.24	2.03E-05
Transcript_86447	G-protein coupled receptor 54	-2.30	3.74E-02
Transcript_380362	glyceraldehyde-3-phosphate dehydrogenase	-3.84	1.53E-02
Transcript_205220	glycine receptor subunit alpha-4	-2.27	6.61E-12
Transcript_288548	glycine-rich cell wall structural protein 1 glycine-rich protein DOT1	-2.14	3.14E-02
Transcript_305980	golgin subfamily A member 6-like protein 22	-2.25	1.60E-02
Transcript_264943	GTP-binding protein Rit1-like GTP-binding protein Rit1 pseudogene	-2.07	4.07E-03
Transcript_281300	hairy/enhancer-of-split related with YRPW motif protein uncharacterized protein LOC593175	-2.17	2.97E-02
Transcript_281299	heat shock cognate 71 kDa protein heat shock 70kDa protein 8	-2.96	1.97E-04
Transcript_300969	heat shock cognate 71 kDa protein heat shock 70kDa protein 8	-2.37	8.25E-03
Transcript_200327	histamine H2 receptor-like	-4.30	7.87E-04
Transcript_338151	histidine triad nucleotide-binding protein 3	-2.68	4.10E-03
Transcript_161417	histone H3, embryonic	-3.59	1.41E-02
Transcript_276623	histone H4	-4.81	4.60E-02
Transcript_212508	histone H4	-3.12	3.75E-02
Transcript_339518	homeobox protein Hox-A7	-2.50	3.18E-02
Transcript_394760	homeodomain protein	-4.44	2.56E-03
Transcript_436417	IgGFc-binding protein Fc fragment of IgG binding protein zonadhesin	-2.19	6.67E-03
Transcript_374429	ileal sodium/bile acid cotransporter-like	-4.01	8.60E-03
Transcript_279040	kelch-like protein 2	-2.18	3.64E-05
Transcript_219771	Krueppel-like factor 13	-2.29	2.33E-03

Transcript_376962	lactase-phlorizin hydrolase	-2.76	3.76E-02
Transcript_274293	lambda-crystallin homolog	-2.16	2.13E-05
Transcript_429112	large neutral amino acids transporter small subunit 2	-2.27	1.22E-05
Transcript_204036	serine/threonine-protein kinase mos	-2.13	2.72E-04
Transcript_229121	serine/threonine-protein kinase mos	-2.02	2.54E-03
Transcript_257994	LOW QUALITY PROTEIN: MMP37-like protein, mitochondrial MMP37-like protein, mitochondrial	-2.04	4.07E-02
Transcript_391508	LOW QUALITY PROTEIN: tubulin alpha-1 chain	-2.73	2.20E-08
Transcript_362387	LOW QUALITY PROTEIN: tubulin alpha-1 chain	-2.36	6.65E-04
Transcript_420771	LOW QUALITY PROTEIN: tubulin alpha-1C chain	-2.16	2.86E-02
Transcript_364074	LOW QUALITY PROTEIN: uncharacterized protein LOC588722	-3.12	4.00E-04
Transcript_339876	LOW QUALITY PROTEIN: zinc finger protein 708-like	-3.37	1.48E-02
Transcript_273801	metabotropic glutamate receptor 8	-2.22	4.80E-05
Transcript_59717	methylmalonic aciduria and homocystinuria type C protein homolog	-2.07	3.76E-03
Transcript_343882	microfibril-associated glycoprotein 4	-4.38	4.85E-03
Transcript_216921	microfibril-associated glycoprotein 4	-2.53	1.48E-04
Transcript_410262	microfibril-associated glycoprotein 4-like	-4.02	2.18E-02
Transcript_179645	microfibril-associated glycoprotein 4-like	-2.94	3.25E-03
Transcript_445086	microfibril-associated glycoprotein 4-like	-2.41	1.99E-03
Transcript_429455	microfibril-associated glycoprotein 4-like	-2.38	4.46E-03
Transcript_220874	microfibril-associated glycoprotein 4 tenascin-N	-9.00	5.41E-03
Transcript_362512	microfibril-associated glycoprotein 4 tenascin-N	-4.39	4.85E-03
Transcript_335205	microfibril-associated glycoprotein 4 tenascin-N	-2.89	8.65E-03
Transcript_367362	microfibril-associated glycoprotein 4 tenascin-N	-2.64	5.42E-03
Transcript_343707	microfibril-associated glycoprotein 4 tenascin-N	-2.25	3.28E-02
Transcript_365407	microfibril-associated glycoprotein 4 tenascin-N	-2.22	8.36E-06
Transcript_343323	microfibril-associated glycoprotein 4 tenascin-N	-2.11	9.52E-03
Transcript_264072	monocarboxylate transporter 12 retinol dehydrogenase 8 Short-chain dehydrogenase/reductase SDR domain containing protein	-2.68	5.62E-03
Transcript_429832	muscle-specific protein 20	-2.01	3.32E-04
Transcript_414296	NADPH oxidase 5	-2.55	1.02E-03
Transcript_341092	neurogenic differentiation factor 4	-2.19	2.56E-02
Transcript_398720	neuronal acetylcholine receptor subunit alpha-3	-2.89	3.68E-13
Transcript_183115	neurotrophin 5 prepro-neurotrophin	-2.35	3.71E-07

Transcript_254653	nucleolar GTP-binding protein 2	-2.17	7.10E-05
Transcript_420284	orexin receptor type 2	-2.50	2.06E-04
Transcript_321671	oxytocin receptor gonadotropin-releasing hormone receptor	-3.48	5.51E-04
Transcript_196171	paired box protein Pax-2a	-2.30	3.24E-04
Transcript_335269	peptidyl-prolyl cis-trans isomerase	-4.41	2.41E-03
Transcript_418613	phospholipid scramblase 2 phospholipid scramblase family member 5	-2.09	6.80E-03
Transcript_391646	PIN2/TERF1-interacting telomerase inhibitor 1	-2.41	2.09E-04
Transcript_348719	popeye domain-containing protein 3	-2.49	8.96E-13
Transcript_208618	potassium channel subfamily K member 9	-2.68	4.58E-04
Transcript_297999	probable cationic amino acid transporter putative cationic amino acid transporter solute carrier family 7 (orphan transporter), member 14	-2.43	2.93E-03
Transcript_255002	probable threonine protease PRSS50	-2.87	9.99E-09
Transcript_217497	protein giant	-2.12	1.54E-04
Transcript_303695	protein PLANT CADMIUM RESISTANCE 3-like	-2.66	6.01E-04
Transcript_409861	protein SSUH2 homolog	-2.28	1.53E-02
Transcript_380758	protein SSUH2 homolog	-2.22	4.36E-05
Transcript_315415	protein Tob1	-2.75	1.53E-02
Transcript_405702	putative uncharacterized protein CXorf58	-2.53	9.26E-04
Transcript_483697	rab3 GTPase	-2.08	1.81E-03
Transcript_426847	ras-related protein ORAB-1	-4.04	8.23E-03
Transcript_182361	retinol dehydrogenase 8	-2.15	1.46E-02
Transcript_269277	rho GTPase-activating protein 25	-2.73	7.41E-03
Transcript_367031	ribosomal protein S14	-3.32	1.75E-02
Transcript_350598	ribosome biogenesis protein bop1-B	-2.08	4.29E-03
Transcript_373223	RNA 3'-terminal phosphate cyclase-like protein	-2.05	3.54E-03
Transcript_253908	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	-2.44	3.37E-05
Transcript_300509	ryncolin-1-like	-3.08	4.21E-03
Transcript_370378	serine/threonine-protein kinase mos	-2.03	3.42E-02
Transcript_381580	serine/threonine-protein kinase NLK serine/threonine-protein kinase NLK2	-2.27	3.18E-02
Transcript_285582	short-chain collagen C4	-2.84	5.23E-04
Transcript_285813	splicing factor 3A subunit 2	-2.31	1.66E-04
Transcript_309701	sugar phosphate exchanger 3	-2.12	3.13E-02
Transcript_179855	sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1	-2.49	3.74E-03
Transcript_236683	synaptotagmin-15	-2.28	2.41E-03
Transcript_275400	synaptotagmin-17-like	-2.77	1.50E-02
Transcript_229301	synaptotagmin-7	-2.73	2.00E-06
Transcript_324193	tubulin alpha chain	-3.36	3.81E-20
Transcript_332311	tubulin alpha chain	-2.85	6.61E-12

Transcript_285898	tubulin alpha chain	-2.15	3.71E-04
Transcript_49445	tubulin alpha-1 chain	-3.02	2.93E-09
Transcript_327532	tubulin alpha-1 chain	-2.96	1.46E-12
Transcript_285897	tubulin alpha-1 chain	-2.41	1.12E-03
Transcript_229300	tubulin alpha-1 chain	-2.04	1.20E-04
Transcript_207127	tubulin alpha-1 chain tubulin alpha-1A chain	-2.23	2.67E-03
Transcript_306226	tubulin alpha-1A chain	-5.73	2.00E-03
Transcript_354200	tubulin alpha-1A chain	-4.12	8.00E-04
Transcript_89028	tubulin alpha-1A chain	-3.17	1.17E-02
Transcript_367771	tubulin alpha-1A chain	-3.12	4.06E-05
Transcript_362085	tubulin alpha-1A chain	-2.62	1.04E-04
Transcript_262388	tubulin alpha-1A chain	-2.56	7.67E-05
Transcript_377194	tubulin alpha-1A chain	-2.54	1.27E-06
Transcript_222321	tubulin alpha-1A chain	-2.05	5.62E-04
Transcript_412907	tubulin alpha-1A chain	-2.04	7.70E-04
Transcript_323033	tubulin alpha-2/alpha-4 chain	-2.83	1.99E-02
Transcript_367619	tubulin beta chain	-3.62	3.14E-04
Transcript_277435	tubulin beta chain	-2.20	2.18E-02
Transcript_230874	tyrosine-protein phosphatase non-receptor type 9	-2.10	4.46E-02
Transcript_196821	ubiquitin	-2.88	2.92E-02
Transcript_433726	UDP-glucuronosyltransferase 2C1 UDP-glucuronosyltransferase 1-2 UDP-glucuronosyltransferase 2A2	-2.73	2.97E-02
Transcript_402138	uncharacterized protein LOC100888048	-3.85	4.20E-04
Transcript_355756	uncharacterized protein LOC100888517	-2.19	9.35E-05
Transcript_369230	uncharacterized protein LOC100891189	-2.61	8.60E-04
Transcript_40273	uncharacterized protein LOC105446839	-3.22	6.08E-03
Transcript_349228	uncharacterized protein LOC576450	-2.43	1.07E-07
Transcript_331800	uncharacterized protein LOC591826	-2.18	1.06E-02
Transcript_247803	uncharacterized protein LOC592324	-2.48	6.86E-03
Transcript_456195	uncharacterized protein LOC753087 185/333 D1 alpha 185/333 D5 epsilon 185/333 E6 alpha	-2.11	1.73E-04
Transcript_399035	uncharacterized protein LOC756005 protein of unknown function DUF2181 containing protein	-3.38	7.19E-08
Transcript_199904	uncharacterized protein LOC756131	-2.05	1.38E-04
Transcript_448557	vasoactive intestinal polypeptide receptor 1 parathyroid hormone 2 receptor	-2.04	4.20E-03
Transcript_339985	von Willebrand factor A domain-containing protein 5B1	-2.40	3.64E-04
Transcript_223195	zinc finger SWIM domain-containing protein 8 zinc finger SWIM domain-containing protein KIAA0913-like	-2.01	3.14E-02

*Highlighted transcripts in yellow are nervous system associated genes

Table S9. Differentially expressed transcription factors

ID	Annotated name	Abbreviation	Log2FC	Adjusted p-value
Transcript_319952	Transcription factor SOX-4	SOX4	4.50	9.30E-34
Transcript_263596	Transcription factor BTF3 homolog 4	BTF3L4	4.16	2.16E-11
Transcript_175325	Thyroid transcription factor 1-associated protein 26 homolog	TAP26	3.00	2.98E-11
Transcript_290528	Transcription factor VBP	TEF	5.74	1.06E-06
Transcript_423204	Forkhead transcription factor A	FOXA	-3.83	3.80E-05
Transcript_287026	Transcription factor 25	TCF25	1.77	1.29E-04
Transcript_443183	Myc protein	MYC	2.72	2.63E-04
Transcript_387814	Transcription factor IIIA	GTF3A	1.86	5.36E-04
Transcript_239737	Pre-B-cell leukemia transcription factor 1	PBX3	1.36	1.46E-03
Transcript_265397	Transcription factor soxd1	SOXD1	1.43	1.90E-03
Transcript_373546	Nuclear transcription factor Y subunit gamma	NFYC	1.35	2.20E-03
Transcript_244221	Transcription factor AP-1	AP-1	-1.81	3.44E-03
Transcript_269278	Transcription factor HES-4	HES4	-2.55	6.28E-03
Transcript_286791	General transcription factor IIH subunit 1	GTF2H1	1.27	1.13E-02
Transcript_220104	Homeobox protein Hox-A10	HOXA10	1.55	1.20E-02
Transcript_321671	Paired box protein Pax-2a	PAX2A	1.50	1.69E-02
Transcript_441452	LIM homeobox transcription factor 1-beta	LMX1B	-1.61	1.83E-02
Transcript_304792	ETS-related transcription factor Elf-3	ELF3	1.33	2.47E-02
Transcript_211042	Myelin transcription factor 1-like protein	MYT1L1	1.04	2.47E-02
Transcript_274240	Beta-catenin	CTNNB	1.03	2.96E-02
Transcript_224155	Zinc-finger transcription factor Snail	SNAIL	1.19	9.00E-02
Transcript_291169	GATA transcription factor e	GATAE	-1.97	1.20E-01
Transcript_441904	Transcription factor E2F5	E2F5	1.01	1.21E-01
Transcript_39673	Transcription factor AP-2-alpha	TFAP2A	2.43	1.31E-01
Transcript_307462	Homeobox transcription factor Nk1	NK1	-1.93	2.44E-01
Transcript_361564	Forkhead transcription factor J1	FOXJ1	-1.08	3.06E-01
Transcript_107633	LIM domain transcription factor LMO4-B	LMO4	1.23	3.40E-01
Transcript_76067	Winged helix transcription factor Forkhead-1	FKH1	1.05	3.58E-01
Transcript_168671	Elongation factor 1 alpha	EEF1A1	7.32	8.38E-05
Transcript_345735	Homeobox protein DLX-5 homeobox protein Hox-B4	DLX5	3.07	4.06E-02
Transcript_429867	Homeobox protein Hmx	HMX	3.59	8.86E-17
Transcript_279040	Krueppel-like factor 13	KLF13	3.21	1.17E-06
Transcript_433953	Periodic tryptophan protein 1 homolog	PWP1	3.35	4.80E-12
Transcript_432532	Rhombotin-2	LMO2	2.95	1.48E-10
Transcript_236625	Homeobox protein CDX-2	CDX1	-8.64	2.33E-03
Transcript_271521	Fos-related antigen 1	FOSL2	-4.85	5.48E-03

Transcript_438891	Homeobox domain-containing protein	HLX	-4.10	1.38E-17
Transcript_173387	Hepatocyte nuclear factor 4-gamma	HNF4G	-3.38	1.70E-03
Transcript_438353	Homeobox protein EMX1	EMX1	-4.28	1.09E-03
Transcript_459460	THAP domain-containing protein 5	THAP4	2.86	1.08E-02
Transcript_433507	Homeobox protein Mohawk-like	MKX	2.61	7.15E-06
Transcript_284772	TATA box-binding protein-associated factor RNA polymerase I subunit A	TAF1A	2.54	2.14E-04
Transcript_189718	Myb-binding protein 1A-like protein	MYBBP1A	2.38	1.71E-05
Transcript_459696	Myoneurin	MYNN	2.11	4.88E-05
Transcript_268430	Gastrula zinc finger protein xlcgf57.1 isoform X5	ZNF	-3.06	8.46E-03
Transcript_247937	Early growth response protein 1-B	EGR1	-2.75	1.42E-04
Transcript_330100	Basic leucine zipper domain, Maf-type	BSL78	-2.45	5.85E-05

Table S10. Gene ontology analysis from day 1 downregulated genes using DAVID

Category	Term	Count	PValue	List.Total	Pop.Hits	Pop.Total	Fold.Enrichment	Bonferroni	Benjamini	FDR	Description
BP	GO:0007155	5	9.67E-04	39	14	1094	10.02	0.31	0.31	1.33	cell adhesion
BP	GO:0022610	5	1.29E-03	39	15	1094	9.35	0.38	0.22	1.76	biological adhesion
BP	GO:0006082	7	1.15E-02	39	57	1094	3.44	0.99	0.58	14.81	organic acid metabolic process
BP	GO:0044699	28	1.97E-02	39	586	1094	1.34	1.00	0.66	24.03	single-organism process
BP	GO:0046394	4	3.34E-02	39	21	1094	5.34	1.00	0.80	37.47	carboxylic acid biosynthetic process
BP	GO:0044763	26	3.49E-02	39	548	1094	1.33	1.00	0.77	38.79	single-organism cellular process
BP	GO:0002376	3	4.44E-02	39	10	1094	8.42	1.00	0.79	46.60	immune system process
BP	GO:0032501	5	4.98E-02	39	41	1094	3.42	1.00	0.80	50.65	multicellular organismal process
BP	GO:0044283	4	6.36E-02	39	27	1094	4.16	1.00	0.85	59.72	small molecule biosynthetic process
CC	GO:0031224	26	6.01E-03	47	445	1253	1.56	0.42	0.42	6.35	intrinsic component of membrane
CC	GO:0016020	29	7.78E-03	47	531	1253	1.46	0.50	0.30	8.15	membrane
CC	GO:0016021	25	1.32E-02	47	444	1253	1.50	0.70	0.33	13.43	integral component of membrane
CC	GO:0044425	26	2.30E-02	47	489	1253	1.42	0.88	0.41	22.35	membrane part
MF	GO:0016798	5	1.02E-03	54	12	1277	9.85	0.16	0.16	1.24	hydrolase activity, acting on glycosyl bonds
MF	GO:0005044	4	3.26E-03	54	8	1277	11.82	0.43	0.24	3.91	scavenger receptor activity
MF	GO:0038024	4	3.26E-03	54	8	1277	11.82	0.43	0.24	3.91	cargo receptor activity
MF	GO:0004872	8	1.19E-02	54	62	1277	3.05	0.87	0.49	13.56	receptor activity
MF	GO:0060089	8	1.19E-02	54	62	1277	3.05	0.87	0.49	13.56	molecular transducer activity
MF	GO:0008237	4	1.78E-02	54	14	1277	6.76	0.95	0.53	19.65	metallopeptidase activity
MF	GO:0003824	34	2.42E-02	54	614	1277	1.31	0.98	0.57	25.83	catalytic activity
MF	GO:0016491	10	2.50E-02	54	105	1277	2.25	0.99	0.51	26.58	oxidoreductase activity
MF	GO:0004553	3	5.05E-02	54	9	1277	7.88	1.00	0.72	46.84	hydrolase activity, hydrolyzing O-glycosyl compounds
MF	GO:0005509	5	8.00E-02	54	40	1277	2.96	1.00	0.83	63.85	calcium ion binding
MF	GO:0016805	2	8.13E-02	54	2	1277	23.65	1.00	0.80	64.47	dipeptidase activity
MF	GO:0003796	2	8.13E-02	54	2	1277	23.65	1.00	0.80	64.47	lysozyme activity
MF	GO:0004497	3	9.84E-02	54	13	1277	5.46	1.00	0.83	71.75	monooxygenase activity

Table S11. Gene ontology analysis from day 1 upregulated genes using DAVID

Category	Term	Count	PValue	List.Total	Pop.Hits	Pop.Total	Fold.Enrichment	Bonferroni	Benjamini	FDR	Description
BP	GO:0022613	23	1.28E-08	99	68	1094	3.74	1.02E-05	1.02E-05	1.97E-05	ribonucleoprotein complex biogenesis
BP	GO:0016072	12	1.52E-05	99	29	1094	4.57	1.21E-02	4.05E-03	2.34E-02	rRNA metabolic process
BP	GO:0034660	15	2.45E-05	99	47	1094	3.53	1.94E-02	4.87E-03	3.76E-02	ncRNA metabolic process
BP	GO:0071840	38	3.45E-04	99	250	1094	1.68	2.41E-01	4.49E-02	5.28E-01	cellular component organization or biogenesis
BP	GO:0010467	41	5.40E-04	99	284	1094	1.60	3.50E-01	5.97E-02	8.25E-01	gene expression
BP	GO:0044085	25	6.48E-04	99	140	1094	1.97	4.04E-01	6.27E-02	9.90E-01	cellular component biogenesis
BP	GO:0006413	6	9.15E-04	99	10	1094	6.63	5.18E-01	7.80E-02	1.40E+00	translational initiation
BP	GO:0034641	53	1.09E-03	99	416	1094	1.41	5.83E-01	8.37E-02	1.67E+00	cellular nitrogen compound metabolic process
BP	GO:0006412	17	1.49E-03	99	82	1094	2.29	6.96E-01	1.02E-01	2.26E+00	translation
BP	GO:0006807	54	2.72E-03	99	441	1094	1.35	8.86E-01	1.44E-01	4.09E+00	nitrogen compound metabolic process
BP	GO:1990542	5	3.20E-03	99	8	1094	6.91	9.23E-01	1.57E-01	4.81E+00	mitochondrial transmembrane transport
BP	GO:0006396	16	3.23E-03	99	80	1094	2.21	9.24E-01	1.49E-01	4.85E+00	RNA processing
BP	GO:1901566	24	4.64E-03	99	151	1094	1.76	9.76E-01	1.86E-01	6.89E+00	organonitrogen compound biosynthetic process
BP	GO:0044260	56	4.67E-03	99	472	1094	1.31	9.76E-01	1.78E-01	6.93E+00	cellular macromolecule metabolic process
BP	GO:1902582	6	5.43E-03	99	14	1094	4.74	9.87E-01	1.95E-01	8.01E+00	single-organism intracellular transport
BP	GO:0043603	18	6.25E-03	99	102	1094	1.95	9.93E-01	2.04E-01	9.18E+00	cellular amide metabolic process
BP	GO:0017038	5	8.34E-03	99	10	1094	5.53	9.99E-01	2.43E-01	1.21E+01	protein import
BP	GO:0006839	5	8.34E-03	99	10	1094	5.53	9.99E-01	2.43E-01	1.21E+01	mitochondrial transport
BP	GO:0043170	56	8.50E-03	99	483	1094	1.28	9.99E-01	2.38E-01	1.23E+01	macromolecule metabolic process
BP	GO:0007005	8	1.12E-02	99	29	1094	3.05	1.00E+00	2.93E-01	1.59E+01	mitochondrion organization
BP	GO:0071826	8	1.12E-02	99	29	1094	3.05	1.00E+00	2.93E-01	1.59E+01	ribonucleoprotein complex subunit organization
BP	GO:0071806	4	1.87E-02	99	7	1094	6.31	1.00E+00	4.16E-01	2.52E+01	protein transmembrane transport
BP	GO:0051246	10	1.96E-02	99	47	1094	2.35	1.00E+00	4.20E-01	2.62E+01	regulation of protein metabolic process
BP	GO:0016070	28	2.24E-02	99	210	1094	1.47	1.00E+00	4.53E-01	2.94E+01	RNA metabolic process
BP	GO:0070585	4	2.80E-02	99	8	1094	5.53	1.00E+00	5.19E-01	3.53E+01	protein localization to mitochondrion
BP	GO:0044267	32	3.19E-02	99	256	1094	1.38	1.00E+00	5.55E-01	3.92E+01	cellular protein metabolic process
BP	GO:0044271	32	3.36E-02	99	257	1094	1.38	1.00E+00	5.63E-01	4.09E+01	cellular nitrogen compound biosynthetic process
BP	GO:0032268	9	3.65E-02	99	44	1094	2.26	1.00E+00	5.82E-01	4.35E+01	regulation of cellular protein metabolic process
BP	GO:0090304	31	4.15E-02	99	251	1094	1.36	1.00E+00	6.20E-01	4.78E+01	nucleic acid metabolic process
BP	GO:0044237	66	4.44E-02	99	632	1094	1.15	1.00E+00	6.25E-01	5.02E+01	cellular metabolic process
BP	GO:0006457	6	4.77E-02	99	23	1094	2.88	1.00E+00	6.41E-01	5.27E+01	protein folding
BP	GO:1901564	25	4.86E-02	99	194	1094	1.42	1.00E+00	6.39E-01	5.34E+01	organonitrogen compound metabolic process
BP	GO:0046483	38	4.97E-02	99	327	1094	1.28	1.00E+00	6.38E-01	5.43E+01	heterocycle metabolic process
BP	GO:0019538	32	5.01E-02	99	265	1094	1.33	1.00E+00	6.32E-01	5.45E+01	protein metabolic process
BP	GO:0006139	37	5.07E-02	99	317	1094	1.29	1.00E+00	6.28E-01	5.50E+01	nucleobase-containing compound metabolic process
BP	GO:0010608	4	5.26E-02	99	10	1094	4.42	1.00E+00	6.33E-01	5.63E+01	posttranscriptional regulation of gene expression
BP	GO:0071704	66	5.62E-02	99	638	1094	1.14	1.00E+00	6.50E-01	5.89E+01	organic substance metabolic process
BP	GO:0006725	38	5.66E-02	99	330	1094	1.27	1.00E+00	6.44E-01	5.91E+01	cellular aromatic compound metabolic process
BP	GO:0044238	63	6.62E-02	99	608	1094	1.15	1.00E+00	6.88E-01	6.51E+01	primary metabolic process
BP	GO:0000469	3	6.64E-02	99	5	1094	6.63	1.00E+00	6.81E-01	6.52E+01	cleavage involved in rRNA processing
BP	GO:0051345	3	6.64E-02	99	5	1094	6.63	1.00E+00	6.81E-01	6.52E+01	positive regulation of hydrolase activity

BP	GO:0009894	4	6.77E-02	99	11	1094	4.02	1.00E+00	6.81E-01	6.59E+01	regulation of catabolic process
BP	GO:0034248	4	6.77E-02	99	11	1094	4.02	1.00E+00	6.81E-01	6.59E+01	regulation of cellular amide metabolic process
BP	GO:1901360	38	6.97E-02	99	335	1094	1.25	1.00E+00	6.77E-01	6.70E+01	organic cyclic compound metabolic process
BP	GO:0090501	3	9.39E-02	99	6	1094	5.53	1.00E+00	7.80E-01	7.80E+01	RNA phosphodiester bond hydrolysis
BP	GO:0000470	3	9.39E-02	99	6	1094	5.53	1.00E+00	7.80E-01	7.80E+01	maturation of LSU-rRNA
BP	GO:0032543	3	9.39E-02	99	6	1094	5.53	1.00E+00	7.80E-01	7.80E+01	mitochondrial translation
CC	GO:0005730	13	1.67E-07	108	25	1253	6.03	3.48E-05	3.48E-05	2.11E-04	nucleolus
CC	GO:0031974	25	8.06E-06	108	113	1253	2.57	1.68E-03	8.38E-04	1.02E-02	membrane-enclosed lumen
CC	GO:0030529	25	1.80E-05	108	118	1253	2.46	3.74E-03	1.25E-03	2.27E-02	intracellular ribonucleoprotein complex
CC	GO:1990904	25	1.80E-05	108	118	1253	2.46	3.74E-03	1.25E-03	2.27E-02	ribonucleoprotein complex
CC	GO:0030684	8	9.92E-05	108	15	1253	6.19	2.04E-02	5.14E-03	1.25E-01	preribosome
CC	GO:0032991	47	8.50E-04	108	363	1253	1.50	1.62E-01	2.50E-02	1.07E+00	macromolecular complex
CC	GO:0044428	22	1.15E-03	108	125	1253	2.04	2.13E-01	2.94E-02	1.44E+00	nuclear part
CC	GO:0043228	28	1.70E-03	108	183	1253	1.78	2.99E-01	3.86E-02	2.13E+00	non-membrane-bounded organelle
CC	GO:0043232	28	1.70E-03	108	183	1253	1.78	2.99E-01	3.86E-02	2.13E+00	intracellular non-membrane-bounded organelle
CC	GO:0044452	5	2.69E-03	108	8	1253	7.25	4.29E-01	5.45E-02	3.34E+00	nucleolar part
CC	GO:0070993	4	5.34E-03	108	5	1253	9.28	6.71E-01	9.62E-02	6.53E+00	translation preinitiation complex
CC	GO:0033290	4	5.34E-03	108	5	1253	9.28	6.71E-01	9.62E-02	6.53E+00	eukaryotic 48S preinitiation complex
CC	GO:0005622	86	1.03E-02	108	869	1253	1.15	8.83E-01	1.64E-01	1.22E+01	intracellular
CC	GO:0005762	4	1.64E-02	108	7	1253	6.63	9.68E-01	2.33E-01	1.89E+01	mitochondrial large ribosomal subunit
CC	GO:0022624	4	1.64E-02	108	7	1253	6.63	9.68E-01	2.33E-01	1.89E+01	proteasome accessory complex
CC	GO:0098798	6	2.27E-02	108	20	1253	3.48	9.92E-01	2.89E-01	2.51E+01	mitochondrial protein complex
CC	GO:0044424	80	2.45E-02	108	812	1253	1.14	9.94E-01	2.91E-01	2.69E+01	intracellular part
CC	GO:0043234	32	2.72E-02	108	264	1253	1.41	9.97E-01	3.01E-01	2.93E+01	protein complex
CC	GO:0005634	36	2.96E-02	108	308	1253	1.36	9.98E-01	3.07E-01	3.15E+01	nucleus
CC	GO:0005623	91	3.12E-02	108	959	1253	1.10	9.99E-01	3.07E-01	3.30E+01	cell
CC	GO:0005852	3	3.87E-02	108	4	1253	8.70	1.00E+00	3.36E-01	3.92E+01	eukaryotic translation initiation factor 3 complex
CC	GO:0005615	6	5.52E-02	108	25	1253	2.78	1.00E+00	4.15E-01	5.12E+01	extracellular space
CC	GO:0005732	3	6.09E-02	108	5	1253	6.96	1.00E+00	4.33E-01	5.47E+01	small nucleolar ribonucleoprotein complex
CC	GO:0005739	15	6.72E-02	108	108	1253	1.61	1.00E+00	4.53E-01	5.84E+01	mitochondrion
CC	GO:0044422	40	8.38E-02	108	377	1253	1.23	1.00E+00	5.03E-01	6.68E+01	organelle part
CC	GO:0032040	3	8.63E-02	108	6	1253	5.80	1.00E+00	5.01E-01	6.80E+01	small-subunit processome
CC	GO:0005758	3	8.63E-02	108	6	1253	5.80	1.00E+00	5.01E-01	6.80E+01	mitochondrial intermembrane space
CC	GO:0031970	3	8.63E-02	108	6	1253	5.80	1.00E+00	5.01E-01	6.80E+01	organelle envelope lumen
MF	GO:0003723	21	1.85E-06	98	86	1277	3.18	4.64E-04	4.64E-04	2.40E-03	RNA binding
MF	GO:0008135	10	8.01E-06	98	21	1277	6.21	2.01E-03	1.00E-03	1.04E-02	translation factor activity, RNA binding
MF	GO:0003743	7	4.71E-04	98	15	1277	6.08	1.11E-01	3.86E-02	6.10E-01	translation initiation factor activity
MF	GO:0008565	4	1.80E-02	98	8	1277	6.52	9.89E-01	6.80E-01	2.10E+01	protein transporter activity
MF	GO:0003676	29	4.59E-02	98	274	1277	1.38	1.00E+00	9.05E-01	4.57E+01	nucleic acid binding
MF	GO:1901363	48	5.68E-02	98	515	1277	1.21	1.00E+00	9.13E-01	5.32E+01	heterocyclic compound binding
MF	GO:0097159	48	6.47E-02	98	519	1277	1.21	1.00E+00	9.09E-01	5.81E+01	organic cyclic compound binding
MF	GO:0034062	3	7.00E-02	98	6	1277	6.52	1.00E+00	8.98E-01	6.11E+01	RNA polymerase activity
MF	GO:0003899	3	7.00E-02	98	6	1277	6.52	1.00E+00	8.98E-01	6.11E+01	DNA-directed RNA polymerase activity
MF	GO:0016779	4	8.38E-02	98	14	1277	3.72	1.00E+00	9.13E-01	6.79E+01	nucleotidyltransferase activity

Table S12. Gene ontology analysis from day 3 downregulated genes using DAVID

Category	Term	Count	PValue	List.Total	Pop.Hits	Pop.Total	Fold.Enrichment	Bonferroni	Benjamini	FDR	Description
BP	GO:0099537	3	3.22E-02	33	10	1094	9.95	1.00	1.00	35.00	trans-synaptic signaling
BP	GO:0098916	3	3.22E-02	33	10	1094	9.95	1.00	1.00	35.00	anterograde trans-synaptic signaling
BP	GO:0099536	3	3.22E-02	33	10	1094	9.95	1.00	1.00	35.00	synaptic signaling
BP	GO:0007268	3	3.22E-02	33	10	1094	9.95	1.00	1.00	35.00	chemical synaptic transmission
BP	GO:0007186	4	4.13E-02	33	27	1094	4.91	1.00	1.00	42.55	G-protein coupled receptor signaling pathway
BP	GO:0007154	10	5.60E-02	33	175	1094	1.89	1.00	0.99	53.11	cell communication
BP	GO:0044699	23	5.70E-02	33	586	1094	1.30	1.00	0.98	53.80	single-organism process
BP	GO:0007155	3	6.06E-02	33	14	1094	7.10	1.00	0.97	56.04	cell adhesion
BP	GO:0022610	3	6.87E-02	33	15	1094	6.63	1.00	0.96	60.76	biological adhesion
CC	GO:0031224	33	1.77E-06	47	445	1253	1.98	0.00	0.00	0.00	intrinsic component of membrane
CC	GO:0016021	32	7.07E-06	47	444	1253	1.92	0.00	0.00	0.01	integral component of membrane
CC	GO:0016020	35	1.02E-05	47	531	1253	1.76	0.00	0.00	0.01	membrane
CC	GO:0031226	12	1.35E-05	47	67	1253	4.77	0.00	0.00	0.02	intrinsic component of plasma membrane
CC	GO:0005887	12	1.35E-05	47	67	1253	4.77	0.00	0.00	0.02	integral component of plasma membrane
CC	GO:0044425	33	1.91E-05	47	489	1253	1.80	0.00	0.00	0.02	membrane part
CC	GO:0071944	14	3.05E-05	47	101	1253	3.70	0.00	0.00	0.04	cell periphery
CC	GO:0044459	12	5.36E-05	47	77	1253	4.15	0.01	0.00	0.06	plasma membrane part
CC	GO:0005886	13	1.11E-04	47	98	1253	3.54	0.02	0.00	0.13	plasma membrane
CC	GO:0005576	5	4.71E-02	47	38	1253	3.51	1.00	0.58	44.16	extracellular region
MF	GO:0060089	12	2.23E-05	54	62	1277	4.58	0.00	0.00	0.03	molecular transducer activity
MF	GO:0004872	12	2.23E-05	54	62	1277	4.58	0.00	0.00	0.03	receptor activity
MF	GO:0004871	8	1.19E-02	54	62	1277	3.05	0.89	0.31	13.74	signal transducer activity
MF	GO:0016491	10	2.50E-02	54	105	1277	2.25	0.99	0.49	26.90	oxidoreductase activity
MF	GO:0005044	3	4.03E-02	54	8	1277	8.87	1.00	0.61	39.90	scavenger receptor activity
MF	GO:0038024	3	4.03E-02	54	8	1277	8.87	1.00	0.61	39.90	cargo receptor activity
MF	GO:1901618	2	8.13E-02	54	2	1277	23.65	1.00	0.83	64.99	organic hydroxy compound transmembrane transporter activity
MF	GO:0052689	3	8.55E-02	54	12	1277	5.91	1.00	0.81	66.91	carboxylic ester hydrolase activity
MF	GO:0004497	3	9.84E-02	54	13	1277	5.46	1.00	0.82	72.26	monooxygenase activity

Table S13. Gene ontology analysis from day 3 Upregulated genes using DAVID

Category	Term	Count	PValue	List.Total	Pop.Hits	Pop.Total	Fold.Enrichment	Bonferroni	Benjamini	FDR	Description
BP	GO:0051246	9	7.48E-04	50	47	1094	4.19	0.35	0.35	1.10	regulation of protein metabolic process
BP	GO:0032268	8	2.51E-03	50	44	1094	3.98	0.77	0.52	3.63	regulation of cellular protein metabolic process
BP	GO:0006396	10	6.99E-03	50	80	1094	2.74	0.98	0.64	9.80	RNA processing
BP	GO:0034470	7	9.04E-03	50	42	1094	3.65	0.99	0.65	12.50	ncRNA processing
BP	GO:0009894	4	1.08E-02	50	11	1094	7.96	1.00	0.65	14.78	regulation of catabolic process
BP	GO:0034660	7	1.56E-02	50	47	1094	3.26	1.00	0.68	20.61	ncRNA metabolic process
BP	GO:0006457	5	1.68E-02	50	23	1094	4.76	1.00	0.67	22.02	protein folding
BP	GO:0000470	3	2.63E-02	50	6	1094	10.94	1.00	0.79	32.40	maturation of LSU-rRNA
BP	GO:0022613	8	2.77E-02	50	68	1094	2.57	1.00	0.77	33.86	ribonucleoprotein complex biogenesis
BP	GO:0044260	29	3.08E-02	50	472	1094	1.34	1.00	0.78	36.91	cellular macromolecule metabolic process
BP	GO:0071806	3	3.57E-02	50	7	1094	9.38	1.00	0.80	41.45	protein transmembrane transport
BP	GO:0065002	3	3.57E-02	50	7	1094	9.38	1.00	0.80	41.45	intracellular protein transmembrane transport
BP	GO:0042273	4	3.69E-02	50	17	1094	5.15	1.00	0.79	42.46	ribosomal large subunit biogenesis
BP	GO:0043170	29	4.25E-02	50	483	1094	1.31	1.00	0.79	47.24	macromolecule metabolic process
BP	GO:0044267	18	4.52E-02	50	256	1094	1.54	1.00	0.79	49.33	cellular protein metabolic process
BP	GO:0006626	3	4.63E-02	50	8	1094	8.21	1.00	0.78	50.21	protein targeting to mitochondrion
BP	GO:0009451	4	4.94E-02	50	19	1094	4.61	1.00	0.79	52.50	RNA modification
BP	GO:0010467	19	5.89E-02	50	284	1094	1.46	1.00	0.81	59.08	gene expression
BP	GO:0019538	18	6.08E-02	50	265	1094	1.49	1.00	0.81	60.25	protein metabolic process
BP	GO:0048522	6	6.30E-02	50	49	1094	2.68	1.00	0.81	61.61	positive regulation of cellular process
BP	GO:0048518	6	6.30E-02	50	49	1094	2.68	1.00	0.81	61.61	positive regulation of biological process
BP	GO:0006412	8	6.70E-02	50	82	1094	2.13	1.00	0.80	63.95	translation
BP	GO:0051336	3	7.03E-02	50	10	1094	6.56	1.00	0.80	65.77	regulation of hydrolase activity
BP	GO:0042981	3	7.03E-02	50	10	1094	6.56	1.00	0.80	65.77	regulation of apoptotic process
BP	GO:0006839	3	7.03E-02	50	10	1094	6.56	1.00	0.80	65.77	mitochondrial transport
BP	GO:0010608	3	7.03E-02	50	10	1094	6.56	1.00	0.80	65.77	posttranscriptional regulation of gene expression
BP	GO:0017038	3	7.03E-02	50	10	1094	6.56	1.00	0.80	65.77	protein import
BP	GO:0006413	3	7.03E-02	50	10	1094	6.56	1.00	0.80	65.77	translational initiation
BP	GO:0034641	25	7.27E-02	50	416	1094	1.31	1.00	0.79	67.04	cellular nitrogen compound metabolic process
BP	GO:0043603	9	7.74E-02	50	102	1094	1.93	1.00	0.80	69.42	cellular amide metabolic process
BP	GO:0006807	26	7.95E-02	50	441	1094	1.29	1.00	0.80	70.43	nitrogen compound metabolic process
BP	GO:0034248	3	8.35E-02	50	11	1094	5.97	1.00	0.81	72.27	regulation of cellular amide metabolic process
BP	GO:0044085	11	8.43E-02	50	140	1094	1.72	1.00	0.80	72.60	cellular component biogenesis
BP	GO:0030155	2	8.76E-02	50	2	1094	21.88	1.00	0.80	74.04	regulation of cell adhesion
BP	GO:0030334	2	8.76E-02	50	2	1094	21.88	1.00	0.80	74.04	regulation of cell migration
BP	GO:0032231	2	8.76E-02	50	2	1094	21.88	1.00	0.80	74.04	regulation of actin filament bundle assembly
CC	GO:0030529	16	1.24E-04	58	118	1253	2.93	0.02	0.02	0.15	intracellular ribonucleoprotein complex
CC	GO:1990904	16	1.24E-04	58	118	1253	2.93	0.02	0.02	0.15	ribonucleoprotein complex
CC	GO:0005615	7	6.15E-04	58	25	1253	6.05	0.09	0.05	0.74	extracellular space

CC	GO:0032991	29	8.02E-04	58	363	1253	1.73	0.12	0.04	0.97	macromolecular complex
CC	GO:0022624	4	2.75E-03	58	7	1253	12.34	0.36	0.09	3.27	proteasome accessory complex
CC	GO:0005730	6	4.31E-03	58	25	1253	5.18	0.50	0.11	5.09	nucleolus
CC	GO:0005576	7	6.04E-03	58	38	1253	3.98	0.62	0.13	7.06	extracellular region
CC	GO:0005732	3	1.86E-02	58	5	1253	12.96	0.95	0.29	20.34	small nucleolar ribonucleoprotein complex
CC	GO:0005758	3	2.71E-02	58	6	1253	10.80	0.99	0.36	28.29	mitochondrial intermembrane space
CC	GO:0031970	3	2.71E-02	58	6	1253	10.80	0.99	0.36	28.29	organelle envelope lumen
CC	GO:0030684	4	2.75E-02	58	15	1253	5.76	0.99	0.34	28.65	preribosome
CC	GO:0043228	15	2.91E-02	58	183	1253	1.77	0.99	0.33	30.01	non-membrane-bounded organelle
CC	GO:0043232	15	2.91E-02	58	183	1253	1.77	0.99	0.33	30.01	intracellular non-membrane-bounded organelle
CC	GO:0044424	44	5.45E-02	58	812	1253	1.17	1.00	0.50	49.23	intracellular part
CC	GO:0031974	10	6.36E-02	58	113	1253	1.91	1.00	0.53	54.83	membrane-enclosed lumen
CC	GO:0043234	18	7.16E-02	58	264	1253	1.47	1.00	0.55	59.29	protein complex
CC	GO:0031429	2	8.89E-02	58	2	1253	21.60	1.00	0.61	67.61	box H/ACA snoRNP complex
CC	GO:0042555	2	8.89E-02	58	2	1253	21.60	1.00	0.61	67.61	MCM complex
CC	GO:0005697	2	8.89E-02	58	2	1253	21.60	1.00	0.61	67.61	telomerase holoenzyme complex
MF	GO:0003723	9	7.28E-03	45	86	1277	2.97	0.65	0.65	8.30	RNA binding
MF	GO:0003676	15	6.90E-02	45	274	1277	1.55	1.00	0.99	57.15	nucleic acid binding
MF	GO:0097159	24	7.56E-02	45	519	1277	1.31	1.00	0.98	60.61	organic cyclic compound binding
MF	GO:0061135	2	9.99E-02	45	3	1277	18.92	1.00	0.98	71.30	endopeptidase regulator activity
MF	GO:0061134	2	9.99E-02	45	3	1277	18.92	1.00	0.98	71.30	peptidase regulator activity

Table S14. Pathway enrichment analysis from day 1 downregulated genes using KEGG database

KEGG ID	Pathway	N	Count	Pvalue	GeneRatio
path:spu00010	Glycolysis / Gluconeogenesis	53	5	4.61E-03	9.43E-02
path:spu00040	Pentose and glucuronate interconversions	85	5	3.13E-02	5.88E-02
path:spu00053	Ascorbate and aldarate metabolism	85	5	3.13E-02	5.88E-02
path:spu00071	Fatty acid degradation	57	4	3.01E-02	7.02E-02
path:spu00250	Alanine, aspartate and glutamate metabolism	36	3	3.81E-02	8.33E-02
path:spu00270	Cysteine and methionine metabolism	70	5	1.47E-02	7.14E-02
path:spu00280	Valine, leucine and isoleucine degradation	61	6	1.55E-03	9.84E-02
path:spu00340	Histidine metabolism	37	4	6.91E-03	1.08E-01
path:spu00350	Tyrosine metabolism	28	3	1.97E-02	1.07E-01
path:spu00380	Tryptophan metabolism	74	6	4.15E-03	8.11E-02
path:spu00410	beta-Alanine metabolism	30	3	2.37E-02	1.00E-01
path:spu00620	Pyruvate metabolism	43	5	1.82E-03	1.16E-01
path:spu00730	Thiamine metabolism	17	2	4.77E-02	1.18E-01
path:spu00760	Nicotinate and nicotinamide metabolism	40	3	4.97E-02	7.50E-02
path:spu00790	Folate biosynthesis	48	6	4.25E-04	1.25E-01
path:spu00920	Sulfur metabolism	20	4	6.64E-04	2.00E-01
path:spu01100	Metabolic pathways	1996	66	7.75E-07	3.31E-02
path:spu01200	Carbon metabolism	138	7	2.42E-02	5.07E-02
path:spu04146	Peroxisome	146	9	3.14E-03	6.16E-02
path:spu04512	ECM-receptor interaction	50	4	1.96E-02	8.00E-02

Table S15. Pathway enrichment analysis from day 1 Upregulated genes using KEGG database

KEGG ID	Pathway	N	Count	Pvalue	GeneRatio
path:spu00970	Aminoacyl-tRNA biosynthesis	74	10	1.96E-03	1.35E-01
path:spu03008	Ribosome biogenesis in eukaryotes	91	26	1.41E-14	2.86E-01
path:spu03010	Ribosome	140	30	5.25E-13	2.14E-01
path:spu03013	RNA transport	170	16	5.02E-03	9.41E-02
path:spu03015	mRNA surveillance pathway	72	7	4.76E-02	9.72E-02
path:spu03020	RNA polymerase	31	7	4.21E-04	2.26E-01
path:spu03040	Spliceosome	177	14	3.38E-02	7.91E-02
path:spu03050	Proteasome	48	15	1.70E-09	3.13E-01
path:spu04141	Protein processing in endoplasmic reticulum	166	13	4.28E-02	7.83E-02

Table S16. Pathway enrichment analysis from day 3 downregulated genes using KEGG database

KEGG ID	Pathway	N	Count	Pvalue	GeneRatio
path:spu00340	Histidine metabolism	37	3	2.58E-02	8.11E-02
path:spu00380	Tryptophan metabolism	74	4	3.90E-02	5.41E-02
path:spu00500	Starch and sucrose metabolism	39	3	2.96E-02	7.69E-02
path:spu00620	Pyruvate metabolism	43	3	3.80E-02	6.98E-02
path:spu00670	One carbon pool by folate	17	2	3.43E-02	1.18E-01
path:spu00730	Thiamine metabolism	17	2	3.43E-02	1.18E-01
path:spu01100	Metabolic pathways	1996	43	4.28E-02	2.15E-02
path:spu04145	Phagosome	165	11	1.14E-04	6.67E-02
path:spu04146	Peroxisome	146	7	1.30E-02	4.79E-02

Table S17. Pathway enrichment analysis from day 3 upregulated genes using KEGG database

KEGG ID	Pathway	N	Count	Pvalue	GeneRatio
path:spu03008	Ribosome biogenesis in eukaryotes	91	7	4.94E-03	7.69E-02
path:spu03010	Ribosome	140	24	3.89E-15	1.71E-01
path:spu03050	Proteasome	48	9	1.14E-06	1.88E-01
path:spu04141	Protein processing in endoplasmic reticulum	166	13	1.06E-04	7.83E-02
path:spu04145	Phagosome	165	8	3.73E-02	4.85E-02

Table S18. Clusters of coexpressed transcripts

ID	Description	Cluster	Adjusted P-value	GeneID
Transcript_442613	catalase	1	5.41E-42	548621
Transcript_268943	cytochrome P450 2U1	2	4.53E-38	581885
Transcript_319952	SOX4	2	9.30E-34	593520
Transcript_285077	zinc transporter ZIP14	2	5.19E-31	763759
Transcript_340144	uncharacterized protein K02A2.6-like Reverse transcriptase domain-containing protein	2	9.49E-30	105446129
Transcript_328691	MAM and LDL-receptor class A domain-containing protein 1	1	7.43E-27	574589
Transcript_298293	collagen alpha-1(XII) chain tenascin-X	1	2.46E-26	763365
Transcript_197637	retinol dehydrogenase 12 dehydrogenase/reductase SDR family member 13-like	3	7.29E-26	589120
Transcript_204404	laminin subunit alpha laminin alpha chain	1	2.41E-25	578626
Transcript_298730	laminin subunit beta-1 laminin, beta 1	4	2.59E-24	582206
Transcript_202375	fibrillin-2 uncharacterized protein LOC105436405	3	4.08E-24	105436405
Transcript_287164	nucleolar complex protein 2 homolog	3	8.11E-24	585237
Transcript_243955	glycerol kinase	3	2.87E-23	580504
Transcript_445893	ATPase family AAA domain-containing protein 3-B	3	5.85E-23	588531
Transcript_298217	4-aminobutyrate aminotransferase, mitochondrial	4	4.79E-22	577656
Transcript_264429	sushi domain-containing protein 2 uncharacterized protein K03H1.5	1	4.74E-21	583122
Transcript_172789	neuroblast differentiation-associated protein AHNK-like	1	1.09E-20	105441784
Transcript_442463	probable dimethyladenosine transferase	2	1.72E-20	574553
Transcript_280127	RNA granule protein invertebrate TPA: RNA granule protein invertebrate	2	3.94E-20	580088
Transcript_406209	sulfite oxidase	4	7.13E-20	586173
Transcript_238520	lysyl oxidase-like 2	1	5.75E-19	585092
Transcript_267297	pumilio homolog 3	3	7.79E-19	583455
Transcript_443315	prestalk protein	1	1.77E-18	590178
Transcript_461742	stromelysin-3-like matrix metalloproteinase-24-like	1	2.08E-18	105436437
Transcript_385039	aminopeptidase N	1	2.21E-18	578352
Transcript_438891	HLX	5	1.38E-17	100892685
Transcript_350383	telomerase reverse transcriptase-long telomerase reverse transcriptase-	3	2.59E-17	105447117
Transcript_344692	26S proteasome non-ATPase regulatory subunit 12	3	2.62E-17	593806
Transcript_429867	HMX	3	8.86E-17	579532
Transcript_395263	26S proteasome non-ATPase regulatory subunit 5	2	1.55E-16	588345
Transcript_198009	uncharacterized protein LOC582064 inter-alpha-trypsin inhibitor heavy chain H2	4	2.22E-16	582064
Transcript_246166	diphthine synthase	3	2.57E-16	577892

Transcript_430669	LOW QUALITY PROTEIN: uncharacterized protein LOC580672 apolipoprotein B-100	4	2.78E-16	580672
Transcript_328858	uncharacterized protein LOC100893633 Arylamine N-acetyltransferase	4	2.78E-16	100893633
Transcript_414587	solute carrier family 35 member F2	2	6.89E-16	574685
Transcript_364016	prohibitin	2	7.21E-16	584483
Transcript_431156	GTP-binding protein 8	1	8.05E-16	590744
Transcript_366520	GDP-mannose 4,6 dehydratase	2	1.21E-15	588885
Transcript_288662	microfibril-associated glycoprotein 4 tenascin-N	1	1.84E-15	753235
Transcript_351600	peroxisomal multifunctional enzyme type 2 hydroxysteroid (17-beta) dehydrogenase 4	1	2.44E-15	581580
Transcript_267740	ribosome biogenesis protein WDR12	2	3.19E-15	591474
Transcript_404053	mRNA turnover protein 4 homolog	3	3.39E-15	578804
Transcript_364345	proteasome activator complex subunit 3	3	4.11E-15	585921
Transcript_461114	yrdC domain-containing protein, mitochondrial	2	4.36E-15	588740
Transcript_204651	OTU domain-containing protein 4 putative bifunctional UDP-N-acetylglucosamine transferase a	3	6.67E-15	593098
Transcript_425984	translocator protein	1	7.60E-15	583617
Transcript_179579	methenyltetrahydrofolate synthase domain-containing protein	3	8.49E-15	588795
Transcript_183015	LOW QUALITY PROTEIN: histidine--tRNA ligase, cytoplasmic	3	1.13E-14	105444109
Transcript_206897	actin, muscle	1	1.22E-14	581500
Transcript_421726	ribosome production factor 2 homolog	2	1.23E-14	755131
Transcript_365697	uncharacterized protein LOC589195	3	1.28E-14	589195
Transcript_428650	ammonium transporter Rh type B ammonium transporter Rh type B-A ammonium transporter	1	1.34E-14	584796
Transcript_431326	26S proteasome non-ATPase regulatory subunit 3	3	1.41E-14	578762
Transcript_384474	transmembrane protein KIAA1109	4	1.46E-14	586038
Transcript_365782	LOW QUALITY PROTEIN: eukaryotic translation initiation factor 3 subunit I	2	2.21E-14	589571
Transcript_279405	ATP-dependent RNA helicase HAS1 ATP-dependent RNA helicase DDX18 DEAD (Asp-Glu-Ala-As	3	2.62E-14	577986
Transcript_197448	negative elongation factor C/D negative elongation factor D	2	3.61E-14	581078
Transcript_375637	protein Wnt-6	3	6.03E-14	585147
Transcript_344765	guanine nucleotide-binding protein-like NSN1 guanine nucleotide-binding protein-like 3 homol	2	7.57E-14	577855
Transcript_354584	enolase alpha-enolase-like	1	7.95E-14	579256
Transcript_423794	activator of 90 kDa heat shock protein ATPase homolog 1	2	1.22E-13	575643
Transcript_359489	eukaryotic translation initiation factor 3 subunit K	3	1.62E-13	587575
Transcript_397594	LOW QUALITY PROTEIN: RNA cytidine acetyltransferase N-acetyltransferase 10 (GCN5-related)	2	1.63E-13	576671
Transcript_373223	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	2	1.68E-13	574857
Transcript_460570	alpha-catulin	1	1.81E-13	576107
Transcript_417350	ribosome biogenesis protein NOP53 glioma tumor suppressor candidate region gene 2 protein	2	1.98E-13	593605
Transcript_333973	tubulin polymerization-promoting protein family member 2	1	2.23E-13	577151
Transcript_183358	alpha-actinin alpha-actinin, sarcomeric	1	2.26E-13	592971

Transcript_270919	heterogeneous nuclear ribonucleoprotein C	3	2.92E-13	100893477
Transcript_263624	protein Wnt-9a	3	3.13E-13	575320
Transcript_298954	uncharacterized protein LOC577534	2	3.22E-13	577534
Transcript_202461	opsin Rh5	2	4.05E-13	579899
Transcript_427877	uncharacterized protein LOC593232 Ankyrin repeat-containing domain-containing protein	3	4.30E-13	593232
Transcript_375646	hydroxyacylglutathione hydrolase, mitochondrial	1	5.05E-13	578596
Transcript_373821	mitochondrial intermembrane space import and assembly protein 40	2	5.98E-13	582540
Transcript_256657	carbohydrate sulfotransferase 1	2	7.10E-13	579726
Transcript_412104	probable cation-transporting ATPase 13A3 ATPase type 13A3 putative cation-transporting ATP	1	7.52E-13	577790
Transcript_314464	CMP-N-acetylneuraminate-beta-1,4-galactoside alpha-2,3-sialyltransferase	1	8.96E-13	754196
Transcript_359719	heat shock cognate 71 kDa protein heat shock 70kDa protein 8	2	9.55E-13	576276
Transcript_395874	U3 small nucleolar RNA-associated protein 18 homolog	3	9.76E-13	579700
Transcript_405927	NADPH oxidase 4	2	1.11E-12	100889322
Transcript_448868	IgG Fc-binding protein Fc fragment of IgG binding protein zonadhesin	1	1.14E-12	762415
Transcript_271439	T-complex protein 1 subunit zeta	2	1.41E-12	577393
Transcript_330216	aspartyl/asparaginyl beta-hydroxylase bromodomain-containing protein 4	1	1.92E-12	593797
Transcript_200469	aquaporin-8	1	2.12E-12	589852
Transcript_197881	eukaryotic translation initiation factor 3 subunit E	2	2.28E-12	754815
Transcript_182900	sodium-coupled monocarboxylate transporter 1	1	2.33E-12	580845
Transcript_396851	soluble adenylyl cyclase	3	2.73E-12	574069
Transcript_383783	bone morphogenetic protein 1 homolog	1	2.81E-12	373360
Transcript_431169	T-complex protein 1 subunit theta	3	3.11E-12	583086
Transcript_443125	nucleolar RNA helicase 2	2	3.20E-12	581409
Transcript_277158	ATP-binding cassette sub-family F member 1	2	3.40E-12	576400
Transcript_249697	lupus La protein homolog	2	3.41E-12	105443896
Transcript_442985	asparagine synthetase [glutamine-hydrolyzing]	2	3.42E-12	575946
Transcript_262723	probable serine/threonine-protein kinase DDB_G0278665	1	4.05E-12	577336
Transcript_225361	contactin-associated protein-like 2 contactin-associated protein-like 5	1	4.57E-12	575215
Transcript_433953	PWP1	2	4.80E-12	583947
Transcript_353989	nidogen-1	1	5.18E-12	586685
Transcript_350978	ribosome biogenesis regulatory protein homolog	3	5.94E-12	575632
Transcript_294196	low-density lipoprotein receptor-related protein 1	1	8.65E-12	582052
Transcript_278301	tubulin alpha-1A chain	2	9.88E-12	754102
Transcript_258721	glutamyl aminopeptidase	1	1.03E-11	587683
Transcript_440792	medium-chain acyl-CoA ligase ACSF2, mitochondrial acyl-CoA synthetase family member 2, mit	1	1.35E-11	592091
Transcript_394161	pyrroline-5-carboxylate reductase 1, mitochondrial	2	1.39E-11	583853

Transcript_267275	prohibitin-2	3	1.70E-11	575755
Transcript_263596	BTF3L4	2	2.16E-11	586588
Transcript_267873	H/ACA ribonucleoprotein complex subunit 1	3	2.51E-11	592267
Transcript_385986	midasin	3	2.92E-11	575173
Transcript_336637	eukaryotic peptide chain release factor GTP-binding subunit ERF3A G1 to S phase transition 2	3	2.92E-11	580307
Transcript_175325	TAP26	2	2.98E-11	579591
Transcript_310211	protein arginine N-methyltransferase 1	3	3.24E-11	590987
Transcript_230511	ribosomal RNA processing protein 1 homolog A ribosomal RNA processing protein 1 homolog B	2	3.35E-11	594061
Transcript_68378	uncharacterized protein LOC584236	2	3.50E-11	584236
Transcript_452859	25S rRNA (cytosine-C(5))-methyltransferase nop2	3	3.62E-11	582075
Transcript_352347	RNA-binding protein with serine-rich domain 1	3	3.88E-11	585553
Transcript_354900	mitochondrial import receptor subunit TOM40 homolog	3	3.95E-11	585934
Transcript_365226	protein phosphatase 1G	2	4.53E-11	594091
Transcript_296057	carbohydrate sulfotransferase 15-like	1	4.53E-11	100892795
Transcript_222572	bone morphogenetic protein BMP2/4	3	4.69E-11	373196
Transcript_216724	uncharacterized protein LOC587705 putative sterigmatocystin biosynthesis dehydrogenase stc	1	4.87E-11	587705
Transcript_311413	amassin coelomocyte amassing protein	3	4.95E-11	373503
Transcript_263997	mitochondrial import inner membrane translocase subunit Tim17-B	3	5.59E-11	577928
Transcript_242486	polycomb protein eed-A	3	5.77E-11	581239
Transcript_454730	LOW QUALITY PROTEIN: allene oxide synthase-lipoxygenase protein	1	6.46E-11	584481
Transcript_279511	mucosa-associated lymphoid tissue lymphoma translocation protein 1 mucosa-associated lymph	2	6.81E-11	590194
Transcript_322705	THO complex subunit 6 homolog	3	6.98E-11	580431
Transcript_421292	sphingosine-1-phosphate lyase 1	3	8.18E-11	585643
Transcript_226274	uncharacterized protein LOC583933	1	8.46E-11	583933
Transcript_435175	sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)	1	9.08E-11	594544
Transcript_224605	ribosomal RNA small subunit methyltransferase NEP1	2	9.38E-11	589275
Transcript_342811	epoxide hydrolase 1	1	9.89E-11	588166
Transcript_328958	H/ACA ribonucleoprotein complex subunit DKC1 dyskeratosis congenita 1, dyskerin	2	1.10E-10	584530
Transcript_421302	equilibrative nucleoside transporter 1 microtubule-associated protein 10	4	1.13E-10	592207
Transcript_339471	fibrillin-1	1	1.23E-10	575027
Transcript_431258	methanethiol oxidase selenium-binding protein 1	1	1.23E-10	582523
Transcript_7357	cathepsin Z	2	1.37E-10	580617
Transcript_432532	LMO2	2	1.48E-10	100892046
Transcript_310947	rRNA-processing protein FCF1 homolog	3	1.49E-10	586103
Transcript_407052	C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8 C3 and PZP-like, alpha-2-m	1	1.50E-10	579831
Transcript_461041	eEF1A lysine and N-terminal methyltransferase methyltransferase-like protein 13	2	1.67E-10	754600

Transcript_205415	H/ACA ribonucleoprotein complex subunit 2-like protein	3	1.73E-10	577044
Transcript_254399	vacuolar protein sorting-associated protein 13A vacuolar protein sorting-associated protein 13A	1	1.75E-10	575234
Transcript_439620	uridine-cytidine kinase 2 uridine-cytidine kinase 2-B	2	1.86E-10	588945
Transcript_208693	neutral and basic amino acid transport protein rBAT	1	1.88E-10	586832
Transcript_395337	formin-J	3	2.03E-10	588660
Transcript_184579	RWD domain-containing protein 1	2	2.11E-10	590636
Transcript_282088	39S ribosomal protein L17, mitochondrial	2	2.40E-10	591498
Transcript_271370	rRNA 2'-O-methyltransferase fibrillarin	3	2.46E-10	752335
Transcript_417755	transmembrane protein 69	2	2.59E-10	586174
Transcript_409638	heat shock 70 kDa protein 14	3	2.73E-10	588149
Transcript_259246	pre-mRNA-splicing factor 38B	2	3.02E-10	100889783
Transcript_308724	uncharacterized protein LOC577145	1	3.19E-10	577145
Transcript_330347	stress-70 protein, mitochondrial heat shock 70kDa protein 9 (mortalin)	3	3.20E-10	577721
Transcript_215804	leucine-rich repeat-containing protein 74B	1	3.42E-10	584206
Transcript_204158	cystine/glutamate transporter	4	3.52E-10	579243
Transcript_243187	DNA-directed RNA polymerase I subunit RPA49	2	3.56E-10	588897
Transcript_290985	glycine--tRNA ligase	2	4.15E-10	578936
Transcript_403536	ribosome production factor 1	2	4.37E-10	592162
Transcript_295742	10 kDa heat shock protein, mitochondrial	3	4.72E-10	762428
Transcript_197679	uncharacterized protein LOC105446114	4	4.73E-10	105446114
Transcript_456681	CD82 antigen carbohydrate sulfotransferase 1-like	1	4.92E-10	100889350
Transcript_263817	eukaryotic translation initiation factor 2 subunit 1	3	4.98E-10	586283
Transcript_357723	translation elongation factor 1B beta subunit	3	6.19E-10	574071
Transcript_234345	bromodomain-containing protein 4-like dentin sialophosphoprotein	3	6.36E-10	105441791
Transcript_270485	U3 small nucleolar RNA-interacting protein 2	2	6.67E-10	582919
Transcript_202897	dimethyladenosine transferase 2, mitochondrial	2	6.97E-10	589505
Transcript_427783	uncharacterized protein LOC575162	1	7.09E-10	575162
Transcript_319739	carboxypeptidase B	1	7.54E-10	764971
Transcript_183115	nucleolar GTP-binding protein 2	2	8.38E-10	585370
Transcript_367031	ribosome biogenesis protein bop1-B	2	8.81E-10	575063
Transcript_272225	protein ABHD11 alpha/beta hydrolase domain-containing protein 11	3	8.95E-10	575326
Transcript_288791	ATP-dependent RNA helicase DHX30	2	1.04E-09	577803
Transcript_244563	mitochondrial import inner membrane translocase subunit TIM44	3	1.08E-09	752190
Transcript_438545	all-trans-retinol 13,14-reductase putative all-trans-retinol 13,14-reductase	4	1.09E-09	581285
Transcript_172871	protein RER1	2	1.09E-09	579195
Transcript_417215	alanine--glyoxylate aminotransferase 2, mitochondrial	4	1.13E-09	594821

Transcript_256986	mitochondrial import inner membrane translocase subunit Tim10-B	3	1.16E-09	589835
Transcript_266569	stress-induced-phosphoprotein 1	3	1.17E-09	765087
Transcript_447903	uracil-DNA glycosylase	4	1.29E-09	586702
Transcript_342844	peroxiredoxin	2	1.31E-09	581408
Transcript_411315	propionyl-CoA carboxylase alpha chain, mitochondrial	2	1.40E-09	582365
Transcript_265130	RRP15-like protein	2	1.46E-09	577322
Transcript_358391	ribosome biogenesis protein NSA2 homolog	3	1.55E-09	577954
Transcript_264331	fibrillin-2 fibrillin-1	1	1.72E-09	582487
Transcript_455249	maleylacetoacetate isomerase	5	1.89E-09	580863
Transcript_443343	lysine--tRNA ligase	3	2.22E-09	588700
Transcript_393409	serine-enriched protein	2	2.28E-09	100888499
Transcript_264379	60 kDa heat shock protein, mitochondrial	2	2.33E-09	590510
Transcript_236885	serine/threonine-protein kinase rio2	2	2.44E-09	579218
Transcript_285991	hypoxia up-regulated protein 1 hypoxia up-regulated 1	3	2.63E-09	592339
Transcript_242646	60S ribosomal protein L8	2	2.67E-09	591341
Transcript_204616	T-complex protein 1 subunit delta	2	2.96E-09	579722
Transcript_194648	coiled-coil domain-containing protein 12	3	3.14E-09	585976
Transcript_410118	ATP-dependent RNA helicase DDX24	2	3.23E-09	578876
Transcript_232798	protein arginine N-methyltransferase 3	3	3.24E-09	588858
Transcript_243757	small nuclear ribonucleoprotein Sm D3	3	3.58E-09	105438529
Transcript_431275	eukaryotic translation initiation factor 2 subunit 2	3	3.61E-09	590481
Transcript_237829	gamma-butyrobetaine dioxygenase	1	3.73E-09	577198
Transcript_353055	deoxyhypusine hydroxylase	2	3.81E-09	582221
Transcript_351300	valine--tRNA ligase	3	3.92E-09	590476
Transcript_253045	cytochrome P450 10	2	4.01E-09	576441
Transcript_411364	CCR4-NOT transcription complex subunit 11	2	4.27E-09	594372
Transcript_215364	26S proteasome non-ATPase regulatory subunit 7	3	4.44E-09	575334
Transcript_78944	DNA-directed RNA polymerase I subunit RPA12	2	4.56E-09	100892475
Transcript_331128	deoxynucleotidyltransferase terminal-interacting protein 2	2	4.71E-09	586304
Transcript_285870	26S proteasome regulatory subunit 6A-B 26S protease regulatory subunit 6A-B 26S protease re	2	4.90E-09	576830
Transcript_324100	hydroxyacid oxidase 1	1	4.95E-09	584105
Transcript_280947	26S proteasome non-ATPase regulatory subunit 4	2	5.06E-09	575737
Transcript_279609	26S proteasome non-ATPase regulatory subunit 2	2	5.09E-09	588529
Transcript_367924	T-complex protein 1 subunit alpha	3	5.28E-09	582138
Transcript_359457	alpha-2-macroglobulin	3	5.54E-09	594798
Transcript_272476	leucine-rich repeat-containing protein 46	2	6.23E-09	100889057

Transcript_428533	proteasomal ubiquitin receptor ADRM1	2	6.25E-09	753175
Transcript_461744	serine--tRNA ligase, cytoplasmic	2	7.26E-09	588782
Transcript_437045	betaine--homocysteine S-methyltransferase 1	1	7.59E-09	752628
Transcript_218326	uncharacterized protein LOC100893287	1	7.60E-09	100893287
Transcript_420760	alkaline phosphatase	1	8.51E-09	580300
Transcript_454673	protein SDA1 homolog SDA1 domain containing 1	3	8.75E-09	585590
Transcript_441945	queuosine salvage protein UPF0553 protein C9orf64	2	8.75E-09	584962
Transcript_256633	bifunctional purine biosynthesis protein PURH	2	9.25E-09	588680
Transcript_386779	FRAS1-related extracellular matrix protein 1 FRAS1 related extracellular matrix 1	1	9.46E-09	591943
Transcript_297492	laminin subunit alpha-2 laminin subunit alpha-1	5	9.73E-09	587274
Transcript_397023	cadherin EGF LAG seven-pass G-type receptor 1	1	9.95E-09	105440441
Transcript_190981	superoxide dismutase [Cu-Zn]	1	1.02E-08	579361
Transcript_41462	EF-hand calcium-binding domain-containing protein 6	4	1.06E-08	589273
Transcript_271917	dihydroflavonol 4-reductase putative NADPH-dependent methylglyoxal reductase GRP2 putative	3	1.09E-08	585152
Transcript_268427	steroid 17-alpha-hydroxylase/17,20 lyase	4	1.19E-08	585029
Transcript_384438	thyrotropin-releasing hormone-degrading ectoenzyme	1	1.20E-08	588093
Transcript_298313	spectrin alpha chain, non-erythrocytic 1	1	1.32E-08	580822
Transcript_437221	apoptosis-inducing factor 1, mitochondrial apoptosis-inducing factor, mitochondrion-associated	3	1.37E-08	578253
Transcript_456290	claspin claspin homolog	1	1.37E-08	575148
Transcript_343920	stAR-related lipid transfer protein 5	2	1.37E-08	584940
Transcript_293280	probable ribosome biogenesis protein RLP24	2	1.39E-08	581865
Transcript_245310	stAR-related lipid transfer protein 7, mitochondrial	2	1.42E-08	578525
Transcript_427274	contactin-2	1	1.44E-08	100893855
Transcript_431447	BRCA2 and CDKN1A-interacting protein	2	1.51E-08	586387
Transcript_461384	ATP-binding cassette sub-family C member 9	4	1.53E-08	594397
Transcript_404538	inactive C-alpha-formylglycine-generating enzyme 2	3	1.59E-08	576301
Transcript_185289	uncharacterized protein LOC100887836	1	1.75E-08	100887836
Transcript_381525	uronyl 2-sulfotransferase	1	1.76E-08	593546
Transcript_185057	GDH/6PGL endoplasmic bifunctional protein hexose-6-phosphate dehydrogenase (glucose 1-de	1	2.02E-08	590387
Transcript_360124	cytochrome c	3	2.03E-08	575347
Transcript_295374	KH domain-containing, RNA-binding, signal transduction-associated protein 2	2	2.09E-08	588527
Transcript_386824	WD repeat-containing protein 74	2	2.16E-08	587044
Transcript_302605	proliferation-associated protein 2G4	2	2.23E-08	576641
Transcript_442775	Y+L amino acid transporter 2	2	2.24E-08	577249
Transcript_217735	protein RRP5 homolog programmed cell death 11	3	2.75E-08	584784
Transcript_298943	LOW QUALITY PROTEIN: small nuclear ribonucleoprotein F	3	2.75E-08	592177

Transcript_276778	electron transfer flavoprotein beta subunit lysine methyltransferase methyltransferase-like pro	3	2.88E-08	589785
Transcript_309454	microtubule-actin cross-linking factor 1 microtubule-actin cross-linking factor 1, isoforms 1/2/3	1	2.94E-08	756550
Transcript_395351	protein CDV3 homolog	2	3.00E-08	593799
Transcript_271655	RRP12-like protein	2	3.25E-08	587536
Transcript_444753	asparagine--tRNA ligase, cytoplasmic	2	3.27E-08	574833
Transcript_428848	26S proteasome non-ATPase regulatory subunit 6 proteasome (prosome, macropain) 26S subu	3	3.43E-08	590942
Transcript_431583	-	3	3.70E-08	100891280
Transcript_240340	tRNA methyltransferase 10 homolog A	3	3.72E-08	100889803
Transcript_199752	echinoidin-like	1	3.72E-08	105446729
Transcript_337159	ergothioneine biosynthesis protein 1 meiotically up-regulated gene 158 protein	1	4.12E-08	584365
Transcript_282269	dipeptidase 1	1	4.12E-08	592585
Transcript_393109	ran-specific GTPase-activating protein	2	4.20E-08	587798
Transcript_342318	aldehyde dehydrogenase, mitochondrial	1	4.23E-08	581706
Transcript_326720	U3 small nucleolar ribonucleoprotein protein IMP3	2	4.47E-08	590066
Transcript_214014	glutamate-rich WD repeat-containing protein 1	3	4.70E-08	581222
Transcript_240901	suppressor of SWI4 1 homolog	2	4.85E-08	582546
Transcript_306776	eukaryotic translation initiation factor 5B	3	5.25E-08	763128
Transcript_404542	uncharacterized protein LOC576204	4	5.64E-08	576204
Transcript_221851	deleted in malignant brain tumors 1 protein-like	1	5.78E-08	105440890
Transcript_322501	protein FAM199X	3	5.93E-08	100893786
Transcript_344436	replication termination factor 2 UPF0549 protein C20orf43 homolog protein RTF2 homolog	2	5.99E-08	754268
Transcript_404038	39S ribosomal protein L19, mitochondrial	3	6.18E-08	589881
Transcript_283496	mitochondrial import inner membrane translocase subunit Tim23-like	3	6.32E-08	105440270
Transcript_376962	lambda-crystallin homolog	2	6.42E-08	589657
Transcript_265994	nascent polypeptide-associated complex subunit alpha	2	7.11E-08	576369
Transcript_311969	uncharacterized protein RAB51F homolog uncharacterized protein C20orf24 homolog	3	7.24E-08	576217
Transcript_340792	WD repeat-containing protein 82	3	7.30E-08	100888929
Transcript_219894	serine/arginine repetitive matrix protein 2	1	7.35E-08	100888995
Transcript_438464	FAD synthase	2	7.76E-08	593348
Transcript_311263	eukaryotic translation initiation factor 3 subunit M	2	7.76E-08	589955
Transcript_323033	tubulin beta chain	2	8.07E-08	373275
Transcript_359669	T-complex protein 1 subunit epsilon chaperonin containing TCP1, subunit 5 (epsilon)	2	8.22E-08	575808
Transcript_215999	elongation factor Ts, mitochondrial	3	9.32E-08	578811
Transcript_430621	alkylglycerol monooxygenase	4	9.45E-08	579307
Transcript_229332	ADP-ribose pyrophosphatase, mitochondrial	4	1.04E-07	756760
Transcript_457631	zinc finger protein 330 homolog	2	1.05E-07	579935

Transcript_375389	N-terminal Xaa-Pro-Lys N-methyltransferase 1	3	1.06E-07	579562
Transcript_322851	nucleolar and coiled-body phosphoprotein 1	3	1.07E-07	591574
Transcript_225582	ADP-ribosylation factor	2	1.25E-07	763814
Transcript_205826	protein ABHD14B abhydrolase domain-containing protein 14A-like alpha/beta hydrolase domain	1	1.26E-07	585657
Transcript_448021	proteasome subunit alpha type-6	3	1.28E-07	589393
Transcript_434118	voltage dependent calcium channel L-type	1	1.32E-07	578128
Transcript_331800	uncharacterized protein LOC592324	2	1.33E-07	592324
Transcript_365923	insulin-like growth factor-binding protein complex acid labile subunit	1	1.33E-07	105447591
Transcript_403056	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)-like	3	1.33E-07	754239
Transcript_205321	leucine-rich PPR motif-containing protein, mitochondrial	2	1.39E-07	755486
Transcript_291904	uncharacterized protein LOC105438010 Glycoside hydrolase family 31 domain containing protein	4	1.47E-07	105438010
Transcript_394693	folylpolyglutamate synthase, mitochondrial	2	1.49E-07	592205
Transcript_50290	uncharacterized protein LOC100890372	1	1.53E-07	100890372
Transcript_216838	LOW QUALITY PROTEIN: lipase maturation factor 2	4	1.57E-07	583944
Transcript_434160	ubiquitin-conjugating enzyme E2 N	3	1.57E-07	590968
Transcript_223216	uncharacterized protein LOC100892961	4	1.58E-07	100892961
Transcript_385327	amidophosphoribosyltransferase	2	1.71E-07	582049
Transcript_316114	eukaryotic translation initiation factor 2 subunit 3 eukaryotic translation initiation factor 2 subunit	3	1.91E-07	582011
Transcript_364746	insulin-like growth factor 2 mRNA-binding protein 1	3	1.93E-07	576835
Transcript_334779	3'(2'),5'-bisphosphate nucleotidase 1	4	1.94E-07	580070
Transcript_185684	nucleolar protein 6	2	1.95E-07	577631
Transcript_196408	DNA mismatch repair protein Mlh3	2	1.97E-07	575007
Transcript_443664	acid phosphatase type 7 iron/zinc purple acid phosphatase-like protein	1	2.13E-07	580652
Transcript_429248	histone-binding protein RBBP4 retinoblastoma binding protein 4	3	2.13E-07	579451
Transcript_351461	28S ribosomal protein S22, mitochondrial	2	2.16E-07	589317
Transcript_454778	protein LLP homolog	2	2.26E-07	764101
Transcript_349228	uncharacterized protein LOC591826	2	2.30E-07	591826
Transcript_187299	transcription initiation protein SPT3 homolog	2	2.34E-07	586422
Transcript_361302	sideroflexin-5	1	2.64E-07	577642
Transcript_416648	nucleolar protein 14	3	2.78E-07	578764
Transcript_225955	endoribonuclease YbeY putative ribonuclease rRNA maturation factor homolog	1	2.82E-07	588773
Transcript_267958	regulator of chromosome condensation	3	2.90E-07	754700
Transcript_352669	zinc finger protein 593	2	2.96E-07	592435
Transcript_384255	zinc finger protein 362	2	2.99E-07	583226
Transcript_422610	hydroxyacid-oxoacid transhydrogenase, mitochondrial	1	3.05E-07	575433
Transcript_424059	acetyl-coenzyme A transporter 1	2	3.05E-07	589856

Transcript_332395	uncharacterized protein LOC591223	5	3.06E-07	591223
Transcript_225467	heat shock protein 75 kDa, mitochondrial	3	3.10E-07	578227
Transcript_444809	eukaryotic peptide chain release factor subunit 1	3	3.11E-07	591483
Transcript_195493	CTP synthase 1	2	3.11E-07	575088
Transcript_428926	menin	2	3.22E-07	589807
Transcript_197652	LOW QUALITY PROTEIN: tubulin alpha-1C chain	2	3.23E-07	762594
Transcript_203588	DDB1- and CUL4-associated factor 13	3	3.39E-07	589486
Transcript_280848	nudC domain-containing protein 1	2	3.39E-07	590657
Transcript_429226	uncharacterized protein LOC590843	4	3.46E-07	590843
Transcript_451457	PHD finger protein 24	3	3.49E-07	100892446
Transcript_343741	proteasome maturation protein	3	3.84E-07	579892
Transcript_185040	endothelin-converting enzyme 1	1	3.84E-07	755783
Transcript_282876	spermidine synthase	2	4.12E-07	591935
Transcript_427763	major facilitator superfamily domain-containing protein 9	2	4.19E-07	577847
Transcript_425248	T-complex protein 1 subunit gamma	3	4.26E-07	574601
Transcript_286893	proteasome subunit beta type-1	2	4.31E-07	754955
Transcript_323172	sialic acid synthase N-acetylneuraminic acid synthase	2	4.43E-07	577884
Transcript_373212	fibrillin-1 latent-transforming growth factor beta-binding protein 4	1	4.48E-07	100887851
Transcript_177898	sodium- and chloride-dependent GABA transporter 1	1	4.60E-07	581958
Transcript_377252	neural-cadherin	1	4.62E-07	589984
Transcript_364897	FAST kinase domain-containing protein 4 protein TBRG4	3	4.73E-07	580380
Transcript_238012	G patch domain-containing protein 4 protein FAM133-like	3	4.75E-07	581552
Transcript_240840	uncharacterized protein LOC105439633 Autophagy-related protein 27	1	4.78E-07	105439633
Transcript_359750	glucosamine-6-phosphate isomerase 2	3	5.05E-07	585301
Transcript_309937	solute carrier organic anion transporter family member 2A1-like	2	5.28E-07	752367
Transcript_208822	lysophosphatidylserine lipase ABHD12 monoacylglycerol lipase ABHD12	2	5.35E-07	100891460
Transcript_418613	PIN2/TERF1-interacting telomerase inhibitor 1	2	5.37E-07	591382
Transcript_294332	60S ribosome subunit biogenesis protein NIP7 homolog	2	5.43E-07	579986
Transcript_353843	poly [ADP-ribose] polymerase tankyrase poly(ADP-ribose) polymerase pme-5	4	5.86E-07	588883
Transcript_205105	uncharacterized protein LOC578177 low-density lipoprotein receptor-related protein 1B	1	5.99E-07	578177
Transcript_364601	acetolactate synthase-like protein	2	6.53E-07	593426
Transcript_321936	RNA-binding protein 34	3	6.77E-07	576551
Transcript_367437	secreted frizzled-related protein 3-like	3	6.84E-07	581781
Transcript_367877	vesicular integral-membrane protein VIP36 VIP36-like protein	3	7.04E-07	578461
Transcript_399833	serine/threonine-protein phosphatase CPPED1 calcineurin-like phosphoesterase domain-conta	2	7.07E-07	583499
Transcript_323748	cryptochrome-1	1	7.23E-07	580742

Transcript_394678	di-N-acetylchitinase	2	7.28E-07	578451
Transcript_232547	protein LMBR1L	3	7.31E-07	578121
Transcript_340709	DNA polymerase beta	2	7.47E-07	582628
Transcript_393067	signal peptide, CUB and EGF-like domain-containing protein 1	1	8.42E-07	577317
Transcript_262552	cytochrome P450 3A9	1	8.45E-07	588156
Transcript_226152	myosin-16 myosin-6	1	8.72E-07	580674
Transcript_367772	tubulin alpha-1 chain	2	8.81E-07	105439767
Transcript_204519	mitochondrial-processing peptidase subunit alpha peptidase (mitochondrial processing) alpha	3	9.15E-07	100889464
Transcript_6160	60S ribosomal protein L27a	2	9.97E-07	580148
Transcript_228286	elongation factor Tu, mitochondrial	3	1.02E-06	583958
Transcript_320536	4-hydroxyphenylpyruvate dioxygenase-like protein	3	1.03E-06	576414
Transcript_290528	TEF	3	1.06E-06	580363
Transcript_359106	GPI ethanolamine phosphate transferase 3	3	1.10E-06	584071
Transcript_302349	bystin	2	1.11E-06	578981
Transcript_260705	sorbin and SH3 domain-containing protein 1 vinexin	1	1.13E-06	574636
Transcript_205888	CDGSH iron-sulfur domain-containing protein 2 homolog A	1	1.13E-06	586672
Transcript_279040	KLF13	2	1.17E-06	576795
Transcript_230031	importin-7	2	1.18E-06	586884
Transcript_365373	ankyrin repeat and protein kinase domain-containing protein 1	3	1.24E-06	100889589
Transcript_278797	protein transport protein Sec24A basic proline-rich protein-like	2	1.25E-06	579127
Transcript_305867	actin-5C	2	1.26E-06	581650
Transcript_303652	derlin-1	3	1.30E-06	592785
Transcript_344547	T-complex protein 1 subunit beta	2	1.33E-06	580864
Transcript_366717	uncharacterized protein LOC582810 Tudor domain-containing protein	2	1.33E-06	582810
Transcript_358088	fucose mutarotase	4	1.37E-06	100888310
Transcript_329212	eukaryotic translation initiation factor 3 subunit J	2	1.40E-06	578606
Transcript_344098	nucleolar GTP-binding protein 1 GTP binding protein 4	3	1.40E-06	575126
Transcript_374375	X-ray radiation resistance-associated protein 1	3	1.45E-06	584905
Transcript_198110	DNA-directed RNA polymerases I and III subunit RPAC1	3	1.45E-06	590827
Transcript_409226	CD151 antigen	4	1.46E-06	592232
Transcript_185863	interaptin nuclear anchorage protein 1 nucleoprotein TPR uncharacterized protein LOC588428	1	1.63E-06	588428
Transcript_411421	wnt inhibitory factor 1	1	1.70E-06	100892419
Transcript_393713	multifunctional protein ADE2	2	1.76E-06	575874
Transcript_212609	NHL repeat-containing protein 2	2	1.83E-06	591178
Transcript_441990	uncharacterized protein LOC100888048	1	1.85E-06	100888048
Transcript_243213	protein-serine O-palmitoleoyltransferase porcupine protein-cysteine N-palmitoyltransferase pc	2	1.98E-06	577959

Transcript_249746	DNA-directed RNA polymerase, mitochondrial	2	1.98E-06	762772
Transcript_286756	GDP-fucose protein O-fucosyltransferase 1	3	2.03E-06	585387
Transcript_235731	MAM and LDL-receptor class A domain-containing protein 2	1	2.05E-06	755161
Transcript_440018	nucleolar complex protein 4 homolog	2	2.11E-06	591488
Transcript_341101	A disintegrin and metalloproteinase with thrombospondin motifs 18 ADAM metalloproteinase w	3	2.36E-06	574964
Transcript_180918	phosphopantothienoylcysteine decarboxylase subunit SIS2-like	1	2.38E-06	105438224
Transcript_439703	protein CBFA2T1 protein CBFA2T3-like	1	2.40E-06	576535
Transcript_405538	uncharacterized protein LOC100891656	1	2.45E-06	100891656
Transcript_292194	FERM domain-containing protein 1	1	2.46E-06	592633
Transcript_110850	60S ribosomal protein L3	2	2.89E-06	586477
Transcript_434866	uncharacterized protein LOC589939 Harbinger transposase-derived nuclease domain-containin	3	2.92E-06	589939
Transcript_438152	DNA excision repair protein ERCC-6-like transcriptional regulator ATRX	1	2.95E-06	575953
Transcript_446005	2-oxoglutarate-dependent dioxygenase htyE UPF0676 protein C1494.01	1	3.10E-06	752472
Transcript_286899	uncharacterized protein LOC587999	2	3.21E-06	587999
Transcript_325335	uncharacterized protein LOC593876	1	3.21E-06	593876
Transcript_249330	eukaryotic translation initiation factor 3 subunit H-B	2	3.27E-06	575080
Transcript_443947	uncharacterized protein LOC579607 putative oxidoreductase YteT-like	1	3.33E-06	579607
Transcript_190658	pyrroline-5-carboxylate reductase 3	2	3.41E-06	586502
Transcript_443207	Bardet-Biedl syndrome 1 protein	2	3.41E-06	578507
Transcript_350598	RNA 3'-terminal phosphate cyclase-like protein	2	3.67E-06	592597
Transcript_239281	cholinesterase 1 thyroglobulin	1	3.85E-06	583460
Transcript_367596	transitional endoplasmic reticulum ATPase	3	3.99E-06	575609
Transcript_381250	prostaglandin E synthase 2	3	4.04E-06	584887
Transcript_409717	isochorismatase domain-containing protein 2 isochorismatase domain-containing protein 2, mi	4	4.04E-06	590365
Transcript_185238	multifunctional methyltransferase subunit TRM112-like protein tRNA methyltransferase 112 hc	2	4.21E-06	579707
Transcript_444350	melanotransferrin	3	4.37E-06	581063
Transcript_306787	methyltransferase-like protein 24	1	4.40E-06	100891683
Transcript_271897	HEAT repeat-containing protein 1	3	4.60E-06	589888
Transcript_302913	L-lactate dehydrogenase	1	4.65E-06	586683
Transcript_386663	pancreatic lipase-related protein 2	1	4.67E-06	592851
Transcript_432931	NADPH oxidase 5	1	4.74E-06	752031
Transcript_306891	graves disease carrier protein homolog	2	4.80E-06	584753
Transcript_382713	60S ribosomal protein L19	2	4.80E-06	593861
Transcript_416522	uncharacterized protein LOC100888035	2	4.85E-06	100888035
Transcript_431677	coatamer subunit beta'	2	4.95E-06	589321
Transcript_185030	DNA-dependent protein kinase catalytic subunit	1	5.16E-06	586799

Transcript_381229	Golgi SNAP receptor complex member 1	2	5.23E-06	593134
Transcript_301702	unconventional myosin-XVI formin-like protein 20 myosin XVI putative F-box protein At1g473	1	5.29E-06	587143
Transcript_197661	LOW QUALITY PROTEIN: tubulin alpha-1 chain	2	5.35E-06	588319
Transcript_206262	cleavage stimulation factor subunit 2	2	5.44E-06	753333
Transcript_316435	neprilysin-1 endothelin-converting enzyme 1	1	5.66E-06	580325
Transcript_266841	tuftelin	4	5.71E-06	576303
Transcript_319974	uncharacterized protein LOC100890537	1	5.79E-06	100890537
Transcript_223102	transducin beta-like protein 3	3	6.10E-06	100891641
Transcript_234991	ADAMTS-like protein 1	2	6.11E-06	580296
Transcript_277138	uncharacterized protein LOC100891149	3	6.28E-06	100891149
Transcript_43695	b(0,+)-type amino acid transporter 1 B(0,+)-type amino acid transporter 1-like	1	6.33E-06	579553
Transcript_447128	maltase 1 alpha-glucosidase	1	6.40E-06	583103
Transcript_190954	uncharacterized protein LOC593642 CAP domain-containing protein	4	6.55E-06	593642
Transcript_84237	actin Cyl, cytoplasmic	1	6.60E-06	592912
Transcript_412252	protein SEC13 homolog	3	6.76E-06	583776
Transcript_284067	programmed cell death protein 2-like	2	6.81E-06	576484
Transcript_262309	N-alpha-acetyltransferase 11	2	6.82E-06	580091
Transcript_396324	phosphopantothenate--cysteine ligase	3	6.92E-06	763180
Transcript_302120	cadherin-23 fat-like cadherin-related tumor suppressor homolog protocadherin Fat 1	1	6.98E-06	594286
Transcript_433507	MKX	2	7.15E-06	105436421
Transcript_205651	lysophosphatidylcholine acyltransferase 2	1	7.37E-06	579107
Transcript_202496	ribosome biogenesis protein BRX1 homolog	3	7.55E-06	583114
Transcript_425468	dnaJ homolog subfamily B member 1	2	7.82E-06	752244
Transcript_315415	putative uncharacterized protein CXorf58	2	7.85E-06	593302
Transcript_244512	aspartate--tRNA ligase, cytoplasmic	3	8.02E-06	588558
Transcript_272010	proto-oncogene Wnt-3	3	8.05E-06	585683
Transcript_285582	splicing factor 3A subunit 2	2	8.28E-06	576257
Transcript_438398	U2 small nuclear ribonucleoprotein B'' U1 small nuclear ribonucleoprotein A-like	3	8.35E-06	584276
Transcript_289715	uncharacterized protein LOC763307 ZU5 domain-containing protein	3	8.56E-06	763307
Transcript_328267	40S ribosomal protein S26	2	8.78E-06	576654
Transcript_356949	ubiquitin-conjugating enzyme E2 K	2	9.01E-06	585095
Transcript_440889	serine/threonine-protein phosphatase 4 catalytic subunit	2	9.06E-06	594644
Transcript_405218	40S ribosomal protein S11	2	9.09E-06	579026
Transcript_375963	uncharacterized protein LOC581850	1	9.12E-06	581850
Transcript_299201	mesencephalic astrocyte-derived neurotrophic factor homolog	3	9.30E-06	755636
Transcript_215281	decaprenyl-diphosphate synthase subunit 2	2	9.56E-06	580439

Transcript_368597	ubiquitin carboxyl-terminal hydrolase 14	2	1.00E-05	581896
Transcript_346637	nuclear migration protein nudC	2	1.01E-05	589717
Transcript_351605	26S proteasome non-ATPase regulatory subunit 10	3	1.02E-05	576864
Transcript_244261	acidic leucine-rich nuclear phosphoprotein 32 family member E	2	1.02E-05	100892466
Transcript_440816	tyrosine aminotransferase	2	1.02E-05	592114
Transcript_381701	rho-related BTB domain-containing protein 1	1	1.02E-05	575159
Transcript_445237	39S ribosomal protein S30, mitochondrial 28S ribosomal protein S30, mitochondrial	3	1.06E-05	591808
Transcript_298879	DNA-directed RNA polymerase III subunit RPC6	2	1.08E-05	580860
Transcript_275685	uncharacterized protein LOC587541	4	1.09E-05	587541
Transcript_381489	papilin	1	1.12E-05	584177
Transcript_362661	ribosome-recycling factor, mitochondrial	3	1.13E-05	587941
Transcript_179642	tetraspanin-5	1	1.14E-05	582219
Transcript_404610	uncharacterized protein F13E9.13, mitochondrial Membrane complex biogenesis protein, BtpA	3	1.14E-05	579795
Transcript_310943	tryptophan--tRNA ligase, cytoplasmic	2	1.16E-05	574927
Transcript_180218	proton-coupled amino acid transporter 1	4	1.20E-05	587558
Transcript_277419	protein SET	2	1.23E-05	583082
Transcript_316855	deleted in malignant brain tumors 1 protein galectin-3-binding protein pseudogene scavenger	1	1.25E-05	754160
Transcript_217175	mitochondrial import inner membrane translocase subunit Tim22	3	1.27E-05	592058
Transcript_271076	carbohydrate sulfotransferase 15	4	1.34E-05	582046
Transcript_434835	alpha-aminoacidic semialdehyde dehydrogenase	1	1.34E-05	588376
Transcript_412907	tubulin alpha-2/alpha-4 chain	2	1.35E-05	582621
Transcript_429645	N-acetylated-alpha-linked acidic dipeptidase 2-like	1	1.36E-05	583418
Transcript_235859	sucrase-isomaltase, intestinal	1	1.40E-05	588081
Transcript_267184	28S ribosomal protein S5, mitochondrial	3	1.43E-05	583862
Transcript_380459	cryptochrome-2	4	1.46E-05	583959
Transcript_453750	uncharacterized protein LOC581715 probable enoyl-CoA hydratase echA8-like probable enoyl-	4	1.49E-05	581715
Transcript_213782	nicalin-1	3	1.50E-05	587749
Transcript_323832	aminoacylase-1	1	1.70E-05	577570
Transcript_402336	mitochondrial ribonuclease P catalytic subunit mitochondrial ribonuclease P protein 3	3	1.71E-05	578934
Transcript_359571	LOW QUALITY PROTEIN: uncharacterized protein LOC577952	1	1.71E-05	577952
Transcript_189718	MYBBP1A	2	1.71E-05	583345
Transcript_388247	mitochondrial glutamate carrier 2	2	1.74E-05	753367
Transcript_369099	protein Abitram protein FAM206A-like protein Simiate	3	1.75E-05	757335
Transcript_305359	metabotropic glutamate receptor 1 extracellular calcium-sensing receptor-like	3	1.75E-05	577623
Transcript_456418	ficolin-2-like	1	1.80E-05	583514
Transcript_433359	probable serine/threonine-protein kinase drkD putative serine/threonine-protein kinase drkD	2	1.85E-05	577165

Transcript_360852	ribosomal RNA-processing protein 7 homolog A	3	1.88E-05	580493
Transcript_236563	protein FAM166B-like	5	1.92E-05	105439658
Transcript_322912	39S ribosomal protein L13, mitochondrial	3	2.04E-05	585375
Transcript_373532	putative helicase MOV-10	3	2.05E-05	583129
Transcript_374213	uncharacterized protein LOC763830	3	2.06E-05	763830
Transcript_442862	zinc finger CCCH domain-containing protein 15	2	2.07E-05	580460
Transcript_401581	protein canopy homolog 2	3	2.08E-05	588644
Transcript_453440	glutamate receptor 2	1	2.10E-05	591929
Transcript_343792	elongation factor 1-delta-like	3	2.16E-05	575168
Transcript_371946	uncharacterized protein LOC100889820	4	2.23E-05	100889820
Transcript_337768	coiled-coil domain-containing protein 58	3	2.23E-05	576818
Transcript_230454	exportin-5	3	2.31E-05	592021
Transcript_314891	periodic tryptophan protein 2 homolog	3	2.43E-05	752047
Transcript_321961	organic cation transporter protein	1	2.46E-05	582688
Transcript_299268	39S ribosomal protein L52, mitochondrial	3	2.49E-05	752505
Transcript_227249	cytochrome P450 2J6	1	2.49E-05	575697
Transcript_329073	uncharacterized protein LOC100889633	2	2.50E-05	100889633
Transcript_449172	transcription initiation factor IIA subunit 1	2	2.52E-05	100888038
Transcript_66007	cytospin-A	1	2.56E-05	583396
Transcript_423340	inverted formin-2	1	2.58E-05	579910
Transcript_423272	phe13-bombesin receptor	1	2.75E-05	100888815
Transcript_276375	uncharacterized protein LOC584281	1	2.75E-05	584281
Transcript_243879	carbonyl reductase [NADPH] 1	4	2.76E-05	574551
Transcript_310622	actin related protein 1	1	2.83E-05	373192
Transcript_380140	cardiolipin synthase (CMP-forming) probable cardiolipin synthase (CMP-forming)	2	2.86E-05	587370
Transcript_378334	DNA-directed RNA polymerase II subunit RPB7	3	2.88E-05	752151
Transcript_298921	development-specific protein LVN1.2	1	2.90E-05	100888941
Transcript_393283	LOW QUALITY PROTEIN: xanthine dehydrogenase/oxidase	1	3.15E-05	576712
Transcript_388184	serine/arginine repetitive matrix protein 1	1	3.16E-05	575766
Transcript_401245	uncharacterized protein LOC593760	4	3.16E-05	593760
Transcript_434004	hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	3	3.18E-05	582126
Transcript_384548	salivary glue protein Sgs-3	3	3.18E-05	100892638
Transcript_380262	cytochrome P450 4V2	4	3.20E-05	581875
Transcript_42693	40S ribosomal protein S13	2	3.25E-05	581196
Transcript_206502	nucleolar protein 56 NOP56 ribonucleoprotein homolog	2	3.29E-05	590067
Transcript_195549	sodium-dependent phosphate transporter 2	2	3.35E-05	582615

Transcript_331211	probable Na(+)/H(+) antiporter nhx-9	1	3.38E-05	591586
Transcript_372883	protein dispatched homolog 1-like	1	3.39E-05	580689
Transcript_308094	sodium-dependent dopamine transporter solute carrier family 6 (neurotransmitter transporter	1	3.48E-05	584179
Transcript_438519	degenerin deg-1	1	3.53E-05	100891272
Transcript_307696	ATP-binding cassette sub-family B member 8, mitochondrial	3	3.69E-05	754756
Transcript_370380	serine/threonine-protein kinase NLK serine/threonine-protein kinase NLK2	2	3.73E-05	574783
Transcript_402303	GTP 3',8-cyclase, mitochondrial cyclic pyranopterin monophosphate synthase, mitochondrial n	4	3.77E-05	578700
Transcript_340758	proteasome subunit alpha type-2	3	3.77E-05	579111
Transcript_423204	FOXA	1	3.80E-05	578584
Transcript_443748	pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2 pyridine nucleotide-d	4	3.86E-05	587519
Transcript_426155	mitotic apparatus protein p62	3	3.98E-05	105443132
Transcript_373050	dihydropteridine reductase	1	4.06E-05	575893
Transcript_268252	39S ribosomal protein L47, mitochondrial	3	4.15E-05	588415
Transcript_261599	elongation factor 1 alpha	2	4.40E-05	548620
Transcript_315154	peroxisomal membrane protein 11A	1	4.41E-05	576910
Transcript_254082	probable ATP-dependent RNA helicase DDX56	2	4.51E-05	585968
Transcript_394798	band 7 protein AGAP004871-like	1	4.55E-05	578433
Transcript_253869	uncharacterized protein LOC100889419 IgGfC-binding protein, N-terminal domain containing p	1	4.65E-05	100889419
Transcript_258821	transcription initiation factor TFIID subunit 10	2	4.67E-05	752563
Transcript_433800	proteasome subunit alpha type-7	2	4.80E-05	579458
Transcript_459696	MYNN	2	4.88E-05	100893972
Transcript_347359	ectonucleotide pyrophosphatase/phosphodiesterase family member 7-like	5	4.90E-05	577518
Transcript_355848	NACHT domain- and WD repeat-containing protein 1 NACHT and WD repeat domain-containing	1	4.97E-05	591208
Transcript_196171	peptidyl-prolyl cis-trans isomerase	2	5.02E-05	585216
Transcript_139365	deleted in malignant brain tumors 1 protein	1	5.10E-05	753862
Transcript_267269	39S ribosomal protein L23, mitochondrial	2	5.29E-05	587414
Transcript_219950	citrate synthase, mitochondrial	2	5.60E-05	590444
Transcript_223195	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	4	5.63E-05	591898
Transcript_230867	RNA N6-adenosine-methyltransferase mettl16 methyltransferase-like protein 16	3	5.67E-05	588854
Transcript_279744	eukaryotic translation initiation factor 4 gamma 3 eukaryotic translation initiation factor 4 gam	2	5.68E-05	588274
Transcript_330100	NRL/MAF	1	5.85E-05	581716
Transcript_254029	uncharacterized protein LOC105441448	1	6.12E-05	105441448
Transcript_431131	proteasome subunit beta type-7	3	6.38E-05	588252
Transcript_263253	E3 ubiquitin-protein ligase TRIM23	1	6.38E-05	591350
Transcript_364264	DNA polymerase epsilon subunit 4	2	6.53E-05	763808
Transcript_181686	patched domain-containing protein 3	2	6.55E-05	100888465

Transcript_203172	uncharacterized protein LOC577523 malate dehydrogenase-like	1	6.68E-05	577523
Transcript_427147	carbohydrate sulfotransferase 11	1	6.68E-05	589022
Transcript_414827	guanine nucleotide exchange factor MSS4	2	6.83E-05	591831
Transcript_197695	quinone oxidoreductase-like uncharacterized protein LOC764164 Alcohol dehydrogenase, C-te	2	7.08E-05	764164
Transcript_269277	ribosomal protein S14	2	7.19E-05	574895
Transcript_246683	PMS1 protein homolog 1	1	7.21E-05	592483
Transcript_447058	coiled-coil domain-containing protein 86 uncharacterized protein LOC100889012	3	7.35E-05	100889012
Transcript_428449	COX assembly mitochondrial protein homolog	3	7.46E-05	754298
Transcript_373487	leucine-rich repeat-containing protein 58	2	7.64E-05	592464
Transcript_297301	isthmin	2	8.01E-05	762678
Transcript_274172	60S ribosomal protein L31	2	8.02E-05	589085
Transcript_214012	RNA transcription, translation and transport factor protein UPF0568 protein C14orf166 homolo	3	8.11E-05	586176
Transcript_180063	endothelin-converting enzyme homolog	1	8.20E-05	594281
Transcript_335203	cyclin-dependent kinase 2	1	8.26E-05	585950
Transcript_436916	scavenger receptor cysteine-rich domain-containing group B protein	1	8.28E-05	577634
Transcript_168671	EEF1A1	2	8.38E-05	548620
Transcript_196792	hydroxyproline dehydrogenase	1	8.47E-05	576696
Transcript_437063	serine/threonine-protein kinase TBK1	3	8.56E-05	579073
Transcript_269134	octopamine receptor	2	8.60E-05	100893874
Transcript_280627	methylenetetrahydrofolate reductase	1	8.96E-05	589576
Transcript_317810	kin of IRRE-like protein 1	1	9.04E-05	762504
Transcript_387048	peptidyl-prolyl cis-trans isomerase-like 1	2	9.09E-05	575873
Transcript_316602	DNA mismatch repair protein Msh2 mutS homolog 2, colon cancer, nonpolyposis type 1	1	9.13E-05	589363
Transcript_263803	phosphate carrier protein, mitochondrial	2	9.29E-05	577743
Transcript_249042	thioredoxin-like protein 1	3	9.29E-05	581305
Transcript_323338	probable assembly chaperone of rpl4 UPF0661 TPR repeat-containing protein C16D10.01c	2	9.32E-05	100891594
Transcript_218894	40S ribosomal protein S15a ribosomal protein S24	2	9.49E-05	373469
Transcript_77032	cubilin	2	9.56E-05	580195
Transcript_214740	glycerophosphocholine phosphodiesterase GPCPD1	1	9.94E-05	594641
Transcript_381580	short-chain collagen C4	1	9.95E-05	100893425
Transcript_373705	tctex1 domain-containing protein 1	1	0.000100228	588988
Transcript_255002	protein giant	2	0.000100627	105444027
Transcript_328974	GRAM domain-containing protein 4	1	0.00010098	581215
Transcript_294422	persulfide dioxygenase ETHE1, mitochondrial	5	0.000102325	585574
Transcript_203149	DNA-directed RNA polymerases I, II, and III subunit RPABC1	3	0.00010449	578317
Transcript_360539	methionine adenosyltransferase	3	0.00010822	548618

Transcript_73952	aminoacyl tRNA synthase complex-interacting multifunctional protein 2	2	0.00010822	575132
Transcript_303046	U3 small nucleolar RNA-associated protein 14 homolog A	3	0.000111727	585850
Transcript_199821	probable ATP-dependent RNA helicase DDX47	3	0.000112486	581057
Transcript_175282	uncharacterized protein LOC105442054	4	0.000113657	105442054
Transcript_267731	39S ribosomal protein L12, mitochondrial	3	0.000120962	585458
Transcript_461577	deoxyribodipyrimidine photo-lyase	1	0.000123123	593941
Transcript_448396	receptor for egg jelly protein	1	0.000127512	576647
Transcript_88669	40S ribosomal protein S5	2	0.000129515	592668
Transcript_383623	histidine ammonia-lyase	1	0.000131478	583726
Transcript_247937	EGR1	1	0.000141967	100892559
Transcript_368914	protein CNPPD1	2	0.000154939	752566
Transcript_428975	RING finger protein 215	4	0.000155181	753231
Transcript_235182	programmed cell death protein 2	3	0.000155446	585086
Transcript_280475	major facilitator superfamily domain-containing protein 6	3	0.000157081	763022
Transcript_459174	notchless protein homolog 1	2	0.000161391	585438
Transcript_411220	RING-box protein 1	3	0.000167486	591601
Transcript_88201	40S ribosomal protein S4	2	0.000169885	583495
Transcript_339559	lysozyme 3	1	0.000170656	583337
Transcript_195407	xylulose kinase xylulokinase homolog (H. influenzae)	1	0.000170904	589304
Transcript_265718	sodium-dependent phosphate transport protein 2C	2	0.000171783	576137
Transcript_253116	dynein regulatory complex subunit 6 F-box/LRR-repeat protein 13	1	0.000175152	577951
Transcript_448836	tubulointerstitial nephritis antigen-like	1	0.000176097	576823
Transcript_215764	U6 snRNA-associated Sm-like protein LSm2	3	0.000186826	587779
Transcript_443991	oxidoreductase HTATIP2-like	3	0.000191678	592505
Transcript_276623	histone H4	2	0.000196637	752213
Transcript_360643	nucleoside diphosphate kinase B	3	0.000199818	594617
Transcript_345101	serine/threonine-protein kinase Nek6	1	0.00020157	100893147
Transcript_445434	28S ribosomal protein S17, mitochondrial	3	0.000201605	753889
Transcript_352645	arginine--tRNA ligase, cytoplasmic	3	0.000202136	575790
Transcript_199943	lens fiber major intrinsic protein	1	0.000202136	594743
Transcript_253163	venom phosphodiesterase 2	1	0.000202136	579858
Transcript_278701	NHP2-like protein 1	3	0.000206072	587294
Transcript_220262	uncharacterized protein LOC581634	2	0.000206087	581634
Transcript_314700	uncharacterized protein LOC587761	1	0.000207742	587761
Transcript_402975	eukaryotic initiation factor 4A-III	2	0.000209348	580266
Transcript_284772	TAF1A	2	0.000213915	105440467

Transcript_361334	chordin	1	0.000215196	580173
Transcript_457700	lengsin-like	2	0.000216409	591380
Transcript_300296	trimeric intracellular cation channel type 1B.1 trimeric intracellular cation channel type A	4	0.000227596	100890448
Transcript_338151	histone H3, embryonic	2	0.000227596	581030
Transcript_383403	mediator of RNA polymerase II transcription subunit 18	3	0.000232301	576519
Transcript_456392	R1a domain-containing protein 1	3	0.00023765	752632
Transcript_299206	39S ribosomal protein L49, mitochondrial	2	0.000241306	593029
Transcript_383531	natural resistance-associated macrophage protein 2	2	0.000251469	576440
Transcript_327352	macrophage mannose receptor 1	1	0.000256987	100893009
Transcript_172390	protein SSUH2 homolog	1	0.000257132	763611
Transcript_353965	uncharacterized protein LOC100892584	2	0.0002581	100892584
Transcript_454078	RNA-binding protein NOB1	2	0.000262544	575793
Transcript_443183	MYC	2	0.000262997	373385
Transcript_329842	SRA stem-loop-interacting RNA-binding protein, mitochondrial-like	3	0.000265293	754241
Transcript_464404	peroxiredoxin-1	2	0.000271849	590165
Transcript_380053	cholinesterase 1	1	0.000275228	591159
Transcript_462380	metalloproteinase inhibitor 3	3	0.000279283	100889149
Transcript_372078	potassium voltage-gated channel subfamily KQT member 4 potassium voltage-gated channel su	3	0.000280671	579971
Transcript_206791	uncharacterized protein LOC105442064 Death effector domain-containing protein	1	0.000288649	105442064
Transcript_86447	glyceraldehyde-3-phosphate dehydrogenase	2	0.000304165	578260
Transcript_392219	neuropeptide Y receptor type 2-like	3	0.000306609	100891742
Transcript_327467	chromosome transmission fidelity protein 8 homolog	3	0.000309435	763690
Transcript_308925	dnaJ homolog subfamily C member 2	2	0.000310386	583525
Transcript_202368	eukaryotic initiation factor 4a	2	0.000311754	575736
Transcript_166464	translation elongation factor 2	2	0.000315605	592801
Transcript_179487	uncharacterized protein LOC580673	4	0.000318961	580673
Transcript_134695	angiotensin-converting enzyme 2	1	0.000330507	580220
Transcript_280569	TNF receptor-associated factor 6-A	3	0.000332355	585060
Transcript_255311	WD repeat-containing protein 37	1	0.000344097	581583
Transcript_461472	growth hormone secretagogue receptor type 1 neuropeptides capa receptor growth hormone	2	0.000351928	592924
Transcript_345624	40S ribosomal protein S9	2	0.000351928	586110
Transcript_230874	ubiquitin	2	0.000355053	584839
Transcript_25798	ATP synthase F(0) complex subunit C2, mitochondrial ATP synthase lipid-binding protein, mitoc	3	0.000360871	583818
Transcript_397056	coatamer subunit epsilon	3	0.000367007	582090
Transcript_333839	G2/mitotic-specific cyclin-B3	5	0.000367007	591240
Transcript_416611	zinc transporter ZIP12	1	0.000368191	587958

Transcript_196818	UDP-glucuronosyltransferase 2C1 UDP-glucuronosyltransferase 1-2 UDP-glucuronosyltransferase	1	0.000369716	589187
Transcript_280665	uncharacterized protein LOC100890259	1	0.000376789	100890259
Transcript_249751	putative Dol-P-Glc:Glc(2)Man(9)GlcNAc(2)-PP-Dol alpha-1,2-glucosyltransferase	3	0.000383409	590617
Transcript_483697	ras-related protein ORAB-1	2	0.000384483	373418
Transcript_323044	pleiotropic regulator 1	2	0.000388456	756406
Transcript_189980	uncharacterized protein LOC100890349 L-idonate 5-dehydrogenase	1	0.000406171	100890349
Transcript_301658	nucleolar protein 10	2	0.000408603	590723
Transcript_459372	fibrillin-3 bypass of stop codon protein 1	4	0.000410913	591161
Transcript_199327	delta-aminolevulinic acid dehydratase	2	0.00041335	577020
Transcript_183069	glutamate receptor 1	2	0.000415045	587837
Transcript_192833	5-oxoprolinase 5-oxoprolinase (ATP-hydrolysing)	1	0.000427737	589767
Transcript_373239	ras-related protein Rap-2c	2	0.000440545	753090
Transcript_386406	WD repeat-containing protein 43	2	0.000451267	592550
Transcript_238124	protein MAK16 homolog A	2	0.000460165	586606
Transcript_233725	uncharacterized protein C2orf50	1	0.000494308	578348
Transcript_300378	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, mitochondrial	3	0.000520562	581340
Transcript_421581	pre-rRNA-processing protein TSR2 homolog	2	0.000525637	592405
Transcript_236174	40S ribosomal protein S3	2	0.000532436	593744
Transcript_249550	sorbitol dehydrogenase	1	0.000534208	585570
Transcript_234548	angiopoietin-4-like	1	0.0005769	100891514
Transcript_128686	pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 pre-rRNA processing protein FTSJ3	3	0.000590448	582089
Transcript_333875	uncharacterized protein LOC578017	5	0.000597208	578017
Transcript_208042	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	1	0.000631501	586329
Transcript_257273	methylsterol monooxygenase 1	1	0.000641983	100891893
Transcript_308851	alcohol dehydrogenase class-3	1	0.000649203	579220
Transcript_385086	pre-piRNA 3'-exonuclease trimmer poly(A)-specific ribonuclease PARN-like domain-containing	2	0.000665071	100891016
Transcript_408947	phosphopantothienoylcysteine decarboxylase	3	0.000674726	584017
Transcript_273618	SHC SH2 domain-binding protein 1	4	0.000680453	575406
Transcript_418431	ketimine reductase mu-crystallin	1	0.000684468	579068
Transcript_214978	basic leucine zipper and W2 domain-containing protein 1	2	0.000692153	587479
Transcript_432419	beta-lactamase domain-containing protein 2	1	0.000718546	575771
Transcript_196327	creatine kinase, flagellar	5	0.00071996	580751
Transcript_221788	NADPH oxidase	1	0.000721382	757329
Transcript_329183	E3 ubiquitin-protein ligase UHRF1 histone-lysine N-methyltransferase, H3 lysine-9 specific SUV	1	0.000725484	756912
Transcript_346536	cAMP-dependent protein kinase catalytic subunit 1 catalytic subunit of cAMP-dependent histon	2	0.000751818	589947
Transcript_366071	N-acetylgalactosamine-6-sulfatase-like	1	0.000766197	579130

Transcript_235911	phospholipase B1, membrane-associated	1	0.000775871	100890912
Transcript_403482	aldo-keto reductase family 1 member A1 alcohol dehydrogenase	4	0.000784233	576680
Transcript_334842	uncharacterized protein LOC580196	2	0.000786461	580196
Transcript_235072	uncharacterized protein LOC579112	4	0.000788949	579112
Transcript_82280	calmodulin	2	0.000790274	575365
Transcript_424005	soma ferritin	3	0.000806	591499
Transcript_419016	dnaJ homolog subfamily C member 5 cysteine string protein	2	0.000807136	577697
Transcript_12298	40S ribosomal protein S23	2	0.000841834	590530
Transcript_368000	syntenin-1	2	0.000847174	578747
Transcript_448298	protein Wnt-7b	1	0.000850909	581981
Transcript_374203	protein Asterix	3	0.000866756	592477
Transcript_121057	V-type proton ATPase 16 kDa proteolipid subunit	2	0.000903696	593221
Transcript_276903	ERI1 exoribonuclease 2	1	0.00096432	585927
Transcript_388827	ADP/ATP translocase 3	2	0.000969427	575225
Transcript_240937	uracil phosphoribosyltransferase homolog	2	0.000983598	575128
Transcript_444850	probable RNA-binding protein EIF1AD putative RNA-binding protein EIF1AD	3	0.000991161	578771
Transcript_427937	DNA repair protein XRCC3	3	0.00101429	763443
Transcript_286704	extended synaptotagmin-2	5	0.001044619	579674
Transcript_263515	polycystic kidney disease protein 1-like 2	1	0.001052967	579144
Transcript_357605	glutathione S-transferase P	3	0.001055612	580662
Transcript_438353	EMX1	4	0.001088813	577702
Transcript_264220	ADP-ribosylation factor 1 ADP-ribosylation factor-like	3	0.001110619	586151
Transcript_208170	uncharacterized protein LOC105441928	1	0.001110863	105441928
Transcript_383458	probable 60S ribosomal protein L37-A	2	0.001114113	591582
Transcript_51640	RCC1 and BTB domain-containing protein 1 ultraviolet-B receptor UVR8 probable E3 ubiquitin-	4	0.001129851	577290
Transcript_305797	WD repeat-containing protein 31	1	0.001163089	585021
Transcript_240632	calpain small subunit 1	4	0.001196235	100889224
Transcript_171991	protein cornichon homolog 1	3	0.00119957	582532
Transcript_398758	serine/threonine-protein phosphatase PGAM5, mitochondrial	2	0.001214001	588383
Transcript_353555	caspase-6	1	0.001318326	584221
Transcript_188732	tetratricopeptide repeat protein 32	2	0.001350098	588488
Transcript_264574	conserved oligomeric Golgi complex subunit 2 component of oligomeric golgi complex 2	3	0.001377664	589392
Transcript_392565	methionyl-tRNA formyltransferase, mitochondrial	2	0.001379209	586344
Transcript_235778	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 7 TM2 domain-containing protein	1	0.001456409	583563
Transcript_463187	mitochondrial import inner membrane translocase subunit Tim10 B	2	0.001462773	574660
Transcript_359454	dynein light chain LC6, flagellar outer arm	4	0.001472937	591043

Transcript_402965	PRELI domain containing protein 3B protein slowmo homolog 2	2	0.001481224	100889391
Transcript_434653	pre-rRNA-processing protein TSR1 homolog TSR1, 20S rRNA accumulation, homolog	2	0.001486958	594000
Transcript_323407	uncharacterized protein LOC763845	1	0.001498958	763845
Transcript_456790	acyloxyacyl hydrolase	1	0.001508263	592185
Transcript_309275	uncharacterized protein LOC100889927	1	0.001508866	100889927
Transcript_350913	lysozyme	4	0.001579517	587263
Transcript_291331	matrix metalloproteinase-24	2	0.001579939	577128
Transcript_228378	ADP-ribosylation factor-like protein 6	2	0.001582577	591507
Transcript_383671	anoctamin-8	1	0.001595851	588981
Transcript_456874	coiled-coil domain-containing protein 51	2	0.00167281	585678
Transcript_328102	protein Aster-B GRAM domain-containing protein 1B	4	0.001674503	754516
Transcript_173387	HNF4G	1	0.001696184	574894
Transcript_453741	uncharacterized protein LOC100892807	3	0.001833911	100892807
Transcript_396224	sodium/glucose cotransporter 4	1	0.001869933	593500
Transcript_184289	F-box/LRR-repeat protein 7	1	0.001893942	580713
Transcript_435724	coiled-coil domain-containing protein 151	5	0.001915415	100893724
Transcript_278188	leucine-rich repeat-containing protein 15	1	0.001944018	100893380
Transcript_228502	S-crystallin SL11	1	0.001945235	586571
Transcript_430758	uncharacterized protein LOC100888279	1	0.001948734	100888279
Transcript_415734	peptidase M20 domain-containing protein 2	4	0.001958887	584225
Transcript_292151	uncharacterized protein LOC105437474	1	0.002019107	105437474
Transcript_359398	cytochrome P450 26A1 cytochrome P450 26B1	1	0.002045033	763716
Transcript_417667	ER membrane protein complex subunit 8 ER membrane protein complex subunit 8 pseudogene	3	0.002058001	582477
Transcript_363862	RNA-binding protein cabeza	1	0.00208612	105447104
Transcript_257591	fibrillin-2	1	0.002112952	581033
Transcript_224730	cytochrome c oxidase subunit 5B, mitochondrial	3	0.002126058	581274
Transcript_456276	heparan sulfate glucosamine 3-O-sulfotransferase 1	1	0.002149764	764585
Transcript_290553	isoamyl acetate-hydrolyzing esterase 1 homolog	4	0.002263181	591412
Transcript_324078	protein PBDC1 UPF0368 protein Cxorf26-like	2	0.00230034	577502
Transcript_236625	CDX1	1	0.002327014	584191
Transcript_309101	uncharacterized protein LOC105443655	3	0.002403175	105443655
Transcript_350196	ATP-binding cassette sub-family F member 2 ATP-binding cassette, sub-family F (GCN20), mem	2	0.002443557	581859
Transcript_204615	U6 snRNA-associated Sm-like protein LSM7	3	0.002487358	594039
Transcript_284394	EF-hand calcium-binding domain-containing protein 12	1	0.002516391	763537
Transcript_229121	LOW QUALITY PROTEIN: MMP37-like protein, mitochondrial MMP37-like protein, mitochondrial	2	0.002561667	575960
Transcript_310649	receptor-type guanylate cyclase gcy-8 insulin-like growth factor 1 receptor	1	0.002569395	591965

Transcript_239164	3-hydroxyanthranilate 3,4-dioxygenase	1	0.002593445	582154
Transcript_234886	multidrug resistance-associated protein 4 ATP-binding cassette, sub-family C (CFTR/MRP), mem	5	0.002593978	591982
Transcript_326960	uncharacterized protein LOC100891910	1	0.002627634	100891910
Transcript_186728	methylglutaconyl-CoA hydratase, mitochondrial	1	0.002651092	577505
Transcript_189831	L-gulonolactone oxidase	5	0.002653064	764246
Transcript_214947	calcium load-activated calcium channel transmembrane and coiled-coil domain-containing prot	3	0.002669245	100892898
Transcript_444322	tubulin beta-4B chain	5	0.002730604	593362
Transcript_309473	autocrine proliferation repressor protein A	1	0.002840025	100889791
Transcript_254514	14-3-3 family protein artA 14-3-3 protein 3	2	0.002856679	581376
Transcript_187684	bcl-2 homologous antagonist/killer	2	0.002938261	588418
Transcript_54760	testis-specific serine/threonine-protein kinase 4-like	5	0.00297144	575157
Transcript_304049	uncharacterized aarF domain-containing protein kinase 1 putative aarF domain-containing prot	2	0.003065219	574821
Transcript_363577	uncharacterized protein LOC105438509	3	0.003084148	105438509
Transcript_340557	small nuclear ribonucleoprotein polypeptide E-like	3	0.003114499	580958
Transcript_182361	rho GTPase-activating protein 25	2	0.00313536	582939
Transcript_204566	ruvB-like 1	2	0.003144896	577255
Transcript_354492	presenilins-associated rhomboid-like protein, mitochondrial	2	0.003374583	576709
Transcript_374584	28S ribosomal protein S34, mitochondrial	2	0.003395751	753857
Transcript_208329	univin	3	0.003400545	373488
Transcript_243976	S-methylmethionine--homocysteine S-methyltransferase BHMT2-like	1	0.00340357	582542
Transcript_343639	glycine-rich cell wall structural protein 1 glycine-rich protein DOT1	2	0.003455777	764696
Transcript_236992	cyclic nucleotide-gated cation channel alpha-3	3	0.003662216	576815
Transcript_326935	deleted in malignant brain tumors 1 protein-like neurotrypsin-like	1	0.003695293	762897
Transcript_445886	neurotrypsin	1	0.003720023	578211
Transcript_270797	uncharacterized protein LOC575472	1	0.003755055	575472
Transcript_456555	scavenger receptor cysteine-rich protein type 12	1	0.003772405	373431
Transcript_448686	fibrinogen C domain-containing protein 1-like	1	0.003887687	105440826
Transcript_450213	thioredoxin domain-containing protein 5	2	0.004022943	764720
Transcript_243778	UDP-glucuronosyltransferase 2C1	1	0.004132616	592958
Transcript_179967	condensin complex subunit 3-like	1	0.004145511	105447056
Transcript_187613	solute carrier family 28 member 3	1	0.004382769	574602
Transcript_280373	adenosylhomocysteinase	1	0.004452691	574714
Transcript_317804	uncharacterized protein LOC100891690	3	0.004527764	100891690
Transcript_438092	ATP-binding cassette, sub-family G (WHITE), member 2	1	0.004755746	578540
Transcript_356568	cystathionine gamma-lyase putative cystathionine gamma-lyase 2	2	0.0051019	762952
Transcript_182233	nose resistant to fluoxetine protein 6	1	0.005139831	587932

Transcript_438569	acid-sensing ion channel 1A	1	0.005184244	575477
Transcript_314048	transmembrane 6 superfamily member 1	4	0.005222331	588706
Transcript_376909	5'-nucleotidase	1	0.005354264	753743
Transcript_368980	fumarylacetoacetate hydrolase domain-containing protein 2	5	0.005436549	763463
Transcript_271521	fos-related antigen 1	1	0.0054842	579838
Transcript_28806	queuine tRNA-ribosyltransferase catalytic subunit 1-like	2	0.00553486	579235
Transcript_319918	uncharacterized protein LOC100888641	1	0.005688136	100888641
Transcript_395198	synaptotagmin-14 synaptotagmin-16	5	0.005940282	577619
Transcript_330815	fibronectin-like	3	0.005999686	105447587
Transcript_271208	glycine-rich cell wall structural protein-like	4	0.006002727	105447344
Transcript_200340	uncharacterized protein YER152C	4	0.006272248	753534
Transcript_269278	HES4	1	0.006281806	592057
Transcript_443316	balbiani ring protein 3 prestalk protein whey acidic protein-like	1	0.006407029	755393
Transcript_74981	DNA-directed RNA polymerases I, II, and III subunit RPABC3	2	0.006545429	591688
Transcript_308440	dimethylaniline monooxygenase [N-oxide-forming] 5	1	0.006648833	580981
Transcript_190979	leucine-rich repeat-containing protein 69	1	0.006656512	579382
Transcript_326137	LOW QUALITY PROTEIN: tRNA (adenine(37)-N6)-methyltransferase nef-associated protein 1	3	0.006798408	577363
Transcript_462766	sodium-dependent multivitamin transporter	2	0.006889503	578787
Transcript_234973	nitric oxide-associated protein 1	2	0.006984558	576629
Transcript_437119	amassin-3	3	0.007112091	580528
Transcript_201140	ficolin-1-like	1	0.007272042	587736
Transcript_299780	rRNA methyltransferase 2, mitochondrial	3	0.00755268	582250
Transcript_315513	sushi domain-containing protein 2	1	0.007619095	580458
Transcript_443412	E3 ubiquitin-protein ligase MARCH8	3	0.007636877	579071
Transcript_282963	acetoacetyl-CoA synthetase	3	0.007722755	590598
Transcript_426847	retinol dehydrogenase 8	2	0.007781435	574716
Transcript_341560	cytochrome b-c1 complex subunit 6, mitochondrial	3	0.007857858	590393
Transcript_231242	ATP-citrate synthase	1	0.008053833	594785
Transcript_392370	methyltransferase-like protein 22	1	0.008061862	100894107
Transcript_50022	60S ribosomal protein L30	2	0.00815734	577852
Transcript_219767	lactase-phlorizin hydrolase	1	0.008398588	581938
Transcript_268430	ZNF260	4	0.008456303	100892543
Transcript_198022	P-selectin	2	0.008474676	105437801
Transcript_433401	proteasome assembly chaperone 3	2	0.008654302	100892637
Transcript_230273	dynein heavy chain 8, axonemal dynein, axonemal, heavy chain 8	1	0.008769573	763294
Transcript_402513	acidic phospholipase A2 basic phospholipase A2 nigroxin A	1	0.00888625	757121

Transcript_326493	sodium-independent sulfate anion transporter	1	0.008989487	574650
Transcript_388333	ribonuclease H2 subunit C	3	0.009211094	752797
Transcript_462732	nesprin-1	5	0.009332795	105437706
Transcript_193119	titin muscle M-line assembly protein unc-89 putative titin-like	3	0.00939858	590007
Transcript_210888	diamine acetyltransferase 2	3	0.009551632	100893060
Transcript_440549	uncharacterized protein LOC577038	1	0.010145783	577038
Transcript_48454	40S ribosomal protein S16	2	0.010706301	577040
Transcript_459460	THAP6	3	0.010762146	577120
Transcript_336905	uncharacterized protein LOC100888517	1	0.010835345	100888517
Transcript_437026	uncharacterized protein K02A2.6-like	5	0.010979249	105444440
Transcript_449725	calcineurin B homologous protein 1	2	0.010979249	576455
Transcript_354357	APOBEC1 complementation factor	1	0.011175702	575684
Transcript_258396	uncharacterized protein LOC588928	1	0.011267375	588928
Transcript_453256	WD repeat-containing protein 86	3	0.01200482	100888294
Transcript_226806	cytochrome P450 3A24	4	0.012022093	576854
Transcript_413396	3-ketoacyl-CoA thiolase A, peroxisomal	1	0.012424432	587557
Transcript_280723	scavenger receptor cysteine-rich protein	1	0.012532041	373211
Transcript_61404	dynein heavy chain 5, axonemal	1	0.012843572	577371
Transcript_13256	protein disulfide-isomerase A5	5	0.013269666	576717
Transcript_292279	dnaJ homolog subfamily C member 28	1	0.013626876	587875
Transcript_256585	microfibril-associated glycoprotein 4	1	0.013830912	582445
Transcript_453252	N-acetyltransferase 9-like protein	2	0.014015317	586164
Transcript_374389	alpha-(1,3)-fucosyltransferase 6	4	0.014272136	579774
Transcript_265355	protein boule-like bromodomain-containing protein 4-like	1	0.014681263	100892519
Transcript_297498	EH domain-containing protein 1 EH domain-containing protein 3-like	2	0.014744428	587455
Transcript_204631	tyrosine-protein kinase receptor Tie-2-like	1	0.014745656	105439696
Transcript_352756	protein TFG	3	0.014753533	594769
Transcript_400118	uncharacterized protein LOC100893690	1	0.015012477	100893690
Transcript_451319	40S ribosomal protein S12	2	0.015117118	590740
Transcript_440408	N-fatty-acyl-amino acid synthase/hydrolase PM20D1 probable carboxypeptidase PM20D1 putative	4	0.015510861	579513
Transcript_285315	N-alpha-acetyltransferase 40	2	0.015578148	577667
Transcript_361820	L-threonine 3-dehydrogenase, mitochondrial inactive L-threonine 3-dehydrogenase, mitochond	2	0.015611387	584440
Transcript_189682	peroxisomal carnitine O-octanoyltransferase	1	0.015664898	585404
Transcript_214210	late histone H2A.L3	3	0.015709704	373348
Transcript_367907	uncharacterized protein LOC586472 Small GTPase superfamily domain containing protein	1	0.015758585	586472
Transcript_393644	SAFB-like transcription modulator	2	0.01587077	585734

Transcript_257884	uncharacterized protein LOC583434 urease	1	0.016315729	583434
Transcript_195199	arylsulfatase	1	0.016536437	582391
Transcript_257979	echinoderm microtubule-associated protein-like 4 uncharacterized protein LOC581284	1	0.016740806	581284
Transcript_321307	mitochondrial fission regulator 2 mitochondrial fission regulator 1	3	0.016869408	764790
Transcript_240999	cyclin-dependent kinases regulatory subunit	1	0.017248255	100891492
Transcript_2061	mitochondrial ATP synthase alpha subunit precursor	2	0.018413908	373382
Transcript_355725	protein disulfide-isomerase A3	2	0.018926929	577673
Transcript_258178	zinc finger protein 474-like	5	0.01959868	100888783
Transcript_225983	histamine N-methyltransferase	4	0.019730461	582038
Transcript_388758	uncharacterized protein LOC591506 UPF0394 inner membrane protein yeeE-like	1	0.020558406	591506
Transcript_252605	cation-dependent mannose-6-phosphate receptor-like	1	0.020779714	105438545
Transcript_307974	malignant fibrous histiocytoma-amplified sequence 1 homolog	3	0.020863101	100888805
Transcript_325168	zonadhesin-like	1	0.021381996	105438765
Transcript_269460	probable D-lactate dehydrogenase, mitochondrial lactate dehydrogenase D	4	0.021486102	591812
Transcript_256749	peptidyl-prolyl cis-trans isomerase G serine/arginine repetitive matrix protein 2-like	1	0.021654179	100890356
Transcript_258900	KRP170	4	0.021974774	373241
Transcript_386762	uncharacterized protein LOC100892326	4	0.022071669	100892326
Transcript_392136	somatostatin receptor type 2	1	0.022255228	100889243
Transcript_405707	ADP-ribosyl cyclase ADP-ribosyl cyclase beta	1	0.022643114	580868
Transcript_280991	phytanoyl-CoA dioxygenase domain-containing protein 1	1	0.022977014	753147
Transcript_314947	microfibril-associated glycoprotein 4-like	3	0.022996409	581168
Transcript_396061	putative ISG12 protein	1	0.023872748	403119
Transcript_412518	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	1	0.025975248	586141
Transcript_246157	LOW QUALITY PROTEIN: tubulin beta chain	5	0.026130789	594231
Transcript_351435	medium-chain acyl-CoA ligase ACSF2, mitochondrial-like acyl-CoA synthetase family member 2,	1	0.02642635	593582
Transcript_200945	cathepsin L1	3	0.027167837	575203
Transcript_308628	protein PRY1 golgi-associated plant pathogenesis-related protein 1	1	0.027167837	100893059
Transcript_398823	uncharacterized protein LOC589927 CUB domain-containing protein	1	0.027751362	589927
Transcript_343503	LOW QUALITY PROTEIN: very early blastula protein 4 very early blastula protein 4	5	0.02946305	373489
Transcript_194733	uncharacterized protein LOC579958	1	0.029757117	579958
Transcript_241860	denticleless protein homolog	4	0.030087247	584715
Transcript_265286	tumor suppressor candidate 2	2	0.030240058	594794
Transcript_254071	actin, cytoskeletal 3B actin, cytoskeletal 3	3	0.03034686	100890099
Transcript_459535	transmembrane protein 187	4	0.031438231	100887935
Transcript_193614	somatostatin receptor type 5	2	0.031787754	105444813
Transcript_386066	zinc finger protein 236	2	0.031981685	100890022

Transcript_407578	solute carrier family 23 member 1	1	0.032288234	581718
Transcript_373383	uncharacterized protein LOC581986 proteinase T	1	0.032789184	581986
Transcript_284740	uncharacterized protein C16orf96 homolog uncharacterized protein C16orf96 uncharacterized	5	0.033005953	755388
Transcript_57336	profilin spCoel1	3	0.034328683	373409
Transcript_299519	uncharacterized protein LOC105447398	2	0.034769137	105447398
Transcript_289174	annexin A7	3	0.035301747	764615
Transcript_453447	NAD kinase	3	0.035404269	584340
Transcript_346874	alpha-tocopherol transfer protein-like	3	0.035599419	575290
Transcript_324882	uncharacterized protein LOC105440703	3	0.035609898	105440703
Transcript_375307	uncharacterized protein LOC100888794	1	0.037345332	100888794
Transcript_285525	uncharacterized protein LOC100891603	3	0.037526216	100891603
Transcript_315280	meiosis 1 arrest protein	1	0.037581022	100893539
Transcript_54635	uncharacterized protein LOC100891675	3	0.03765683	100891675
Transcript_359165	calponin homology domain-containing protein DDB_G0272472 intracellular protein transport p	1	0.037852399	100890558
Transcript_281352	centrosomal protein of 290 kDa-like	2	0.038176421	105442844
Transcript_117530	D(2) dopamine receptor A-like	1	0.038798225	105439410
Transcript_82652	mitochondrial ribosome-associated GTPase 1	4	0.039178574	588789
Transcript_427415	paraneoplastic antigen Ma3-like	2	0.039625395	105447116
Transcript_345735	DLX5	3	0.04058574	593496
Transcript_218552	cytosolic beta-glucosidase	1	0.04098007	589416
Transcript_322346	triple QxxK/R motif-containing protein-like acyl-CoA synthetase family member 3, mitochondria	4	0.041155658	105440874
Transcript_300712	protein DDI1 homolog 2	2	0.04169834	590177
Transcript_67216	cGMP-dependent protein kinase 1	2	0.042140028	589462
Transcript_390895	vesicular inhibitory amino acid transporter-like	1	0.043654839	755450
Transcript_366842	bindin	5	0.044607927	373276
Transcript_207308	uncharacterized protein LOC587864	1	0.045911275	587864
Transcript_177363	LOW QUALITY PROTEIN: aromatic-L-amino-acid decarboxylase	1	0.04611209	577767
Transcript_371808	dexamethasone-induced Ras-related protein 1	3	0.04725451	578089
Transcript_206242	uncharacterized protein LOC756858 Solute-binding protein family 3/N-terminal domain of Mltf	1	0.047665727	756858
Transcript_64977	40S ribosomal protein S15	3	0.048248049	574998
Transcript_364074	LOW QUALITY PROTEIN: zinc finger protein 708-like	2	0.048728883	593726

Table S19. Functional analysis of coexpressed clusters

Cluster	Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
1	Biological Process	GO:0044699~single-organism process	23	7.565789474	2.70E-04	591943, 591159, 592958, 755450, 100891492, 577570, 757121, 581938, 105439410, 577952, 580868,	28	81	162	1.642857143	0.086471814	0.090428842	0.090428842
	Biological Process	GO:0044763~single-organism cellular process	20	6.578947368	0.006625553	591943, 591159, 592958, 755450, 100891492, 577570, 757121, 105439410, 577952, 580868, 1008892,	28	76	162	1.522556391	0.892142638	1	1
	Biological Process	GO:0005975~carbohydrate metabolic process	4	1.315789474	0.030874466	586329, 586832, 581938, 583563,	28	5	162	4.628571429	0.999987273	1	1
	Biological Process	GO:0044710~single-organism metabolic process	9	2.960526316	0.050405274	100891893, 592958, 586329, 574714, 577570, 757121, 581938, 583563, 100891910	28	27	162	1.928571429	0.99999997	1	1
	Biological Process	GO:0044707~single-multicellular organism process	4	1.315789474	0.058741299	591159, 373360, 580173, 105439410	28	6	162	3.857142857	0.999999998	1	1
	Biological Process	GO:0098609~cell-cell adhesion	3	0.986842105	0.072334369	591943, 591159, 105440441	28	3	162	5.785714286	1	1	1
	Biological Process	GO:006082~organic acid metabolic process	5	1.644736842	0.088248913	100891893, 592958, 574714, 577570, 100891910	28	11	162	2.62987013	1	1	1
	Biological Process	GO:0032501~multicellular organismal process	4	1.315789474	0.091301958	591159, 373360, 580173, 105439410	28	7	162	3.306122449	1	1	1
	Biological Process	GO:0022610~biological adhesion	4	1.315789474	0.091301958	591943, 591159, 576823, 105440441	28	7	162	3.306122449	1	1	1
	Biological Process	GO:0007155~cell adhesion	4	1.315789474	0.091301958	591943, 591159, 576823, 105440441	28	7	162	3.306122449	1	1	1
	Cellular Component	GO:0016020~membrane	28	9.210526316	3.25E-08	591159, 373211, 373431, 755450, 585092, 578540, 100893380, 105439410, 592585, 105437474, 5769	38	61	183	2.210526316	2.18E-06	1.25E-06	1.21E-06
	Cellular Component	GO:0031224~intrinsic component of membrane	25	8.223684211	3.73E-08	591159, 755450, 578540, 100893380, 105439410, 592585, 105437474, 576910, 582219, 586832, 1054	38	49	183	2.457035446	2.50E-06	1.25E-06	1.21E-06
	Cellular Component	GO:0016021~integral component of membrane	24	7.894736842	1.79E-07	591943, 586672, 591159, 592958, 755450, 578540, 100893380, 100888815, 105439410, 105437474, 5	38	48	183	2.407894737	1.20E-05	3.99E-06	3.87E-06
	Cellular Component	GO:0044425~membrane part	25	8.223684211	5.07E-07	591159, 755450, 578540, 100893380, 105439410, 592585, 105437474, 576910, 582219, 586832, 1054	38	54	183	2.229532164	3.40E-05	8.49E-06	8.24E-06
	Cellular Component	GO:0071944~cell periphery	6	1.973684211	0.017738484	580868, 100889243, 591159, 582219, 105440441, 589852	38	9	183	3.210526316	0.698548349	0.198079733	0.192166905
	Cellular Component	GO:005886~plasma membrane	6	1.973684211	0.017738484	580868, 100889243, 591159, 582219, 105440441, 589852	38	9	183	3.210526316	0.698548349	0.198079733	0.192166905
	Molecular Function	GO:0060089~molecular transducer activity	8	2.631578947	0.002391091	100889243, 591159, 576823, 373431, 373211, 585092, 105439410, 100888815	46	10	183	3.182608696	0.318209368	0.191287272	0.191287272
	Molecular Function	GO:0004872~receptor activity	8	2.631578947	0.002391091	100889243, 591159, 576823, 373431, 373211, 585092, 105439410, 100888815	46	10	183	3.182608696	0.318209368	0.191287272	0.191287272
	Molecular Function	GO:0038024~cargo receptor activity	4	1.315789474	0.046606505	576823, 373431, 373211, 585092	46	4	183	3.97826087	0.999517442	1	1
	Molecular Function	GO:0005044~scavenger receptor activity	4	1.315789474	0.046606505	576823, 373431, 373211, 585092	46	4	183	3.97826087	0.999517442	1	1
	Molecular Function	GO:0043167~ion binding	12	3.947368421	0.060239568	591943, 575697, 100891893, 373360, 577570, 757121, 585092, 580652, 105440441, 592971, 592585,	46	29	183	1.646176912	0.999951834	1	1
	Molecular Function	GO:0005509~calcium ion binding	5	1.644736842	0.063060918	591943, 373360, 577121, 105440441, 592971	46	7	183	2.841614907	0.999970227	1	1
	Molecular Function	GO:0003824~catalytic activity	27	8.881578947	0.067218842	591159, 577570, 585092, 578540, 577198, 592585, 574714, 585404, 373360, 580652, 586832, 588773	46	86	183	1.248988878	0.999985386	1	1
	Molecular Function	GO:0016787~hydrolase activity	14	4.605263158	0.07561082	591159, 577570, 757121, 578540, 581938, 592585, 580868, 576823, 574714, 373360, 583337, 580652	46	37	183	1.505287897	0.999996558	1	1
	Molecular Function	GO:0043169~cation binding	11	3.618421053	0.086149331	591943, 575697, 100891893, 373360, 577570, 757121, 585092, 580652, 105440441, 592971, 592585	46	27	183	1.620772947	0.999999945	1	1
	Molecular Function	GO:0046872~metal ion binding	11	3.618421053	0.086149331	591943, 575697, 100891893, 373360, 577570, 757121, 585092, 580652, 105440441, 592971, 592585	46	27	183	1.620772947	0.999999945	1	1
	Molecular Function	GO:0016788~hydrolase activity, acting on ester bonds	4	1.315789474	0.096329578	591159, 577121, 580652, 580300	46	5	183	3.182608696	0.999999908	1	1
	Molecular Function	GO:0008237~metallopeptidase activity	4	1.315789474	0.096329578	373360, 577570, 588773, 592585	46	5	183	3.182608696	0.999999908	1	1
	Biological Process	GO:1901566~organonitrogen compound biosynthetic process	23	7.324840764	9.44E-04	593029, 593744, 575080, 591935, 588945, 577040, 762952, 591341, 593861, 577020, 591498, 590740	58	38	162	1.690562613	0.378755347	0.475805574	0.475805574
	Biological Process	GO:0044271~cellular nitrogen compound biosynthetic process	26	8.280254777	0.006317447	752563, 588945, 591935, 577255, 591498, 590740, 574895, 575225, 584839, 581865, 100892475, 373	58	48	162	1.512931034	0.812649242	0.835996592	0.835996592
	Biological Process	GO:1901564~organonitrogen compound metabolic process	23	7.324840764	0.00631878	593029, 593744, 575080, 591935, 588945, 577040, 762952, 591341, 593861, 577020, 591498, 590740	58	42	162	1.52955665	0.959024032	1	1
	Biological Process	GO:0044249~cellular biosynthetic process	28	8.917197452	0.013615712	752563, 754268, 588945, 591935, 577255, 591498, 590740, 574895, 575225, 584839, 581865, 100892	58	57	162	1.372050817	0.999001708	1	1
	Biological Process	GO:0043043~peptide biosynthetic process	16	5.095541401	0.014924636	593029, 593744, 575080, 577040, 591341, 593861, 591498, 590740, 373469, 577852, 574895, 575225	58	27	162	1.655172414	0.999488781	1	1
	Biological Process	GO:0006412~translation	16	5.095541401	0.014924636	593029, 593744, 575080, 577040, 591341, 593861, 591498, 590740, 373469, 577852, 574895, 575225	58	27	162	1.655172414	0.999488781	1	1
	Biological Process	GO:0043604~amide biosynthetic process	16	5.095541401	0.014924636	593029, 593744, 575080, 577040, 591341, 593861, 591498, 590740, 373469, 577852, 574895, 575225	58	27	162	1.655172414	0.999488781	1	1
	Biological Process	GO:0009058~biosynthetic process	28	8.917197452	0.01872805	752563, 754268, 588945, 591935, 577255, 591498, 590740, 574895, 575225, 584839, 581865, 100892	58	58	162	1.348394768	0.999927247	1	1
	Biological Process	GO:1901576~organic substance biosynthetic process	28	8.917197452	0.01872805	752563, 754268, 588945, 591935, 577255, 591498, 590740, 574895, 575225, 584839, 581865, 100892	58	58	162	1.348394768	0.999927247	1	1
	Biological Process	GO:0006518~peptide metabolic process	16	5.095541401	0.034271009	593029, 593744, 575080, 577040, 591341, 593861, 591498, 590740, 373469, 577852, 574895, 575225	58	29	162	1.541022592	0.999999977	1	1
	Biological Process	GO:0043603~cellular amide metabolic process	16	5.095541401	0.049078681	593029, 593744, 575080, 577040, 591341, 593861, 591498, 590740, 373469, 577852, 574895, 575225	58	30	162	1.489655172	1	1	1
	Biological Process	GO:0034645~cellular macromolecule biosynthetic process	21	6.687898089	0.0528505	591688, 752563, 593029, 754268, 593744, 575080, 577040, 591341, 593861, 577255, 591498, 590740	58	43	162	1.364073777	1	1	1
Biological Process	GO:0009059~macromolecule biosynthetic process	21	6.687898089	0.0528505	591688, 752563, 593029, 754268, 593744, 575080, 577040, 591341, 593861, 577255, 591498, 590740	58	43	162	1.364073777	1	1	1	
Biological Process	GO:0034641~cellular nitrogen compound metabolic process	32	10.1910828	0.070295793	592405, 752563, 754268, 579591, 588945, 591935, 577255, 591498, 590740, 582919, 574895, 575225	58	74	162	1.207828518	1	1	1	
Biological Process	GO:0006807~nitrogen compound metabolic process	33	10.50955414	0.073219103	592405, 752563, 754268, 579591, 588945, 591935, 577255, 591498, 590740, 582919, 574895, 575225	58	77	162	1.197044335	1	1	1	
Cellular Component	GO:0005840~ribosome	14	4.458598726	2.43E-04	593029, 593744, 577040, 580091, 591341, 593861, 591498, 590740, 373469, 577852, 574895, 584839	59	18	183	2.412429379	0.033490967	0.03406049	0.032357465	
Cellular Component	GO:0044391~ribosomal subunit	10	3.184713376	0.001873756	577852, 593029, 581865, 593744, 577040, 591341, 593861, 587414, 591498, 590740	59	12	183	2.584745763	0.230928925	0.131162907	0.124604762	
Cellular Component	GO:0005829~cytosol	10	3.184713376	0.004539866	577852, 581865, 593744, 588945, 577040, 580091, 591341, 593861, 590740	59	13	183	2.385919166	0.471138308	0.139107249	0.132151887	
Cellular Component	GO:0022626~cytosolic ribosome	8	2.547770701	0.004968116	577852, 581865, 593744, 577040, 580091, 591341, 593861, 590740	59	9	183	2.757062147	0.502057038	0.139107249	0.132151887	
Cellular Component	GO:0044445~cytosolic part	8	2.547770701	0.004968116	57								

3	Biological Process	GO:0006139~nucleobase-containing compound metabolic process	24	9.795918367	0.034737512	584340, 588854, 590968, 752151, 577044, 594039, 575790, 373348, 592267, 593496, 578317, 574069	61	47	162	1.356121381	0.999999999	1	1	1
	Biological Process	GO:0046483~heterocycle metabolic process	24	9.795918367	0.047021722	584340, 588854, 590968, 752151, 577044, 594039, 575790, 373348, 592267, 593496, 578317, 574069	61	48	162	1.327868852	1	1	1	1
	Biological Process	GO:0022613~ribonucleoprotein complex biogenesis	14	5.714285714	0.050722687	587575, 588854, 585590, 577044, 592267, 577954, 575632, 575126, 574998, 105438529, 589486, 582	61	24	162	1.549180328	1	1	1	1
	Biological Process	GO:0016043~cellular component organization	18	7.346938776	0.060468956	587575, 588415, 589835, 585590, 373348, 373503, 580307, 763690, 580528, 583958, 585934, 589392	61	34	162	1.405978785	1	1	1	1
	Biological Process	GO:0044248~cellular catabolic process	8	3.265306122	0.060621815	590942, 591601, 575334, 575203, 752151, 100889149, 585921, 578762	61	11	162	1.931445604	1	1	1	1
	Biological Process	GO:0010467~gene expression	26	10.6122449	0.060796025	587575, 586283, 575790, 593496, 578317, 580958, 574998, 576519, 105438529, 589486, 582011, 580	61	54	162	1.278688525	1	1	1	1
	Biological Process	GO:0006725~cellular aromatic compound metabolic process	24	9.795918367	0.062339684	584340, 588854, 590968, 752151, 577044, 594039, 575790, 373348, 592267, 593496, 578317, 574069	61	49	162	1.300769488	1	1	1	1
	Biological Process	GO:1990542~mitochondrial transmembrane transport	5	2.040816327	0.06318405	589835, 585934, 589195, 577928, 581274	61	5	162	2.655737705	1	1	1	1
	Biological Process	GO:0006839~mitochondrial transport	5	2.040816327	0.06318405	589835, 585934, 589195, 577928, 581274	61	5	162	2.655737705	1	1	1	1
	Biological Process	GO:0030163~protein catabolic process	7	2.857142857	0.064304928	590942, 591601, 575334, 575203, 100889149, 585921, 578762	61	9	162	2.065573777	1	1	1	1
	Biological Process	GO:0051649~establishment of localization in cell	7	2.857142857	0.064304928	575632, 589835, 585590, 585934, 589195, 577928, 581274	61	9	162	2.065573777	1	1	1	1
	Biological Process	GO:0046907~intracellular transport	7	2.857142857	0.064304928	575632, 589835, 585590, 585934, 589195, 577928, 581274	61	9	162	2.065573777	1	1	1	1
	Biological Process	GO:0044265~cellular macromolecule catabolic process	7	2.857142857	0.064304928	590942, 591601, 575334, 575203, 752151, 585921, 578762	61	9	162	2.065573777	1	1	1	1
	Biological Process	GO:0042254~ribosome biogenesis	11	4.489795918	0.072996416	575632, 577954, 588854, 575126, 585590, 574998, 577044, 589486, 580493, 592267, 586103	61	18	162	1.62295082	1	1	1	1
	Biological Process	GO:006996~organelle organization	14	5.714285714	0.073674626	588415, 589835, 585590, 373348, 373503, 763690, 580528, 583958, 585934, 589392, 574998, 589195	61	25	162	1.487213115	1	1	1	1
	Biological Process	GO:0044085~cellular component biogenesis	16	6.530612245	0.079112304	587575, 588854, 585590, 577044, 592267, 373503, 577954, 575632, 580528, 575126, 574998, 1054068	61	30	162	1.416393443	1	1	1	1
	Biological Process	GO:1901360~organic cyclic compound metabolic process	24	9.795918367	0.081036534	584340, 588854, 590968, 752151, 577044, 594039, 575790, 373348, 592267, 593496, 578317, 574069	61	50	162	1.274754098	1	1	1	1
	Biological Process	GO:006396~RNA processing	10	4.081632653	0.081966607	575632, 577954, 588854, 580958, 105438529, 577044, 594039, 589486, 580493, 586103	61	16	162	1.659836066	1	1	1	1
	Biological Process	GO:0034641~cellular nitrogen compound metabolic process	33	13.46938776	0.090703903	584340, 587575, 586283, 590968, 575790, 592267, 593496, 578317, 580958, 575347, 105443655, 574	61	74	162	1.184315463	1	1	1	1
	Biological Process	GO:0044238~primary metabolic process	41	16.73469388	0.095328282	584340, 587575, 590942, 586283, 590968, 575790, 592267, 593496, 578762, 578317, 575203, 580958	61	96	162	1.134221311	1	1	1	1
	Cellular Component	GO:0044428~nuclear part	18	7.346938776	3.36E-05	591601, 752151, 577044, 594039, 373348, 592267, 591574, 578317, 577954, 575632, 575126, 580958	67	22	183	2.234735414	0.0060654	0.006083767	0.005848483	
	Cellular Component	GO:0031981~nuclear lumen	14	5.714285714	0.001168745	752151, 577044, 373348, 592267, 591574, 578317, 577954, 575632, 575126, 576519, 583455, 589486	67	18	183	2.124378109	0.190765557	0.091662373	0.08811742	
	Cellular Component	GO:0043234~protein complex	24	9.795918367	0.001519266	587575, 590942, 591601, 589835, 586283, 752151, 574071, 594039, 373348, 578762, 578317, 575334	67	40	183	1.63880597	0.240576906	0.091662373	0.08811742	
	Cellular Component	GO:0032991~macromolecular complex	33	13.46938776	0.003446902	587575, 590942, 589835, 586283, 592267, 578762, 578317, 580958, 574998, 585921, 576519, 105438	67	64	183	1.408348881	0.464720854	0.124304455	0.1194971	
	Cellular Component	GO:0031974~membrane-enclosed lumen	17	6.93877551	0.00401343	588415, 589835, 752151, 577044, 373348, 592267, 591574, 578317, 577954, 575632, 575126, 575347	67	26	183	1.785878301	0.51707435	0.124304455	0.1194971	
	Cellular Component	GO:0005622~intracellular	56	22.85714286	0.00412059	590968, 575290, 579451, 591499, 592785, 592267, 591574, 578762, 578317, 575126, 575203, 580958	67	130	183	1.176578645	0.526388345	0.124304455	0.1194971	
	Cellular Component	GO:0005730~nucleolus	11	4.489795918	0.00575559	578317, 575632, 577954, 575126, 583455, 577044, 589486, 580493, 592267, 591574, 586103	67	14	183	2.146055437	0.649504234	0.149339452	0.143563893	
	Cellular Component	GO:0070013~intracellular organelle lumen	15	6.12244898	0.008795471	588415, 752151, 577044, 373348, 592267, 591574, 578317, 577954, 575632, 575126, 576519, 583455	67	23	183	1.781310837	0.797906061	0.17688669	0.170045769	
	Cellular Component	GO:0043233~organelle lumen	15	6.12244898	0.008795471	588415, 752151, 577044, 373348, 592267, 591574, 578317, 577954, 575632, 575126, 576519, 583455	67	23	183	1.781310837	0.797906061	0.17688669	0.170045769	
	Cellular Component	GO:0005634~nucleus	24	9.795918367	0.013239748	591601, 588854, 590968, 752151, 578771, 577044, 594039, 579451, 373348, 592267, 593496, 591574	67	45	183	1.456716418	0.910399978	0.203917025	0.196030731	
	Cellular Component	GO:0043231~intracellular membrane-bounded organelle	36	14.69387755	0.013519361	589835, 590968, 579451, 592785, 592267, 593496, 591574, 578317, 575126, 575203, 580958, 575347	67	76	183	1.293794187	0.914880224	0.203917025	0.196030731	
	Cellular Component	GO:0043227~membrane-bounded organelle	36	14.69387755	0.013519361	589835, 590968, 579451, 592785, 592267, 593496, 591574, 578317, 575126, 575203, 580958, 575347	67	76	183	1.293794187	0.914880224	0.203917025	0.196030731	
	Cellular Component	GO:0005615~extracellular space	7	2.857142857	0.02670786	580528, 575203, 37488, 100889149, 373196, 585147, 373503	67	8	183	2.389925373	0.9925523	0.328818067	0.316101346	
	Cellular Component	GO:0044421~extracellular region part	7	2.857142857	0.02670786	580528, 575203, 37488, 100889149, 373196, 585147, 373503	67	8	183	2.389925373	0.9925523	0.328818067	0.316101346	
	Cellular Component	GO:0044424~intracellular part	52	21.2244898	0.027250116	590968, 579451, 591499, 592785, 592267, 591574, 578762, 578317, 575126, 575203, 580958, 574998	67	124	183	1.145402022	0.993266902	0.328818067	0.316101346	
	Cellular Component	GO:0005623~cell	58	23.67346939	0.040687985	590968, 575290, 579451, 591499, 592785, 592267, 591574, 578762, 578317, 575126, 575203, 580958	67	144	183	1.100124378	0.999457076	0.460282831	0.442481838	
	Cellular Component	GO:0044422~organelle part	29	11.83673469	0.047921827	589835, 592785, 592267, 591574, 578317, 575126, 580958, 575347, 574998, 576519, 105438529, 577	67	62	183	1.277563794	0.999862043	0.481880589	0.463244323	
	Cellular Component	GO:0044446~intracellular organelle part	29	11.83673469	0.047921827	589835, 592785, 592267, 591574, 578317, 575126, 580958, 575347, 574998, 576519, 105438529, 577	67	62	183	1.277563794	0.999862043	0.481880589	0.463244323	
	Cellular Component	GO:0005576~extracellular region	7	2.857142857	0.057043871	580528, 575203, 37488, 100889149, 373196, 585147, 373503	67	9	183	2.124378109	0.999975848	0.543417932	0.522401769	
	Cellular Component	GO:0044464~cell part	56	22.85714286	0.071033853	590968, 575290, 579451, 591499, 592785, 592267, 591574, 578762, 578317, 575126, 575203, 580958	67	140	183	1.092537313	0.999998386	0.642856373	0.617994525	
	Molecular Function	GO:0003676~nucleic acid binding	21	8.571428571	3.97E-04	587575, 586283, 752151, 574071, 589939, 578771, 577044, 594039, 580307, 583958, 100893477, 574998, 105	55	37	183	1.888452088	0.064153823	0.066290996	0.066290996	
	Molecular Function	GO:0003723~RNA binding	14	5.714285714	0.002018721	587575, 586283, 752151, 574071, 578771, 577044, 594039, 580307, 583958, 100893477, 574998, 105	55	22	183	2.117355372	0.286424619	0.168563229	0.168563229	
	Molecular Function	GO:1901363~heterocyclic compound binding	30	12.24489796	0.004679523	587575, 586283, 590968, 589939, 575790, 593496, 577721, 578317, 575126, 575347, 105443655, 574	55	70	183	1.425974026	0.543110853	0.260493427	0.260493427	
	Molecular Function	GO:0097159~organic cyclic compound binding	30	12.24489796	0.006280826	587575, 586283, 590968, 589939, 575790, 593496, 577721, 578317, 575126, 575347, 105443655, 574	55	71	183	1.405889885	0.650833305	0.262224501	0.262224501	
	Molecular Function	GO:008135~translation factor activity, RNA binding	7	2.857142857	0.066618535	587575, 580307, 583958, 586283, 574071, 578771, 582011	55	11	183	2.117355372	0.999990003	1	1	1
	Molecular Function	GO:008856~protein transporter activity	4	1.632653061	0.077764695	589835, 585934, 589392, 577928	55	4	183	3.327272727	0.999998655	1		