

Supplemental Table 1. RNA seq analysis of differentially expressed hippocampal genes

Supplemental Table 1a. BPA exposed females vs control females					
Significantly ($padj \leq 0.05$) altered genes in 2.5BPA ♀ vs. Control ♀					
Gene Symbol	Description	Fold Change	log2FC	p value	padj
Hdlbp	high density lipoprotein binding protein	-1.332	-0.414	1.500E-06	0.013
Clk4	CDC-like kinase 4	1.646	0.719	1.600E-05	0.036
Plrg1	pleiotropic regulator 1	1.359	0.443	2.080E-05	0.036
Thoc1	THO complex 1	1.581	0.661	2.380E-05	0.036
Rmnd1	required for meiotic nuclear division 1 homolog	1.342	0.424	2.820E-05	0.036
Rsrc2	arginine and serine rich coiled-coil 2	1.452	0.538	2.970E-05	0.036
Krr1	small subunit processome component homolog	1.362	0.446	3.550E-05	0.036
Slc25a36l1	solute carrier family 25 (pyrimidine nucleotide carrier), member 36-like 1	1.490	0.575	4.030E-05	0.036
Exosc7	exosome component 7	1.410	0.496	4.080E-05	0.036
Eng	endoglin	-1.520	-0.604	4.300E-05	0.036
Trappc9	trafficking protein particle complex 9	-1.358	-0.441	4.950E-05	0.038
Luc7l3	LUC7-like 3 pre-mRNA splicing factor	1.590	0.669	6.700E-05	0.047
ENSRNOG00000017758	similar to NICE-3	1.331	0.412	7.450E-05	0.048
Significantly ($padj \leq 0.05$) altered genes in 2500BPA ♀ vs. Control ♀					
None					

Supplemental Table 1b. BPA exposed males vs control males					
Significantly ($padj \leq 0.05$) altered genes in 2.5BPA ♂ vs. Control ♂					
Gene Symbol	Description	Fold Change	log2FC	p value	padj
Ruvbl2	RuvB-like AAA ATPase 2	-1.285	-0.362	6.65E-07	0.014
Significantly ($padj \leq 0.05$) altered genes in 2500BPA ♂ vs. Control ♂					
Gene Symbol	Description	Fold Change	log2FC	p value	padj
Nradd	neurotrophin receptor associated death domain	-1.754	-0.811	1.760E-06	0.012
Edem1	ER degradation enhancing alpha-mannosidase like protein 1	1.695	0.761	1.800E-06	0.012
Cchcr1	coiled-coil alpha-helical rod protein 1	-1.591	-0.670	4.610E-06	0.019
Ppp2r5c	protein phosphatase 2, regulatory subunit B', gamma	1.320	0.400	6.000E-06	0.019
Elovl1	ELOVL fatty acid elongase 1	-1.538	-0.621	1.860E-05	0.047
Actr2	ARP2 actin-related protein 2 homolog	1.506	0.591	2.700E-05	0.048
Lrrc71	leucine rich repeat containing 71	-1.494	-0.579	3.280E-05	0.048
Opcml	Opcml	1.583	0.663	3.390E-05	0.048
Cyb5b	Cyb5b	1.352	0.435	3.430E-05	0.048
Sfxn1	Sfxn1	1.348	0.431	3.760E-05	0.048

Supplemental Table 2. RNA seq analysis of differentially expressed hypothalamic genes

Supplemental Table 2a. BPA exposed females vs control females					
Significantly ($padj \leq 0.05$) altered genes in 2.5BPA ♀ vs. Control ♀					
Gene Symbol	Description	Fold Change	log2F C	p value	padj
Csap1	common salivary protein 1	-1.308	-0.387	1.550E-06	0.033
Significantly ($padj \leq 0.05$) altered genes in 2500BPA ♀ vs. Control ♀					
Sparcl1	SPARC like 1	-1.622	-0.698	5.130E-08	1.080E-03
Csap1	common salivary protein 1	-1.321	-0.402	6.460E-07	6.800E-03

Supplemental Table 2b. BPA exposed males vs control males					
Significantly ($padj \leq 0.05$) altered genes in 2.5BPA ♂ vs. Control ♂					
Gene Symbol	Description	Fold Change	log2F C	p value	padj
Ythdc2	YTH domain containing 2	1.501	0.586	5.300E-09	5.820E-05
Ipo4	importin 4	-1.303	-0.382	3.450E-08	1.900E-04
Mat2a	methionine adenosyltransferase II, alpha	1.446	0.532	1.260E-07	4.600E-04
Akap10	A kinase (PRKA) anchor protein 10	1.389	0.474	3.510E-07	8.470E-04
Zfp317	zinc finger protein 317	1.494	0.579	3.850E-07	8.470E-04
Rictor	rapamycin-insensitive companion of mTOR	1.416	0.502	1.740E-06	3.190E-03
Agap3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	-1.318	-0.398	5.410E-06	3.500E-03
C1galt1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	1.488	0.573	5.030E-06	3.500E-03
Dpy19l4	dpy-19-like 4 (C. elegans)	1.461	0.547	5.300E-06	3.500E-03
Drap1	Dr1 associated protein 1 (negative cofactor 2 alpha)	-1.302	-0.381	3.660E-06	3.500E-03
Lcor	ligand dependent nuclear receptor corepressor	1.544	0.627	3.530E-06	3.500E-03
Mtmr10	myotubularin related protein 10	1.387	0.472	5.180E-06	3.500E-03
Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	-1.373	-0.457	3.820E-06	3.500E-03
Rnf170	ring finger protein 170	1.376	0.460	5.210E-06	3.500E-03
Sp1	Sp1 transcription factor	1.417	0.503	5.090E-06	3.500E-03
Ttc39b	Fras1 related extracellular matrix 1	1.494	0.579	4.440E-06	3.500E-03
Uhmk1	U2AF homology motif (UHM) kinase 1	1.422	0.508	5.210E-06	3.500E-03
Atad5	ATPase family, AAA domain containing 5	1.402	0.487	9.630E-06	4.660E-03
Carf	calcium response factor	1.424	0.510	7.810E-06	4.660E-03
Csk	c-src tyrosine kinase	-1.169	-0.225	1.020E-05	4.660E-03
DMD	dystrophin, muscular dystrophy	1.386	0.471	9.800E-06	4.660E-03
Eml2	echinoderm microtubule associated protein like 2	-1.347	-0.430	9.710E-06	4.660E-03
Esyt2	extended synaptotagmin 2	1.386	0.471	9.160E-06	4.660E-03
Fam35a	family with sequence similarity 35, member A	1.472	0.558	8.280E-06	4.660E-03
RGD1562390	similar to RGD, leucine-rich repeat, tropomodulin and proline-rich containing protein	-1.355	-0.438	1.100E-05	4.840E-03
Evi5l	ecotropic viral integration site 5-like	-1.235	-0.305	1.260E-05	5.150E-03
Foxp4	forkhead box P4	-1.370	-0.454	1.310E-05	5.150E-03
Gpr162	G protein-coupled receptor 162	-1.286	-0.363	1.270E-05	5.150E-03
Lrrc4b	leucine rich repeat containing 4B	-1.342	-0.424	1.420E-05	5.180E-03
Tmem132e	transmembrane protein 132E	-1.432	-0.518	1.410E-05	5.180E-03
Dennd4c	DENN domain containing 4C	1.420	0.506	1.990E-05	7.060E-03
Has2	hyaluronan synthase 2	1.456	0.542	2.250E-05	7.720E-03

Atm	ataxia telangiectasia mutated homolog (human)	1.383	0.468	2.710E-05	8.770E-03
Slc32a1	solute carrier family 32 (GABA vesicular transporter), member 1	-1.501	-0.586	2.650E-05	8.770E-03
ATP11B	ATPase, class VI, type 11B	1.421	0.507	2.880E-05	8.900E-03
Gtf3c3	general transcription factor IIIC, polypeptide 3	1.344	0.426	3.000E-05	8.900E-03
Srrd	SRR1 domain containing	-1.408	-0.494	2.980E-05	8.900E-03
Aatk	apoptosis-associated tyrosine kinase	-1.275	-0.350	3.370E-05	9.490E-03
Rbm15b	RNA binding motif protein 15B	-1.247	-0.319	3.360E-05	9.490E-03
Scn9a	sodium channel, voltage-gated, type IX, alpha	1.445	0.531	3.500E-05	9.610E-03
Yip6	Yip1 domain family, member 6	1.452	0.538	3.910E-05	1.050E-02
Adrm1	adhesion regulating molecule 1	-1.263	-0.337	4.070E-05	1.060E-02
Tubg1	tubulin, gamma 1	-1.307	-0.386	4.170E-05	1.060E-02
Cacnb2	calcium channel, voltage-dependent, beta 2 subunit	1.271	0.346	4.380E-05	1.090E-02
Fam179b	family with sequence similarity 179, member B	1.345	0.428	4.720E-05	1.150E-02
Ppp1r9b	protein phosphatase 1, regulatory subunit 9B	-1.204	-0.268	4.880E-05	1.170E-02
Poglut1	protein O-glucosyltransferase 1	1.322	0.403	5.050E-05	1.180E-02
Nufip2	FMR1 interacting protein 2	1.414	0.500	5.470E-05	1.190E-02
Hdac5	histone deacetylase 5	-1.337	-0.419	5.310E-05	1.190E-02
Ssbp3	single stranded DNA binding protein 3	-1.222	-0.289	5.520E-05	1.190E-02
Zdhhc15	zinc finger, DHHC-type containing 15	1.410	0.496	5.290E-05	1.190E-02
Dph6	diphthamine biosynthesis 6	1.361	0.445	6.070E-05	1.280E-02
Foxo6	forkhead box O6	-1.347	-0.430	6.160E-05	1.280E-02
RGD1307365	similar to KIAA1009 protein	1.428	0.514	6.380E-05	1.300E-02
Cacnb1	calcium channel, voltage-dependent, beta 1 subunit	-1.290	-0.367	6.860E-05	1.310E-02
Grik2	glutamate receptor, ionotropic, kainate 2	1.337	0.419	6.910E-05	1.310E-02
Irf2bp1	interferon regulatory factor 2 binding protein 1	-1.282	-0.358	6.930E-05	1.310E-02
Lrrn2	leucine rich repeat neuronal 2	-1.283	-0.359	6.540E-05	1.310E-02
Pianp	PILR alpha associated neural protein	-1.330	-0.411	7.050E-05	1.310E-02
Cilp2	cartilage intermediate layer protein 2	-1.439	-0.525	7.250E-05	1.330E-02
ATG101	autophagy related 101	-1.207	-0.271	7.870E-05	1.370E-02
Mta1	metastasis associated 1	-1.207	-0.271	7.830E-05	1.370E-02
Oaz1	ornithine decarboxylase antizyme 1	-1.231	-0.300	8.160E-05	1.370E-02
Setx	senataxin	1.324	0.405	8.240E-05	1.370E-02
Trappc8	trafficking protein particle complex 8	1.318	0.398	7.730E-05	1.370E-02
Wdr18	WD repeat domain 18	-1.299	-0.377	8.070E-05	1.370E-02
Lmtk3	lemur tyrosine kinase 3	-1.366	-0.450	8.400E-05	1.380E-02
Rnf208	ring finger protein 208	-1.347	-0.430	8.680E-05	1.380E-02
Zfp575	zinc finger protein 575	-1.391	-0.476	8.570E-05	1.380E-02
Bmyc	brain expressed myelocytomatosis oncogene	-1.354	-0.437	9.540E-05	1.500E-02
Cd2ap	CD2-associated protein	1.371	0.455	1.000E-04	1.530E-02
RGD1309995	similar to CG13957-PA	1.404	0.490	9.880E-05	1.530E-02
Clcc1	chloride channel CLIC-like 1	1.245	0.316	1.080E-04	1.540E-02
Cotl1	coactosin-like 1 (Dictyostelium)	-1.388	-0.473	1.060E-04	1.540E-02
Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	-1.317	-0.397	1.070E-04	1.540E-02
Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	-1.293	-0.371	1.060E-04	1.540E-02
Pls3	plastin 3 (T-isoform)	1.360	0.444	1.030E-04	1.540E-02
Polr2e	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	-1.254	-0.326	1.090E-04	1.540E-02
Hcn2	hyperpolarization activated cyclic nucleotide-gated potassium channel 2	-1.308	-0.387	1.160E-04	1.560E-02
Katnbl1	katanin regulatory subunit B1 like 1	1.428	0.514	1.120E-04	1.560E-02
Lrfr3	leucine rich repeat and fibronectin type III domain containing 3	-1.337	-0.419	1.170E-04	1.560E-02
RGD1562608	similar to KIAA1328 protein	1.262	0.336	1.150E-04	1.560E-02

Atxn3	ataxin 3	1.445	0.531	1.190E-04	1.580E-02
Cdk7	cyclin-dependent kinase 7	1.359	0.443	1.210E-04	1.580E-02
Zbtb25	zinc finger and BTB domain containing 25	1.395	0.480	1.250E-04	1.620E-02
Cdc37	cell division cycle 37 homolog (S. cerevisiae)	-1.246	-0.317	1.280E-04	1.630E-02
Ergic3	ERGIC and golgi 3	-1.234	-0.303	1.300E-04	1.630E-02
Krit1	KRIT1, ankyrin repeat containing	1.433	0.519	1.290E-04	1.630E-02
Uba52	ubiquitin A-52 residue ribosomal protein fusion product 1	-1.329	-0.410	1.390E-04	1.710E-02
Atad2	ATPase family, AAA domain containing 2	1.461	0.547	1.430E-04	1.740E-02
Tnk2	tyrosine kinase, non-receptor, 2	-1.283	-0.359	1.450E-04	1.750E-02
Casp8ap2	caspace 8 associated protein 2	1.414	0.500	1.510E-04	1.800E-02
Zfp483	zinc finger protein 483	1.430	0.516	1.550E-04	1.830E-02
Akap17a	A-kinase anchoring protein 17A	-1.204	-0.268	1.590E-04	1.860E-02
Zfp157	zinc finger protein 157	1.380	0.465	1.690E-04	1.950E-02
Pick1	protein interacting with PRKCA 1	-1.255	-0.328	1.740E-04	1.990E-02
Acof7	acyl-CoA thioesterase 7	-1.296	-0.374	2.630E-04	2.020E-02
Actr5	ARP5 actin-related protein 5 homolog (yeast)	-1.274	-0.349	2.430E-04	2.020E-02
Aip	aryl-hydrocarbon receptor-interacting protein	-1.271	-0.346	1.960E-04	2.020E-02
Atl3	atlastin GTPase 3	1.402	0.488	2.100E-04	2.020E-02
BC005561	cDNA sequence BC005561	1.411	0.497	1.950E-04	2.020E-02
Clip2	CAP-GLY domain containing linker protein 2	-1.202	-0.266	1.960E-04	2.020E-02
Ctdspl2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	1.364	0.448	2.160E-04	2.020E-02
Dact3	diacylglycerol lipase, beta	-1.310	-0.390	2.330E-04	2.020E-02
Dlgap4	discs, large homolog-associated protein 4 (Drosophila)	-1.259	-0.332	1.800E-04	2.020E-02
Dtx1	deltex E3 ubiquitin ligase 1	-1.259	-0.332	2.720E-04	2.020E-02
Eid2	EP300 interacting inhibitor of differentiation 2	-1.383	-0.468	2.450E-04	2.020E-02
Eml5	echinoderm microtubule associated protein like 5	1.344	0.427	2.560E-04	2.020E-02
Fbx15	F-box and leucine-rich repeat protein 15	-1.352	-0.435	2.230E-04	2.020E-02
Gas2	growth arrest-specific 2	1.370	0.454	2.700E-04	2.020E-02
Ints2	integrator complex subunit 2	1.358	0.442	2.710E-04	2.020E-02
Itch	itchy E3 ubiquitin protein ligase homolog (mouse)	1.366	0.450	2.540E-04	2.020E-02
Lcorl	ligand dependent nuclear receptor corepressor-like	1.370	0.454	2.190E-04	2.020E-02
Map7d1	MAP7 domain containing 1	-1.223	-0.291	2.150E-04	2.020E-02
Mdm4	Mdm4 p53 binding protein homolog (mouse)	1.398	0.483	1.920E-04	2.020E-02
Med13	mediator complex subunit 13	1.333	0.415	2.390E-04	2.020E-02
Mitd1	MIT, microtubule interacting and transport, domain containing 1	1.415	0.501	2.750E-04	2.020E-02
Mrpl52	mitochondrial ribosomal protein L52	-1.320	-0.401	2.320E-04	2.020E-02
Ndufa13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	-1.240	-0.310	1.980E-04	2.020E-02
Nlgn2	neuroligin 2	-1.341	-0.423	2.620E-04	2.020E-02
Nom1	nodal modulator 1	-1.176	-0.234	2.250E-04	2.020E-02
Nsmf	neutral sphingomyelinase (N-SMase) activation associated factor	1.290	0.367	2.400E-04	2.020E-02
Numbl	numb homolog (Drosophila)-like	-1.330	-0.411	2.220E-04	2.020E-02
Osgin2	oxidative stress induced growth inhibitor family member 2	1.334	0.416	2.230E-04	2.020E-02
PCBP2	poly(rC) binding protein 2	-1.176	-0.234	2.130E-04	2.020E-02
PHF20L1	PHD finger protein 20-like 1	1.317	0.397	2.500E-04	2.020E-02
Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	1.423	0.509	2.550E-04	2.020E-02
Podxl2	podocalyxin-like 2	-1.266	-0.340	2.320E-04	2.020E-02
Ppp2r5d	protein phosphatase 2, regulatory subunit B', delta isoform	-1.162	-0.217	2.750E-04	2.020E-02
Ppwd1	peptidylprolyl isomerase domain and WD repeat	1.385	0.470	2.540E-04	2.020E-02

	containing 1				
Prr3	proline rich 3	-1.207	-0.271	2.410E-04	2.020E-02
Psme4	proteasome (prosome, macropain) activator subunit 4	1.363	0.447	2.750E-04	2.020E-02
Pvrl1	poliovirus receptor-related 1	-1.342	-0.424	2.680E-04	2.020E-02
Rnaseh2a	ribonuclease H2, subunit A	-1.278	-0.354	2.430E-04	2.020E-02
Rnf10	ring finger protein 10	-1.218	-0.284	2.440E-04	2.020E-02
Scand1	SCAN domain-containing 1	-1.359	-0.443	2.370E-04	2.020E-02
Scn1a	sodium channel, voltage-gated, type I, alpha	1.309	0.388	2.120E-04	2.020E-02
Sez6l2	seizure related 6 homolog (mouse)-like 2	-1.301	-0.380	2.440E-04	2.020E-02
Slc25a16	solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16	1.333	0.415	2.580E-04	2.020E-02
Snx13	sorting nexin 13	1.376	0.460	2.460E-04	2.020E-02
Syt4	synaptotagmin IV	1.367	0.451	2.100E-04	2.020E-02
Tesk1	testis-specific kinase 1	-1.271	-0.346	2.630E-04	2.020E-02
Trak1	trafficking kinesin protein 1	-1.188	-0.248	1.830E-04	2.020E-02
Vstm2l	V-set and transmembrane domain containing 2 like	-1.364	-0.448	1.890E-04	2.020E-02
Wdtdc1	WD and tetratricopeptide repeats 1	-1.246	-0.317	2.520E-04	2.020E-02
Zfp579	zinc finger protein 579	-1.275	-0.350	2.760E-04	2.020E-02
Zfp871	zinc finger protein 871	1.407	0.493	1.790E-04	2.020E-02
Zfp9	zinc finger protein 9	1.373	0.457	2.510E-04	2.020E-02
Zmat1	zinc finger, matrin-type 1	1.362	0.446	2.710E-04	2.020E-02
Zufsp	zinc finger with UFM1-specific peptidase domain	1.313	0.393	2.420E-04	2.020E-02
Kcnt2	potassium channel, subfamily T, member 2	1.316	0.396	2.820E-04	2.050E-02
Bok	BCL2-related ovarian killer	-1.260	-0.333	2.890E-04	2.080E-02
Btaf1	BTA1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, <i>S. cerevisiae</i>)	1.363	0.447	2.930E-04	2.080E-02
Cntfr	ciliary neurotrophic factor receptor	-1.370	-0.454	2.900E-04	2.080E-02
MBD3	methyl-CpG binding domain protein 3	-1.299	-0.377	2.910E-04	2.080E-02
Eif6	eukaryotic translation initiation factor 6, pseudogene 1	-1.173	-0.230	3.010E-04	2.120E-02
Tmem87b	transmembrane protein 87B	1.329	0.410	3.080E-04	2.150E-02
Ahctf1	AT hook containing transcription factor 1	1.340	0.422	3.260E-04	2.200E-02
Arid4a	AT rich interactive domain 4A (Rbp1 like)	1.356	0.439	3.220E-04	2.200E-02
Mios	missing oocyte, meiosis regulator, homolog (<i>Drosophila</i>)	1.374	0.458	3.160E-04	2.200E-02
Prpf39	PRP39 pre-mRNA processing factor 39 homolog (<i>S. cerevisiae</i>)	1.423	0.509	3.180E-04	2.200E-02
Ranbp2	RAN binding protein 2	1.418	0.504	3.270E-04	2.200E-02
Smrbc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	-1.220	-0.287	3.230E-04	2.200E-02
Tmem168	transmembrane protein 168	1.399	0.484	3.300E-04	2.200E-02
Trim28	tripartite motif-containing 28	-1.157	-0.211	3.310E-04	2.200E-02
Fam127b	family with sequence similarity 127, member B	-1.261	-0.334	3.380E-04	2.230E-02
Hmx3	H6 family homeobox 3	-1.429	-0.515	3.380E-04	2.230E-02
Zfp715	protein Zfp715 (Fragment)	1.282	0.358	3.470E-04	2.240E-02
Ncapg	non-SMC condensin I complex, subunit G	1.433	0.519	3.430E-04	2.240E-02
Phc3	polyhomeotic homolog 3 (<i>Drosophila</i>)	1.327	0.408	3.470E-04	2.240E-02
Ctbp1	C-terminal binding protein 1	-1.190	-0.251	3.530E-04	2.250E-02
Mvb12b	multivesicular body subunit 12B	-1.267	-0.341	3.570E-04	2.250E-02
Nvl	nuclear VCP-like	1.392	0.477	3.570E-04	2.250E-02
Slc10a4	solute carrier family 10 (sodium/bile acid cotransporter family), member 4	-1.426	-0.512	3.510E-04	2.250E-02
Cpne3	copine III	1.354	0.437	3.650E-04	2.260E-02
Ttf1	transcription termination factor, RNA polymerase I	1.361	0.445	3.600E-04	2.260E-02

Zfp449	zinc finger protein 449	1.345	0.428	3.650E-04	2.260E-02
Atl2	atlastin GTPase 2	1.330	0.411	3.800E-04	2.300E-02
Hcfc1r1	host cell factor C1 regulator 1 (XPO1-dependent)	-1.429	-0.515	3.760E-04	2.300E-02
Hectd2	HECT domain containing 2	1.369	0.453	3.840E-04	2.300E-02
Rfc1	replication factor C (activator 1) 1	1.220	0.287	3.840E-04	2.300E-02
Samd10	sterile alpha motif domain containing 10	-1.241	-0.312	3.760E-04	2.300E-02
Secisbp2l	SECIS binding protein 2-like	1.257	0.330	3.860E-04	2.300E-02
Stub1	STIP1 homology and U-Box containing protein 1	-1.275	-0.350	3.790E-04	2.300E-02
Gnaz	guanine nucleotide binding protein (G protein), alpha z polypeptide	-1.261	-0.334	3.880E-04	2.310E-02
Fam76a	family with sequence similarity 76, member A	1.329	0.410	3.920E-04	2.320E-02
Fam19a5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	-1.229	-0.298	3.960E-04	2.330E-02
Zfp560	zinc finger protein 560	1.343	0.425	3.980E-04	2.330E-02
Nr2f6	nuclear receptor subfamily 2, group F, member 6	-1.295	-0.373	4.140E-04	2.380E-02
Rhob	ras homolog gene family, member B	-1.325	-0.406	4.130E-04	2.380E-02
Zfp192	zinc finger protein 192	1.417	0.503	4.120E-04	2.380E-02
Rps6kb1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	1.326	0.407	4.180E-04	2.390E-02
AABR07054370.1	AABR07054370.1	-1.234	-0.303	4.320E-04	2.430E-02
Lmna	lamin A	-1.261	-0.334	4.300E-04	2.430E-02
Papolg	poly(A) polymerase gamma	1.374	0.458	4.290E-04	2.430E-02
Dzip3	DAZ interacting zinc finger protein 3	1.317	0.397	4.600E-04	2.470E-02
ENSRNOG00000017708	uncharacterized protein	-1.301	-0.380	4.410E-04	2.470E-02
Npat	nuclear protein, ataxia-telangiectasia locus	1.376	0.460	4.640E-04	2.470E-02
Ogdhl	oxoglutarate dehydrogenase-like	-1.305	-0.384	4.590E-04	2.470E-02
Pik3c2a	phosphoinositide-3-kinase, class 2, alpha polypeptide	1.399	0.484	4.480E-04	2.470E-02
Rbm28	RNA binding motif protein 28	1.293	0.371	4.550E-04	2.470E-02
Sf3b4	splicing factor 3b, subunit 4	-1.246	-0.317	4.470E-04	2.470E-02
Thra	thyroid hormone receptor alpha	-1.257	-0.330	4.610E-04	2.470E-02
Ubxn6	UBX domain protein 6	-1.234	-0.303	4.500E-04	2.470E-02
Vegfb	vascular endothelial growth factor B	-1.388	-0.473	4.620E-04	2.470E-02
Xpo4	exportin 4	1.363	0.447	4.520E-04	2.470E-02
Scyl2	SCY1-like 2 (S. cerevisiae)	1.302	0.381	4.690E-04	2.480E-02
Usp37	ubiquitin specific protease 37	1.363	0.447	4.730E-04	2.480E-02
Zfp949	zinc finger protein 949	1.347	0.430	4.710E-04	2.480E-02
Cdk2ap2	CDK2-associated protein 2	-1.361	-0.445	4.760E-04	2.490E-02
Luc7l3	cisplatin resistance-associated overexpressed protein	1.384	0.469	4.870E-04	2.520E-02
Orc3	origin recognition complex, subunit 3	1.295	0.373	4.870E-04	2.520E-02
Prcc	papillary renal cell carcinoma (translocation-associated)	-1.157	-0.210	4.970E-04	2.550E-02
Zfp580	zinc finger protein 580	-1.405	-0.491	4.960E-04	2.550E-02
Ap2a1	adaptor-related protein complex 2, alpha 1 subunit	-1.254	-0.327	5.020E-04	2.560E-02
Pot1	protection of telomeres 1	1.345	0.428	5.110E-04	2.600E-02
Asic1	acid sensing ion channel subunit 1	-1.220	-0.287	5.170E-04	2.620E-02
Cactin	spliceosome C complex subunit	-1.240	-0.310	5.560E-04	2.680E-02
Capn5	calpain 5	-1.254	-0.326	5.510E-04	2.680E-02
Cox5b	cytochrome c oxidase subunit Vb	-1.246	-0.317	5.720E-04	2.680E-02
DAGLB	death-associated protein kinase 3	-1.222	-0.289	5.550E-04	2.680E-02
Fam57b	family with sequence similarity 57, member B	-1.265	-0.339	5.700E-04	2.680E-02
Hdgfrp2	hepatoma-derived growth factor, related protein 2	-1.189	-0.250	5.320E-04	2.680E-02
Hmga1	high mobility group AT-hook 1	-1.340	-0.422	5.640E-04	2.680E-02
Kcnc4	potassium voltage gated channel, Shaw-related subfamily, member 4	-1.318	-0.398	5.360E-04	2.680E-02

Lrfn1	leucine rich repeat and fibronectin type III domain containing 1	-1.322	-0.403	5.560E-04	2.680E-02
Mef2a	myocyte enhancer factor 2a	1.322	0.403	5.610E-04	2.680E-02
Mospd2	motile sperm domain containing 2	1.367	0.451	5.670E-04	2.680E-02
Neurl1a	neuralized E3 ubiquitin protein ligase 1	-1.384	-0.469	5.530E-04	2.680E-02
Sys1	Sys1 golgi trafficking protein	-1.311	-0.391	5.390E-04	2.680E-02
Tia1	TIA1 cytotoxic granule-associated RNA binding protein	1.246	0.317	5.340E-04	2.680E-02
Zfp131	zinc finger protein 131	1.325	0.406	5.640E-04	2.680E-02
ZFP87	zinc finger protein 87	1.407	0.493	5.530E-04	2.680E-02
Zfyve16	zinc finger, FYVE domain containing 16	1.371	0.455	5.490E-04	2.680E-02
Bin1	bridging integrator 1	-1.190	-0.251	5.820E-04	2.710E-02
Irf2bp1	interferon regulatory factor 2 binding protein-like	-1.293	-0.371	5.890E-04	2.710E-02
Klhdc3	kelch domain containing 3	-1.211	-0.276	5.860E-04	2.710E-02
Mrps18a	mitochondrial ribosomal protein S18A	-1.247	-0.319	5.880E-04	2.710E-02
Ubl7	ubiquitin-like 7 (bone marrow stromal cell-derived)	-1.214	-0.280	5.900E-04	2.710E-02
Ptpn4	protein tyrosine phosphatase, non-receptor type 4	1.382	0.467	5.970E-04	2.730E-02
Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	1.371	0.455	6.140E-04	2.740E-02
Gnpda2	glucosamine-6-phosphate deaminase 2	1.376	0.460	6.130E-04	2.740E-02
Pebp1	phosphatidylethanolamine binding protein 1	-1.261	-0.334	6.090E-04	2.740E-02
Stk11	serine/threonine kinase 11	-1.223	-0.290	6.110E-04	2.740E-02
Trim8	tripartite motif-containing 8	-1.208	-0.273	6.070E-04	2.740E-02
Zkscan2	zinc finger with KRAB and SCAN domains 2	1.301	0.380	6.100E-04	2.740E-02
Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	1.399	0.484	6.190E-04	2.750E-02
Edf1	endothelial differentiation-related factor 1	-1.323	-0.404	6.230E-04	2.750E-02
Homer1	homer homolog 1 (Drosophila)	1.382	0.467	6.260E-04	2.750E-02
Smc5	structural maintenance of chromosomes 5	1.376	0.460	6.230E-04	2.750E-02
Ap5m1	adaptor-related protein complex 5, mu 1 subunit	1.358	0.442	6.340E-04	2.770E-02
Ankfy1	ankyrin repeat and FYVE domain containing 1	1.296	0.374	6.430E-04	2.800E-02
Exosc5	exosome component 5	-1.283	-0.360	6.470E-04	2.800E-02
Fmn1	formin-like 1	-1.249	-0.321	6.510E-04	2.800E-02
Rps4y2	ribosomal protein S4, Y-linked 2	-1.406	-0.492	6.540E-04	2.800E-02
Trim3	tripartite motif-containing 3	-1.188	-0.248	6.550E-04	2.800E-02
Wwc3	WWC family member 3	1.340	0.422	6.460E-04	2.800E-02
Eif3h	eukaryotic translation initiation factor 3, subunit H	-1.230	-0.299	6.620E-04	2.810E-02
Elp5	elongator acetyltransferase complex subunit 5	-1.209	-0.274	6.630E-04	2.810E-02
40971	40971	-1.234	-0.303	6.750E-04	2.820E-02
Aspscr1	alveolar soft part sarcoma chromosome region, candidate 1 (human)	-1.240	-0.310	6.750E-04	2.820E-02
Magel2	MAGE-like 2	-1.295	-0.373	6.710E-04	2.820E-02
Suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	1.289	0.366	6.750E-04	2.820E-02
Kbtbd8	kelch repeat and BTB (POZ) domain containing 8	1.404	0.490	6.830E-04	2.840E-02
Strip1	striatin interacting protein 1	-1.164	-0.219	6.870E-04	2.850E-02
Bop1	block of proliferation 1	-1.203	-0.267	7.010E-04	2.890E-02
Chek1	CHK1 checkpoint homolog (S. pombe)	1.377	0.462	7.080E-04	2.910E-02
Paf1	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	-1.170	-0.226	7.100E-04	2.910E-02
Cep95	centrosomal protein 95	1.315	0.395	7.650E-04	2.980E-02
Chm	choroideremia (Rab escort protein 1)	1.370	0.454	7.500E-04	2.980E-02
Clk4	CDC like kinase 4	1.384	0.469	7.530E-04	2.980E-02
Ctdnep1	CTD nuclear envelope phosphatase 1	-1.181	-0.240	7.630E-04	2.980E-02
Jund	Jun D proto-oncogene	-1.382	-0.467	7.620E-04	2.980E-02

Mif	macrophage migration inhibitory factor	-1.371	-0.455	7.410E-04	2.980E-02
Mrpl37	mitochondrial ribosomal protein L37	-1.239	-0.309	7.590E-04	2.980E-02
Phactr3	phosphatase and actin regulator 3	-1.269	-0.344	7.500E-04	2.980E-02
Trnp1	TNFAIP3 interacting protein 1	-1.297	-0.375	7.540E-04	2.980E-02
Tubg2	tubulin, gamma 2	-1.264	-0.338	7.460E-04	2.980E-02
Zfp451	zinc finger protein 451	1.310	0.390	7.480E-04	2.980E-02
Zfp954	zinc finger protein 954	1.301	0.380	7.400E-04	2.980E-02
Zmynd19	zinc finger, MYND-type containing 19	-1.201	-0.264	7.400E-04	2.980E-02
Zzz3	zinc finger, ZZ-type containing 3	1.320	0.400	7.630E-04	2.980E-02
Agap2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	-1.247	-0.319	7.830E-04	2.990E-02
Gipc1	GIPC PDZ domain containing family, member 1	-1.229	-0.297	7.900E-04	2.990E-02
Hiatl1	hippocampus abundant transcript-like 1	1.344	0.426	7.960E-04	2.990E-02
Mad2l2	MAD2 mitotic arrest deficient-like 2 (yeast)	-1.255	-0.328	7.980E-04	2.990E-02
Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	-1.159	-0.213	7.920E-04	2.990E-02
Nup62	nucleoporin 62	-1.159	-0.213	7.870E-04	2.990E-02
Phldb2	pleckstrin homology-like domain, family B, member 2	1.313	0.393	7.910E-04	2.990E-02
Ptms	parathyrosin	-1.213	-0.279	7.770E-04	2.990E-02
R3hdm2	R3H domain containing 2	-1.205	-0.269	7.860E-04	2.990E-02
Tmed5	transmembrane emp24 protein transport domain containing 5	1.370	0.454	7.690E-04	2.990E-02
TVP23A	trans-golgi network vesicle protein 23A	-1.194	-0.256	7.870E-04	2.990E-02
Fam135a	family with sequence similarity 135, member A	1.344	0.427	8.060E-04	3.010E-02
Abhd16a	abhydrolase domain containing 16A	-1.259	-0.332	8.280E-04	3.020E-02
Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)	-1.171	-0.228	8.350E-04	3.020E-02
Ckb	creatine kinase, brain	-1.289	-0.366	8.360E-04	3.020E-02
Flywch2	FLYWCH family member 2	-1.241	-0.312	8.350E-04	3.020E-02
Mtf2	metal response element binding transcription factor 2	1.358	0.441	8.360E-04	3.020E-02
Noc4l	nucleolar complex associated 4 homolog (S. cerevisiae)	-1.253	-0.325	8.240E-04	3.020E-02
Pcmd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	1.323	0.404	8.170E-04	3.020E-02
Prmt2	protein arginine methyltransferase 2	-1.214	-0.280	8.220E-04	3.020E-02
Psm3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	-1.220	-0.287	8.400E-04	3.020E-02
RGD1559904	similar to mKIAA1429 protein	1.331	0.413	8.200E-04	3.020E-02
Zfp853	zinc finger protein 853	-1.291	-0.368	8.340E-04	3.020E-02
Fuz	fuzzy homolog (Drosophila)	-1.260	-0.333	8.450E-04	3.030E-02
B3gat1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	-1.214	-0.280	8.670E-04	3.060E-02
Csm3	CUB and Sushi multiple domains 3	1.317	0.397	8.700E-04	3.060E-02
Glce	glucuronic acid epimerase	1.306	0.385	8.720E-04	3.060E-02
GPX4	glutathione peroxidase 4	-1.217	-0.283	8.580E-04	3.060E-02
Plekhd2	pleckstrin homology domain containing, family M (with RUN domain) member 2	-1.254	-0.326	8.630E-04	3.060E-02
Rock1	Rho-associated coiled-coil containing protein kinase 1	1.351	0.434	8.670E-04	3.060E-02
Uqcrl10	ubiquinol-cytochrome c reductase, complex III subunit X	-1.370	-0.454	8.550E-04	3.060E-02
Birc6	tetratricopeptide repeat domain 27	1.305	0.384	8.990E-04	3.080E-02
Gpr149	G protein-coupled receptor 149	1.390	0.475	8.980E-04	3.080E-02
Osgepl1	O-sialoglycoprotein endopeptidase-like 1	1.320	0.401	9.010E-04	3.080E-02
Rc3h2	ring finger and CCCH-type zinc finger domains 2	1.314	0.394	8.870E-04	3.080E-02
Slx4	SLX4 structure-specific endonuclease subunit	-1.221	-0.288	8.800E-04	3.080E-02
Srek1ip1	SREK1-interacting protein 1	1.387	0.472	8.920E-04	3.080E-02

Tacc2	transforming, acidic coiled-coil containing protein 2	-1.182	-0.241	8.990E-04	3.080E-02
Ypel3	yippee-like 3	-1.230	-0.299	8.960E-04	3.080E-02
Hcrtr2	hypocretin (orexin) receptor 2	1.362	0.446	9.210E-04	3.140E-02
Smarcd3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	-1.240	-0.310	9.220E-04	3.140E-02
Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	-1.250	-0.322	9.330E-04	3.160E-02
Cox6a1	cytochrome c oxidase, subunit VIa, polypeptide 1	-1.313	-0.393	9.380E-04	3.170E-02
Ap4e1	adaptor-related protein complex 4, epsilon 1 subunit	1.319	0.399	9.510E-04	3.180E-02
Sox12	SRY (sex determining region Y)-box 12	-1.284	-0.361	9.530E-04	3.180E-02
Tbc1d15	TBC1 domain family, member 15	1.323	0.404	9.540E-04	3.180E-02
Wash	WAS protein family homolog 1	-1.211	-0.276	9.480E-04	3.180E-02
Aamp	angio-associated, migratory cell protein	-1.146	-0.197	9.650E-04	3.200E-02
Itgb1	integrin beta 1 (fibronectin receptor beta)	1.264	0.338	9.610E-04	3.200E-02
Palm	paralemmin	-1.296	-0.374	9.660E-04	3.200E-02
Mospd3	motile sperm domain containing 3	-1.202	-0.265	9.760E-04	3.210E-02
Zfp706	zinc finger protein 706	-1.306	-0.385	9.770E-04	3.210E-02
Asic2	acid sensing ion channel subunit 2	-1.308	-0.387	9.920E-04	3.250E-02
Fam131c	family with sequence similarity 131, member C	-1.382	-0.467	1.000E-03	3.260E-02
Sf3b1	splicing factor 3b, subunit 1	1.287	0.364	9.990E-04	3.260E-02
Unc119	UNC-119 homolog (C. elegans)	-1.240	-0.310	9.960E-04	3.260E-02
Diras1	DIRAS family, GTP-binding RAS-like 1	-1.265	-0.339	1.020E-03	3.290E-02
Pdpx	pyridoxal (pyridoxine, vitamin B6) phosphatase	-1.270	-0.345	1.010E-03	3.290E-02
Entpd6	ectonucleoside triphosphate diphosphohydrolase 6	-1.242	-0.313	1.020E-03	3.300E-02
Nup155	nucleoporin 155	1.283	0.360	1.030E-03	3.300E-02
Pkig	protein kinase inhibitor, gamma	-1.241	-0.312	1.030E-03	3.300E-02
Smc2	structural maintenance of chromosomes 2	1.356	0.439	1.030E-03	3.300E-02
Kdm5a	lysine demethylase 5A	1.360	0.444	1.040E-03	3.310E-02
Cntn3	contactin 3 (plasmacytoma associated)	1.392	0.477	1.050E-03	3.330E-02
Cc2d1a	coiled-coil and C2 domain containing 1A	-1.227	-0.295	1.080E-03	3.340E-02
MOR9T0	uncharacterized protein	-1.321	-0.402	1.080E-03	3.340E-02
Fam189a1	similar to Protein KIAA0574	-1.339	-0.421	1.060E-03	3.340E-02
H1fx	H1 histone family, member X	-1.378	-0.463	1.050E-03	3.340E-02
Preld1	PRELI domain containing 1	-1.251	-0.323	1.060E-03	3.340E-02
Prrc2a	proline-rich coiled-coil 2A	-1.254	-0.326	1.060E-03	3.340E-02
Rnpc3	RNA-binding region (RNP1, RRM) containing 3	1.342	0.424	1.070E-03	3.340E-02
Slit1	slit homolog 1 (Drosophila)	-1.247	-0.319	1.070E-03	3.340E-02
Tram1	translocation associated membrane protein 1	1.298	0.376	1.080E-03	3.340E-02
Ndst3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	1.371	0.455	1.090E-03	3.350E-02
NOL6	nucleolar protein family 6 (RNA-associated)	-1.188	-0.248	1.090E-03	3.350E-02
Rbfa	ribosome binding factor A	-1.233	-0.302	1.090E-03	3.350E-02
Cdc27	cell division cycle 27 homolog (S. cerevisiae)	1.316	0.396	1.100E-03	3.360E-02
Papd4	PAP associated domain containing 4	1.335	0.417	1.100E-03	3.360E-02
Manea	mannosidase, endo-alpha	1.342	0.424	1.120E-03	3.390E-02
TAOK2	TAO kinase 2	-1.152	-0.204	1.110E-03	3.390E-02
Gzf1	GDNF-inducible zinc finger protein 1	1.296	0.374	1.130E-03	3.410E-02
Trdmt1	tRNA aspartic acid methyltransferase 1	1.352	0.435	1.130E-03	3.410E-02
Vps54	vacuolar protein sorting 54 homolog (S. cerevisiae)	1.331	0.413	1.130E-03	3.410E-02
Ehmt2	euchromatic histone lysine N-methyltransferase 2	-1.229	-0.297	1.170E-03	3.450E-02
Ercc6l2	ERCC excision repair 6 like 2	1.274	0.349	1.150E-03	3.450E-02
Hid1	HID1 domain containing	-1.268	-0.343	1.170E-03	3.450E-02
Lrfn4	leucine rich repeat and fibronectin type III domain containing 4	-1.275	-0.350	1.150E-03	3.450E-02

Map3k11	mitogen-activated protein kinase kinase kinase 11	-1.372	-0.456	1.180E-03	3.450E-02
Pnpt1	polyribonucleotide nucleotidyltransferase 1	1.334	0.416	1.150E-03	3.450E-02
Ptov1	prostate tumor overexpressed 1	-1.271	-0.346	1.180E-03	3.450E-02
Sacs	spastic ataxia of Charlevoix-Saguenay (sacsin)	1.326	0.407	1.180E-03	3.450E-02
Sgta	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	-1.263	-0.337	1.170E-03	3.450E-02
Tmub1	transmembrane and ubiquitin-like domain containing 1	-1.280	-0.356	1.170E-03	3.450E-02
Fam69b	family with sequence similarity 69, member B	-1.207	-0.271	1.190E-03	3.470E-02
Tomm40	translocase of outer mitochondrial membrane 40 homolog (yeast)	-1.268	-0.343	1.190E-03	3.470E-02
Agpat1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	-1.305	-0.384	1.220E-03	3.490E-02
Atp5d	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit	-1.308	-0.387	1.220E-03	3.490E-02
Fbxl19	F-box and leucine-rich repeat protein 19	-1.200	-0.263	1.210E-03	3.490E-02
Hspbp1	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1	-1.236	-0.306	1.200E-03	3.490E-02
Mat2b	methionine adenosyltransferase II, beta	1.326	0.407	1.220E-03	3.490E-02
Snrpd2	small nuclear ribonucleoprotein D2-like	-1.231	-0.300	1.210E-03	3.490E-02
Vsig10l	V-set and immunoglobulin domain containing 10 like	-1.278	-0.354	1.200E-03	3.490E-02
Gmcl1	germ cell-less homolog 1 (Drosophila)	1.319	0.399	1.240E-03	3.520E-02
Papss1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	-1.139	-0.188	1.240E-03	3.520E-02
RGD1306502	similar to hypothetical protein FLJ11193	1.274	0.349	1.230E-03	3.520E-02
Trmt13	tRNA methyltransferase 13 homolog	1.373	0.457	1.240E-03	3.520E-02
Prrt4	similar to hypothetical gene supported by BC063892	-1.287	-0.364	1.250E-03	3.530E-02
Zc3h6	zinc finger CCCH type containing 6	1.339	0.421	1.250E-03	3.530E-02
Sema6b	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	-1.261	-0.335	1.260E-03	3.540E-02
Gk	glycerol kinase	1.332	0.414	1.270E-03	3.560E-02
Bcar1	breast cancer anti-estrogen resistance 1	-1.231	-0.300	1.280E-03	3.570E-02
Eef1g	eukaryotic translation elongation factor 1 gamma	-1.138	-0.187	1.310E-03	3.590E-02
LOC257650	hippyragranin	1.355	0.438	1.310E-03	3.590E-02
AABR07043823.2	AABR07043823.2	1.310	0.390	1.290E-03	3.590E-02
Itpk1	inositol 1,3,4-triphosphate 5/6 kinase	-1.247	-0.319	1.310E-03	3.590E-02
Pcbp4	poly(rC) binding protein 4	-1.236	-0.306	1.310E-03	3.590E-02
Rnd3	Rho family GTPase 3	1.319	0.399	1.300E-03	3.590E-02
Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	1.296	0.374	1.300E-03	3.590E-02
Ufl1	Ufm1-specific ligase 1	1.268	0.342	1.300E-03	3.590E-02
F8a1	coagulation factor VIII-associated (intronic transcript) 1	-1.239	-0.309	1.320E-03	3.600E-02
Gpr98	G protein-coupled receptor 98	1.375	0.459	1.320E-03	3.600E-02
Nfat5	nuclear factor of activated T-cells 5	1.334	0.416	1.320E-03	3.600E-02
Tdp2	tyrosyl-DNA phosphodiesterase 2	1.352	0.435	1.330E-03	3.610E-02
Acsf3	acyl-CoA synthetase family member 3	-1.241	-0.312	1.340E-03	3.630E-02
Dmx1	Dmx-like 1	1.327	0.408	1.340E-03	3.630E-02
Zfp382	zinc finger protein 382	1.179	0.238	1.350E-03	3.630E-02
Api5	apoptosis inhibitor 5	1.324	0.405	1.400E-03	3.640E-02
Bai2	brain-specific angiogenesis inhibitor 2	-1.267	-0.341	1.390E-03	3.640E-02
Ccdc97	coiled-coil domain containing 97	-1.241	-0.311	1.390E-03	3.640E-02
Dusp26	dual specificity phosphatase 26 (putative)	-1.266	-0.340	1.380E-03	3.640E-02
Fam178a	family with sequence similarity 178, member A	1.324	0.405	1.380E-03	3.640E-02
Hap1	huntingtin-associated protein 1	-1.227	-0.295	1.400E-03	3.640E-02
Ipp	intracisternal A particle-promoted polypeptide	1.313	0.393	1.370E-03	3.640E-02

Maz	MYC-associated zinc finger protein (purine-binding transcription factor)	-1.306	-0.385	1.360E-03	3.640E-02
Meaf6	MYST/Esa1-associated factor 6	-1.254	-0.327	1.370E-03	3.640E-02
Med25	mediator complex subunit 25	-1.285	-0.362	1.410E-03	3.640E-02
Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	-1.217	-0.283	1.400E-03	3.640E-02
Ppp1r37	protein phosphatase 1, regulatory subunit 37	-1.268	-0.343	1.410E-03	3.640E-02
RGD1311863	similar to RIKEN cDNA 2410127L17	1.315	0.395	1.390E-03	3.640E-02
Rnf126	ring finger protein 126	-1.312	-0.392	1.360E-03	3.640E-02
Rundc3a	RUN domain containing 3A	-1.281	-0.357	1.400E-03	3.640E-02
Tgfb1i1	transforming growth factor beta 1 induced transcript 1	-1.303	-0.382	1.410E-03	3.640E-02
Wiz	widely-interspaced zinc finger motifs	-1.240	-0.310	1.400E-03	3.640E-02
Zfp386	zinc finger protein 386 (Kruppel-like)	1.348	0.431	1.360E-03	3.640E-02
Angel2	angel homolog 2 (Drosophila)	1.245	0.316	1.460E-03	3.660E-02
C1qtnf4	C1q and tumor necrosis factor related protein 4	-1.349	-0.432	1.440E-03	3.660E-02
Chuk	conserved helix-loop-helix ubiquitous kinase	1.353	0.436	1.450E-03	3.660E-02
Evi5l	protein Evi5l	-1.249	-0.321	1.450E-03	3.660E-02
Epn1	Epsin 1	-1.231	-0.300	1.450E-03	3.660E-02
Lpxn	leupaxin	1.273	0.348	1.440E-03	3.660E-02
Mt3	metallothionein 3	-1.318	-0.398	1.430E-03	3.660E-02
Pelp1	proline, glutamic acid and leucine rich protein 1	-1.149	-0.201	1.450E-03	3.660E-02
Rac3	ras-related C3 botulinum toxin substrate	-1.303	-0.382	1.440E-03	3.660E-02
Sh3rf1	SH3 domain containing ring finger 1	-1.234	-0.303	1.420E-03	3.660E-02
UBE2M	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	-1.255	-0.328	1.430E-03	3.660E-02
Dnajb2	DnaJ (Hsp40) homolog, subfamily B, member 2	-1.146	-0.196	1.460E-03	3.670E-02
Limk1	LIM domain kinase 1	-1.193	-0.254	1.470E-03	3.690E-02
Btd	biotinidase	-1.314	-0.394	1.480E-03	3.700E-02
Cpne5	copine V	-1.296	-0.374	1.490E-03	3.700E-02
Puf60	poly-U binding splicing factor 60	-1.173	-0.230	1.480E-03	3.700E-02
RGD1560394	RGD1560394	-1.350	-0.433	1.490E-03	3.700E-02
Cnot6l	CCR4-NOT transcription complex, subunit 6-like	1.367	0.451	1.510E-03	3.710E-02
Polr2b	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	1.219	0.286	1.510E-03	3.710E-02
Thoc1	THO complex 1	1.350	0.433	1.500E-03	3.710E-02
Caly	calcyon neuron-specific vesicular protein	-1.330	-0.411	1.520E-03	3.720E-02
Ccdc106	coiled-coil domain containing 106	-1.209	-0.274	1.530E-03	3.720E-02
ERCC5	excision repair cross-complementing rodent repair deficiency, complementation group 5	1.261	0.334	1.530E-03	3.720E-02
Madd	MAP-kinase activating death domain	-1.125	-0.170	1.530E-03	3.720E-02
Pigw	phosphatidylinositol glycan anchor biosynthesis, class W	1.324	0.405	1.540E-03	3.720E-02
Samd1	sterile alpha motif domain containing 1	-1.236	-0.306	1.530E-03	3.720E-02
Zmym2	zinc finger, MYM-type 2	1.320	0.400	1.530E-03	3.720E-02
Grina	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	-1.268	-0.342	1.550E-03	3.730E-02
Pdgfa	platelet-derived growth factor alpha polypeptide	-1.258	-0.331	1.550E-03	3.730E-02
Cic	capicua homolog (Drosophila)	-1.246	-0.317	1.570E-03	3.750E-02
Fsd1	fibronectin type III and SPRY domain containing 1	-1.230	-0.299	1.560E-03	3.750E-02
Gadd45gip1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	-1.258	-0.331	1.570E-03	3.750E-02
Gpaa1	glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)	-1.239	-0.309	1.570E-03	3.750E-02
HRAS1	Harvey rat sarcoma virus oncogene	-1.250	-0.322	1.560E-03	3.750E-02
Hfm1	HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae)	1.331	0.413	1.580E-03	3.760E-02

Fam208a	family with sequence similarity 208, member A	1.326	0.407	1.590E-03	3.770E-02
Bag6	BCL2-associated athanogene 6	-1.185	-0.245	1.600E-03	3.790E-02
Csnk1g2	casein kinase 1, gamma 2	-1.251	-0.323	1.620E-03	3.810E-02
Nhlrc2	NHL repeat containing 2	1.339	0.421	1.610E-03	3.810E-02
SCAI	suppressor of cancer cell invasion	1.292	0.370	1.620E-03	3.810E-02
Atp13a2	ATPase type 13A2	-1.254	-0.327	1.640E-03	3.830E-02
Fam20c	family with sequence similarity 20, member C	-1.220	-0.287	1.640E-03	3.830E-02
Fnip1	folliculin interacting protein 1	1.325	0.406	1.640E-03	3.830E-02
Mgat3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	-1.167	-0.223	1.640E-03	3.830E-02
RGD1308134	similar to RIKEN cDNA 1110020A23	-1.250	-0.322	1.650E-03	3.830E-02
Zfp397	zinc finger protein 397	1.364	0.448	1.640E-03	3.830E-02
Glt8d1	glycosyltransferase 8 domain containing 1	1.223	0.290	1.660E-03	3.860E-02
Bcl9l	B-cell CLL/lymphoma 9-like	-1.241	-0.312	1.670E-03	3.870E-02
Chmp4bl1	chromatin modifying protein 4B-like 1	-1.203	-0.267	1.690E-03	3.870E-02
Fam214a	family with sequence similarity 214, member A	1.229	0.297	1.680E-03	3.870E-02
Gsk3a	glycogen synthase kinase 3 alpha	-1.232	-0.301	1.700E-03	3.870E-02
Myl12b	myosin light chain 12B	-1.261	-0.334	1.670E-03	3.870E-02
Nefh	neurofilament, heavy polypeptide	-1.318	-0.398	1.700E-03	3.870E-02
Pard6a	par-6 (partitioning defective 6,) homolog alpha (C. elegans)	-1.324	-0.405	1.680E-03	3.870E-02
Slc17a6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	1.335	0.417	1.700E-03	3.870E-02
Smpdl3a	sphingomyelin phosphodiesterase, acid-like 3A	1.286	0.363	1.690E-03	3.870E-02
Ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)	1.210	0.275	1.730E-03	3.910E-02
Atp11c	ATPase, class VI, type 11C	1.363	0.447	1.740E-03	3.910E-02
Frs3	fibroblast growth factor receptor substrate 3	-1.264	-0.338	1.740E-03	3.910E-02
Kif5b	kinesin family member 5B	1.245	0.316	1.730E-03	3.910E-02
Sirt2	sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)	-1.240	-0.310	1.730E-03	3.910E-02
Zfp26	zinc finger protein 26	1.359	0.443	1.730E-03	3.910E-02
Zmiz2	zinc finger, MIZ-type containing 2	-1.241	-0.312	1.730E-03	3.910E-02
Dlgap3	discs, large (Drosophila) homolog-associated protein 3	-1.268	-0.342	1.750E-03	3.920E-02
Rpl13	ribosomal protein L13	-1.265	-0.339	1.750E-03	3.920E-02
G2E3	G2/M-phase specific E3 ubiquitin ligase	1.348	0.431	1.780E-03	3.960E-02
Git1	G protein-coupled receptor kinase interacting ArfGAP 1	-1.264	-0.338	1.780E-03	3.960E-02
Chst7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	-1.311	-0.391	1.800E-03	3.990E-02
Pigm	phosphatidylinositol glycan anchor biosynthesis, class M	1.340	0.422	1.800E-03	3.990E-02
Mga	MAX gene associated	1.289	0.366	1.810E-03	4.010E-02
Slc25a39	solute carrier family 25, member 39	-1.302	-0.381	1.820E-03	4.020E-02
Msh3	mutS homolog 3 (E. coli)	1.289	0.366	1.850E-03	4.030E-02
Nrsn2	neurensin 2	-1.270	-0.345	1.830E-03	4.030E-02
Nup160	nucleoporin 160	1.281	0.357	1.840E-03	4.030E-02
Phip	pleckstrin homology domain interacting protein	1.318	0.398	1.840E-03	4.030E-02
Vps37d	VPS37D, ESCRT-I subunit	-1.240	-0.310	1.830E-03	4.030E-02
Zfp286a	zinc finger protein 286A	1.290	0.367	1.830E-03	4.030E-02
Fam171a2	family with sequence similarity 171, member A2	-1.308	-0.387	1.860E-03	4.040E-02
Orc5	origin recognition complex, subunit 5	1.249	0.321	1.860E-03	4.040E-02
Aes	amino-terminal enhancer of split	-1.278	-0.354	1.870E-03	4.060E-02
Baz2b	bromodomain adjacent to zinc finger domain, 2B	1.300	0.378	1.880E-03	4.060E-02
Kif15	kinesin family member 15	1.329	0.410	1.880E-03	4.060E-02
Ppp6r3	protein phosphatase 6, regulatory subunit 3	1.218	0.285	1.880E-03	4.060E-02

Ints1	integrator complex subunit 1	-1.237	-0.307	1.900E-03	4.080E-02
RGD1565183	similar to ribosomal protein L28	-1.272	-0.347	1.890E-03	4.080E-02
Adrbk1	adrenergic, beta, receptor kinase 1	-1.129	-0.175	1.910E-03	4.100E-02
Cacng8	calcium channel, voltage-dependent, gamma subunit 8	-1.329	-0.410	1.930E-03	4.120E-02
Fam76b	family with sequence similarity 76, member B	1.355	0.438	1.930E-03	4.120E-02
Rel2	RELT-like 2	-1.320	-0.401	1.930E-03	4.120E-02
Bri3	brain protein I3	-1.298	-0.376	1.940E-03	4.130E-02
Abca5	ATP-binding cassette, sub-family A (ABC1), member 5	1.326	0.407	2.000E-03	4.150E-02
Camk2n2	calcium/calmodulin-dependent protein kinase II inhibitor 2	-1.352	-0.435	2.000E-03	4.150E-02
Ccnt2	cyclin T2	1.303	0.382	1.970E-03	4.150E-02
Fam126b	family with sequence similarity 126, member B	1.341	0.423	1.980E-03	4.150E-02
Htr2a	5-hydroxytryptamine (serotonin) receptor 2A	1.351	0.434	1.990E-03	4.150E-02
Map2k2	mitogen activated protein kinase kinase 2	-1.271	-0.346	2.000E-03	4.150E-02
Mapk8ip1	mitogen-activated protein kinase 8 interacting protein 1	-1.232	-0.301	1.990E-03	4.150E-02
Morc3	microorchidia 3	1.301	0.380	1.980E-03	4.150E-02
Per1	period homolog 1 (Drosophila)	-1.323	-0.404	1.980E-03	4.150E-02
Rhoq	ras homolog gene family, member Q	1.251	0.323	2.000E-03	4.150E-02
Rnf152	ring finger protein 152	1.304	0.383	1.950E-03	4.150E-02
Sgsm1	small G protein signaling modulator 1	-1.231	-0.300	2.000E-03	4.150E-02
Sipa1l3	signal-induced proliferation-associated 1 like 3	-1.239	-0.309	1.980E-03	4.150E-02
Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	-1.173	-0.230	1.980E-03	4.150E-02
Ubald2	UBA-like domain containing 2	-1.309	-0.388	2.010E-03	4.150E-02
Alkbh8	alkB, alkylation repair homolog 8 (E. coli)	1.337	0.419	2.070E-03	4.240E-02
Hcfc2	host cell factor C2	1.226	0.294	2.070E-03	4.240E-02
Lypla2	lysophospholipase 2	-1.187	-0.247	2.060E-03	4.240E-02
Maf1	MAF1 homolog (S. cerevisiae)	-1.131	-0.178	2.060E-03	4.240E-02
Pnmal2	PNMA-like 2	-1.179	-0.237	2.070E-03	4.240E-02
Sf3a2	splicing factor 3a, subunit 2	-1.263	-0.337	2.070E-03	4.240E-02
Atp5g2	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	-1.186	-0.246	2.090E-03	4.260E-02
Lmbrd2	LMBR1 domain containing 2	1.340	0.422	2.090E-03	4.270E-02
Mbtd1	mbt domain containing 1	1.293	0.371	2.110E-03	4.300E-02
Ampd2	adenosine monophosphate deaminase 2 (isoform L)	-1.212	-0.277	2.140E-03	4.320E-02
Myo9a	myosin IXA	1.275	0.350	2.140E-03	4.320E-02
Rpl36	ribosomal protein L36	-1.315	-0.395	2.130E-03	4.320E-02
Slc25a38	solute carrier family 25, member 38	-1.200	-0.263	2.130E-03	4.320E-02
Csnk2b	casein kinase 2, beta subunit	-1.207	-0.271	2.170E-03	4.370E-02
Mast3	microtubule associated serine/threonine kinase 3	-1.272	-0.347	2.170E-03	4.370E-02
Atp13a1	ATPase type 13A1	-1.222	-0.289	2.190E-03	4.410E-02
Ckmt1b	creatine kinase, mitochondrial 1B	-1.268	-0.342	2.230E-03	4.450E-02
Il12rb2	interleukin 12 receptor, beta 2	1.314	0.394	2.220E-03	4.450E-02
Psmb5	proteasome (prosome, macropain) subunit, beta type 5	-1.221	-0.288	2.220E-03	4.450E-02
Klh20	kelch-like 20 (Drosophila)	1.201	0.264	2.240E-03	4.460E-02
Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3	1.341	0.423	2.240E-03	4.460E-02
Dapk3	death-associated protein kinase 3	-1.312	-0.392	2.250E-03	4.470E-02
Dusp8	dual specificity phosphatase 8	-1.211	-0.276	2.260E-03	4.480E-02
Pcm1	pericentriolar material 1	1.288	0.365	2.270E-03	4.480E-02
Zfp882	zinc finger protein 882	1.328	0.409	2.270E-03	4.480E-02
Sf1	splicing factor 1	-1.145	-0.195	2.300E-03	4.540E-02

Med16	mediator complex subunit 16	-1.260	-0.333	2.320E-03	4.560E-02
Lgals3bp	lectin, galactoside-binding, soluble, 3 binding protein	-1.337	-0.419	2.340E-03	4.580E-02
Pkd2	polycystic kidney disease 2 homolog (human)	1.275	0.350	2.340E-03	4.580E-02
Rapgef6	Rap guanine nucleotide exchange factor (GEF) 6	1.274	0.349	2.340E-03	4.580E-02
ENSRNOG00000024507	ENSRNOG00000024507	1.299	0.377	2.360E-03	4.600E-02
Fbxo31	F-box protein 31	-1.227	-0.295	2.360E-03	4.600E-02
Lrif1	ligand dependent nuclear receptor interacting factor 1	1.359	0.443	2.360E-03	4.600E-02
Blzf1	basic leucine zipper nuclear factor 1	1.288	0.365	2.380E-03	4.620E-02
Ccdc92	coiled-coil domain containing 92	-1.225	-0.293	2.380E-03	4.620E-02
Maea	macrophage erythroblast attacher	-1.126	-0.171	2.390E-03	4.630E-02
Mri1	methylothioribose-1-phosphate isomerase homolog (S. cerevisiae)	-1.269	-0.344	2.400E-03	4.630E-02
Otub1	OTU domain, ubiquitin aldehyde binding 1	-1.188	-0.249	2.400E-03	4.630E-02
Vps72	vacuolar protein sorting 72 homolog (S. cerevisiae)	-1.199	-0.262	2.400E-03	4.630E-02
RGD1566386	similar to Hypothetical protein A430033K04	1.337	0.419	2.420E-03	4.640E-02
Tmtc3	transmembrane and tetratricopeptide repeat containing 3	1.357	0.440	2.420E-03	4.640E-02
Zfp644	zinc finger protein 644	1.242	0.313	2.420E-03	4.640E-02
Prkdc	protein kinase, DNA activated, catalytic polypeptide	1.292	0.370	2.470E-03	4.730E-02
RGD1359634	similar to RIKEN cDNA 1700088E04	-1.213	-0.279	2.480E-03	4.740E-02
MGC114464	similar to expressed sequence A1836003	-1.246	-0.317	2.500E-03	4.760E-02
Mrp139	mitochondrial ribosomal protein L39	1.227	0.295	2.500E-03	4.760E-02
Yipf3	Yip1 domain family, member 3	-1.210	-0.275	2.490E-03	4.760E-02
Actb	actin, beta	-1.258	-0.331	2.520E-03	4.770E-02
Edem3	ER degradation enhancer, mannosidase alpha-like 3	1.242	0.313	2.520E-03	4.770E-02
Kih128	kelch-like 28 (Drosophila)	1.316	0.396	2.520E-03	4.770E-02
Mbnl1	muscleblind-like 1 (Drosophila)	1.238	0.308	2.530E-03	4.770E-02
Arl6ip6	ADP-ribosylation-like factor 6 interacting protein 6	1.340	0.422	2.600E-03	4.810E-02
Bad	Bcl2-antagonist of cell death	-1.217	-0.283	2.590E-03	4.810E-02
C2cd2l	transmembrane protein 24	-1.200	-0.263	2.610E-03	4.810E-02
Csnk1e	casein kinase 1, epsilon	-1.229	-0.298	2.570E-03	4.810E-02
Myd8f	myeloid derived growth factor	-1.157	-0.211	2.570E-03	4.810E-02
Fam208b	family with sequence similarity 208, member B	1.289	0.366	2.590E-03	4.810E-02
H2afy2	H2A histone family, member Y2	-1.169	-0.225	2.580E-03	4.810E-02
Psmc4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	-1.138	-0.186	2.600E-03	4.810E-02
RGD1309594	similar to RIKEN cDNA 1810043G02	-1.244	-0.315	2.560E-03	4.810E-02
Slc5a6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	-1.215	-0.281	2.600E-03	4.810E-02
Smardc1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	1.332	0.414	2.600E-03	4.810E-02
Snx17	sorting nexin 17	-1.188	-0.248	2.600E-03	4.810E-02
Ube2d1	ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog (yeast)	-1.326	-0.407	2.580E-03	4.810E-02
Zfp248	zinc finger protein 248	1.333	0.415	2.550E-03	4.810E-02
Csnk1g3	casein kinase 1, gamma 3	1.300	0.378	2.640E-03	4.820E-02
E2f3	E2F transcription factor 3	1.268	0.342	2.640E-03	4.820E-02
Efcab14	EF-hand calcium binding domain 14	1.261	0.335	2.650E-03	4.820E-02
Fam89b	family with sequence similarity 89, member B	-1.247	-0.318	2.650E-03	4.820E-02
Prrt1	proline-rich transmembrane protein 1	-1.353	-0.436	2.650E-03	4.820E-02
Rbm42	RNA binding motif protein 42	-1.258	-0.331	2.640E-03	4.820E-02
Sh2d3c	SH2 domain containing 3C	-1.289	-0.366	2.630E-03	4.820E-02
Sncb	synuclein, beta	-1.297	-0.375	2.620E-03	4.820E-02
Tceal6	transcription elongation factor A (SII)-like 6	-1.235	-0.305	2.640E-03	4.820E-02

Rabac1	Rab acceptor 1 (prenylated)	-1.224	-0.292	2.680E-03	4.840E-02
Traf4	Tnf receptor associated factor 4	-1.185	-0.245	2.670E-03	4.840E-02
Adcy5	adenylate cyclase 5	-1.222	-0.289	2.740E-03	4.890E-02
Chchd10	coiled-coil-helix-coiled-coil-helix domain containing 10	-1.342	-0.424	2.710E-03	4.890E-02
Eefsec	eukaryotic elongation factor, selenocysteine-tRNA-specific	-1.226	-0.294	2.740E-03	4.890E-02
Esf1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	1.326	0.407	2.730E-03	4.890E-02
Fgd1	FYVE, RhoGEF and PH domain containing 1	-1.188	-0.249	2.710E-03	4.890E-02
Rpl27a	ribosomal protein L27a	-1.292	-0.370	2.740E-03	4.890E-02
Rpl35	ribosomal protein L35	-1.278	-0.354	2.740E-03	4.890E-02
Serpinc1	serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	1.317	0.397	2.730E-03	4.890E-02
Zfp59	zinc finger protein 59	1.327	0.408	2.710E-03	4.890E-02
Tmem18	transmembrane protein 18	1.213	0.278	2.760E-03	4.910E-02
Vprbp	Vpr (HIV-1) binding protein	1.242	0.313	2.760E-03	4.910E-02
Vcam1	vascular cell adhesion molecule 1	1.175	0.233	2.780E-03	4.930E-02
Fastkd3	FAST kinase domains 3	1.310	0.390	2.840E-03	4.940E-02
Gdap111	ganglioside-induced differentiation-associated protein 1-like 1	-1.227	-0.295	2.840E-03	4.940E-02
Glrx5	glutaredoxin 5	-1.299	-0.377	2.840E-03	4.940E-02
Ly6h	lymphocyte antigen 6 complex, locus H	-1.256	-0.329	2.810E-03	4.940E-02
Mark4	MAP/microtubule affinity-regulating kinase 4	-1.265	-0.339	2.810E-03	4.940E-02
Paccin2	protein kinase C and casein kinase substrate in neurons 2	-1.170	-0.227	2.830E-03	4.940E-02
Pank3	pantothenate kinase 3	1.311	0.391	2.790E-03	4.940E-02
Prr7	proline rich 7 (synaptic)	-1.312	-0.392	2.830E-03	4.940E-02
Slitrk6	SLIT and NTRK-like family, member 6	1.349	0.432	2.830E-03	4.940E-02
Tceal3	transcription elongation factor A (SII)-like 3	-1.249	-0.321	2.830E-03	4.940E-02
Wbp4	WW domain binding protein 4 (formin binding protein 21)	1.256	0.329	2.790E-03	4.940E-02
Ythdf3	YTH domain family, member 3	1.314	0.394	2.820E-03	4.940E-02
Dscam	Down syndrome cell adhesion molecule	-1.235	-0.305	2.860E-03	4.970E-02
Arrb2	arrestin, beta 2	-1.213	-0.278	2.870E-03	4.980E-02
Zfp445	zinc finger protein 445	1.286	0.363	2.870E-03	4.980E-02
Atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	-1.272	-0.347	2.910E-03	5.000E-02
Fktn	fukutin	1.265	0.339	2.900E-03	5.000E-02
Nanp	N-acetylneuraminic acid phosphatase	1.270	0.345	2.910E-03	5.000E-02
Pnlsr	PNN interacting serine and arginine rich protein	1.308	0.387	2.910E-03	5.000E-02
Wbp2	WW domain binding protein 2	-1.197	-0.259	2.900E-03	5.000E-02

Significantly (padj ≤ 0.05) altered genes in 2500BPA ♂ vs. Control ♂

Gene Symbol	Description	Fold Change	log2FC	p value	padj
Ythdc2	YTH domain containing 2	1.640	0.714	1.010E-12	1.400E-08
Tia1	cytotoxic granule-associated RNA binding protein 1	1.530	0.614	1.760E-11	1.210E-07
Rictor	RPTOR independent companion of MTOR, complex 2	1.545	0.628	2.060E-09	9.480E-06
Atm	ataxia telangiectasia mutated homolog (human)	1.571	0.652	4.740E-09	1.520E-05
Nsmaf	neutral sphingomyelinase (N-SMase) activation associated factor	1.497	0.582	5.490E-09	1.520E-05
Ankhd1	ankyrin repeat and KH domain containing 1	1.532	0.615	7.790E-09	1.790E-05
Cep295	centrosomal protein 295	1.675	0.744	1.840E-08	2.310E-05
Cep95	centrosomal protein 95	1.587	0.666	1.330E-08	2.310E-05
Ints2	integrator complex subunit 2	1.609	0.686	1.420E-08	2.310E-05
Mat2a	methionine adenosyltransferase II, alpha	1.481	0.567	1.710E-08	2.310E-05

Prp211	proline rich protein 2-like 1	1.722	0.784	1.770E-08	2.310E-05
Oaz1	ornithine decarboxylase antizyme 1	-1.343	-0.425	2.260E-08	2.440E-05
Em15	echinoderm microtubule associated protein like 5	1.570	0.651	2.470E-08	2.440E-05
Sacs	sacsin	1.625	0.700	2.460E-08	2.440E-05
Ap5m1	adaptor-related protein complex 5, mu 1 subunit	1.639	0.713	3.280E-08	3.020E-05
Atad5	ATPase family, AAA domain containing 5	1.521	0.605	3.790E-08	3.080E-05
Mdm4	transformed mouse 3T3 cell double minute 4	1.638	0.712	3.730E-08	3.080E-05
Dna2	DNA replication helicase 2 homolog (yeast)	1.614	0.691	5.510E-08	4.230E-05
Slc25a36l1	solute carrier family 25 (pyrimidine nucleotide carrier), member 36-like 1	1.367	0.451	6.210E-08	4.510E-05
Esyt2	family with sequence similarity 62 (C2 domain containing), member B	1.485	0.570	7.730E-08	5.340E-05
Tgds	TDP-glucose 4,6-dehydratase	1.533	0.616	8.820E-08	5.800E-05
Nktr	natural killer tumor recognition sequence	1.476	0.562	9.280E-08	5.830E-05
Drap1	Dr1 associated protein 1 (negative cofactor 2 alpha)	-1.356	-0.439	9.830E-08	5.910E-05
Scn9a	sodium channel, voltage-gated, type IX, alpha	1.597	0.675	1.410E-07	8.140E-05
Cep162	centrosomal protein 162	1.582	0.662	2.550E-07	1.410E-04
Srek1	splicing regulatory glutamic acid and lysine rich protein 1	1.594	0.673	3.190E-07	1.630E-04
Zfp483	zinc finger protein 483	1.622	0.698	3.100E-07	1.630E-04
Cd2ap	CD2-associated protein	1.510	0.595	3.480E-07	1.720E-04
Rbm5	RNA binding motif protein 5	1.564	0.645	4.190E-07	1.990E-04
Itsn2	intersectin 2	1.424	0.510	5.080E-07	2.340E-04
RPL12	ribosomal protein L12	-1.329	-0.410	5.770E-07	2.410E-04
Arr3	arrestin 3, retinal	1.651	0.723	5.660E-07	2.410E-04
Birc6	baculoviral IAP repeat-containing 6	1.493	0.578	5.770E-07	2.410E-04
Gtf3c3	general transcription factor IIIC, polypeptide 3	1.423	0.509	6.120E-07	2.480E-04
Mrs2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	1.529	0.613	6.370E-07	2.510E-04
Fam19a5	family with sequence similarity 19, member A5	-1.337	-0.419	6.570E-07	2.520E-04
Ash11	ash1 (absent, small, or homeotic)-like (Drosophila)	1.352	0.435	7.030E-07	2.570E-04
Dennd4c	DENN/MADD domain containing 4C	1.503	0.588	7.070E-07	2.570E-04
Trdmt1	tRNA aspartic acid methyltransferase 1	1.580	0.660	7.550E-07	2.680E-04
Rps21	ribosomal protein S21	-1.508	-0.593	1.090E-06	3.630E-04
Ccdc62	coiled-coil domain containing 62	1.565	0.646	1.100E-06	3.630E-04
Mfn1	mitofusin 1	1.400	0.485	1.050E-06	3.630E-04
Tnrc6a	trinucleotide repeat containing 6a	1.390	0.475	1.400E-06	4.400E-04
Tubgcp3	tubulin, gamma complex associated protein 3	1.288	0.365	1.400E-06	4.400E-04
PHF20L1	PHD finger protein 20-like 1	1.436	0.522	1.510E-06	4.620E-04
Rplp1	ribosomal protein, large, P1	-1.563	-0.644	1.560E-06	4.700E-04
Setx	senataxin	1.408	0.494	1.600E-06	4.710E-04
Ccnt2	cyclin T2	1.504	0.589	1.850E-06	5.330E-04
Ras10b	RAS-like, family 10, member B	-1.616	-0.692	1.920E-06	5.420E-04
Arnt	aryl hydrocarbon receptor nuclear translocator	1.424	0.510	2.540E-06	6.890E-04
Arhgef6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	1.538	0.621	2.540E-06	6.890E-04
Ddx26b	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	1.540	0.623	2.870E-06	7.300E-04
Fam179b	family with sequence similarity 179, member B	1.406	0.492	2.870E-06	7.300E-04
Fam214a	family with sequence similarity 214, member A	1.358	0.442	2.890E-06	7.300E-04
Golgb1	golgi autoantigen, golgin subfamily b, macrogolgin 1	1.286	0.363	2.910E-06	7.300E-04
Mir770	microRNA 770	1.597	0.675	3.000E-06	7.390E-04
Chuk	conserved helix-loop-helix ubiquitous kinase	1.556	0.638	3.070E-06	7.450E-04
ATP11B	ATPase, class VI, type 11B	1.479	0.565	3.150E-06	7.500E-04
Lcor	ligand dependent nuclear receptor corepressor	1.544	0.627	3.550E-06	8.320E-04

Nfat5	nuclear factor of activated T-cells 5	1.515	0.599	3.740E-06	8.610E-04
Leng8	leukocyte receptor cluster (LRC) member 8	1.506	0.591	3.890E-06	8.800E-04
Supt20	suppressor of Ty 20	1.417	0.503	4.020E-06	8.950E-04
Bri3	brain protein I3	-1.471	-0.557	4.470E-06	9.350E-04
Nf1	neurofibromatosis 1	1.292	0.370	4.290E-06	9.350E-04
Smg1	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)	1.494	0.579	4.380E-06	9.350E-04
Sys1	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	-1.434	-0.520	4.470E-06	9.350E-04
Psm3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	-1.314	-0.394	4.630E-06	9.550E-04
Ttc39b	tetratricopeptide repeat domain 39B	1.493	0.578	4.730E-06	9.620E-04
Adrm1	adhesion regulating molecule 1	-1.298	-0.376	4.820E-06	9.640E-04
Akap10	A kinase (PRKA) anchor protein 10	1.344	0.426	4.910E-06	9.690E-04
AABR07030590.1	AABR07030590.1	1.580	0.660	5.620E-06	1.090E-03
Utp20	UTP20, small subunit (SSU) processome component, homolog (yeast)	1.431	0.517	5.770E-06	1.110E-03
Cdc37	cell division cycle 37 homolog (S. cerevisiae)	-1.296	-0.374	6.470E-06	1.220E-03
Eid2	EP300 interacting inhibitor of differentiation 2	-1.491	-0.576	6.720E-06	1.250E-03
Agap3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	-1.313	-0.393	6.880E-06	1.260E-03
Pnir	PNN-interacting serine/arginine-rich protein	1.499	0.584	6.920E-06	1.260E-03
Ahctf1	AT hook containing transcription factor 1	1.440	0.526	7.710E-06	1.380E-03
Atxn3	ataxin 3	1.533	0.616	7.980E-06	1.380E-03
Cc2d2a	coiled-coil and C2 domain containing 2A	1.465	0.551	7.880E-06	1.380E-03
Dopey1	dopey family member 1	1.417	0.503	7.890E-06	1.380E-03
Rpl32	ribosomal protein L32	-1.495	-0.580	8.340E-06	1.400E-03
Trpm7	transient receptor potential cation channel, subfamily M, member 7	1.528	0.612	8.190E-06	1.400E-03
Tmem121	transmembrane protein 121	-1.357	-0.440	1.010E-05	1.640E-03
Mex3d	mex3 homolog D (C. elegans)	-1.425	-0.511	1.000E-05	1.640E-03
Zfp382	zinc finger protein 382	1.254	0.327	1.000E-05	1.640E-03
Usp40	ubiquitin specific peptidase 40	1.498	0.583	1.030E-05	1.660E-03
Rpl27a	ribosomal protein L27a	-1.458	-0.544	1.070E-05	1.690E-03
Rpl31	ribosomal protein L31	-1.306	-0.385	1.120E-05	1.750E-03
H2afz	H2A histone family, member Z	-1.366	-0.450	1.200E-05	1.860E-03
Uqc10	ubiquinol-cytochrome c reductase, complex III subunit X	-1.513	-0.597	1.210E-05	1.860E-03
Bmyc	brain expressed myelocytomatosis oncogene	-1.404	-0.490	1.260E-05	1.900E-03
Med13	mediator complex subunit 13	1.407	0.493	1.260E-05	1.900E-03
Kpna5	karyopherin subunit alpha 5	1.470	0.556	1.310E-05	1.920E-03
Snrpd2	predicted gene 5449	-1.324	-0.405	1.300E-05	1.920E-03
BC005561	THO complex 2	1.496	0.581	1.350E-05	1.960E-03
Prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	1.532	0.615	1.380E-05	1.980E-03
Cep350	centrosomal protein 350	1.402	0.488	1.400E-05	1.990E-03
Prcc	papillary renal cell carcinoma (translocation-associated)	-1.199	-0.262	1.440E-05	2.040E-03
Rps27a	similar to ribosomal protein S27a	-1.416	-0.502	1.510E-05	2.070E-03
Edrf1	erythroid differentiation regulatory factor 1	1.455	0.541	1.580E-05	2.070E-03
Hfm1	HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae)	1.479	0.565	1.510E-05	2.070E-03
Ppip5k2	histidine acid phosphatase domain containing 1	1.397	0.482	1.570E-05	2.070E-03
Ndufa13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	-1.283	-0.360	1.560E-05	2.070E-03
Rock1	Rho-associated coiled-coil containing protein kinase 1	1.476	0.562	1.560E-05	2.070E-03

Sf3b1	splicing factor 3b, subunit 1	1.393	0.478	1.530E-05	2.070E-03
Jhd1d	jumonji C domain-containing histone demethylase 1 homolog D (<i>S. cerevisiae</i>)	1.539	0.622	1.590E-05	2.080E-03
Pkig	protein kinase inhibitor, gamma	-1.329	-0.410	1.670E-05	2.090E-03
RGD1309995	similar to CG13957-PA	1.456	0.542	1.630E-05	2.090E-03
Vps13c	vacuolar protein sorting 13C (yeast)	1.418	0.504	1.650E-05	2.090E-03
AABR07054370.1	AABR07054370.1	-1.293	-0.371	1.660E-05	2.090E-03
GPX4	glutathione peroxidase 4	-1.288	-0.365	1.760E-05	2.170E-03
Argef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	1.276	0.352	1.800E-05	2.170E-03
Ctnn1	catenin (cadherin associated protein), alpha-like 1	1.429	0.515	1.830E-05	2.170E-03
Fastk1	FAST kinase domains 1	1.408	0.494	1.750E-05	2.170E-03
Pan3	PAN3 polyA specific ribonuclease subunit homolog (<i>S. cerevisiae</i>)	1.285	0.362	1.790E-05	2.170E-03
Usp37	ubiquitin specific peptidase 37	1.461	0.547	1.820E-05	2.170E-03
Trmt13	tRNA methyltransferase 13 homolog	1.522	0.606	1.850E-05	2.180E-03
Alkbh7	alkB, alkylation repair homolog 7 (<i>E. coli</i>)	-1.402	-0.487	1.940E-05	2.260E-03
Sgk494	uncharacterized serine/threonine-protein kinase Sgk494	1.515	0.599	1.940E-05	2.260E-03
Vstm2l	V-set and transmembrane domain containing 2-like	-1.423	-0.509	2.220E-05	2.530E-03
Irf2bp1	interferon regulatory factor 2 binding protein 1	-1.303	-0.382	2.210E-05	2.530E-03
Zfyve16	zinc finger, FYVE domain containing 16	1.472	0.558	2.230E-05	2.530E-03
Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, <i>S. cerevisiae</i>)	1.438	0.524	2.260E-05	2.540E-03
Ctbp1	C-terminal binding protein 1	-1.228	-0.296	2.420E-05	2.620E-03
Rps2	similar to 40S ribosomal protein S2	-1.326	-0.407	2.440E-05	2.620E-03
Ankfy1	ankyrin repeat and FYVE domain containing 1	1.376	0.461	2.490E-05	2.620E-03
D17Wsu104e	DNA segment, Chr 17, Wayne State University 104, expressed	-1.228	-0.296	2.450E-05	2.620E-03
RGD1562608	similar to KIAA1328 protein	1.291	0.368	2.370E-05	2.620E-03
Scn3a	sodium channel, voltage-gated, type III, alpha	1.320	0.401	2.470E-05	2.620E-03
Strn	striatin, calmodulin binding protein	1.272	0.347	2.480E-05	2.620E-03
Tada2a	transcriptional adaptor 2 (ADA2 homolog, yeast)-like	1.300	0.378	2.420E-05	2.620E-03
Paxbp1	PAX3 and PAX7 binding protein 1	1.447	0.533	2.550E-05	2.640E-03
Thoc1	THO complex 1	1.489	0.574	2.540E-05	2.640E-03
Hes5	hairy and enhancer of split 5 (<i>Drosophila</i>)	-1.478	-0.564	2.620E-05	2.660E-03
Ssbp3	single-stranded DNA binding protein 3	-1.232	-0.301	2.620E-05	2.660E-03
Scn1a	sodium channel, voltage-gated, type I, alpha	1.357	0.440	2.640E-05	2.660E-03
Zc3h7a	zinc finger CCCH type containing 7 A	1.424	0.510	2.590E-05	2.660E-03
Ero1b	ERO1-like beta (<i>S. cerevisiae</i>)	1.434	0.520	2.680E-05	2.680E-03
Cilp2	cartilage intermediate layer protein 2	-1.469	-0.555	2.800E-05	2.790E-03
Pycl	pyrroline-5-carboxylate reductase-like	-1.289	-0.366	2.920E-05	2.880E-03
Zufsp	zinc finger with UFM1-specific peptidase domain	1.363	0.447	3.000E-05	2.940E-03
Rpl36	ribosomal protein L36	-1.450	-0.536	3.090E-05	2.960E-03
Brca2	breast cancer 2	1.363	0.447	3.070E-05	2.960E-03
Timm8b	translocase of inner mitochondrial membrane 8 homolog b (yeast)	-1.360	-0.444	3.040E-05	2.960E-03
Atp5j2	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit f, isoform 2	-1.329	-0.410	3.270E-05	2.990E-03
Dock3	dedicator of cyto-kinesis 3	1.336	0.418	3.190E-05	2.990E-03
Dennd4a	DENN/MADD domain containing 4A	1.433	0.519	3.210E-05	2.990E-03
Lmna	lamin A	-1.315	-0.395	3.180E-05	2.990E-03
Nudt3	nudix (nucleotide diphosphate linked moiety X)-type motif 3	-1.196	-0.258	3.270E-05	2.990E-03
Rab12	RAB12, member RAS oncogene family	-1.376	-0.461	3.150E-05	2.990E-03

PCBP1	Poly(RC) Binding Protein 1	-1.366	-0.450	3.260E-05	2.990E-03
Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	-1.443	-0.529	3.350E-05	3.040E-03
Prkdc	protein kinase, DNA activated, catalytic polypeptide	1.420	0.506	3.390E-05	3.060E-03
Zfc3h1	zinc finger, C3H1-type containing	1.476	0.562	3.450E-05	3.090E-03
Psmc4	proteasome (prosome, macropain) activator subunit 4	1.423	0.509	3.480E-05	3.100E-03
Tubg1	tubulin, gamma 1	-1.310	-0.390	3.540E-05	3.130E-03
Zkscan2	zinc finger with KRAB and SCAN domains 2	1.374	0.458	3.710E-05	3.260E-03
Abca5	ATP-binding cassette, sub-family A (ABC1), member 5	1.456	0.542	3.880E-05	3.390E-03
Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	1.392	0.477	3.980E-05	3.450E-03
Rnf10	ring finger protein 10	-1.246	-0.317	4.080E-05	3.520E-03
Nfxl1	nuclear transcription factor, X-box binding-like 1	1.433	0.519	4.310E-05	3.700E-03
Rpl18a	ribosomal protein L18A	-1.287	-0.364	4.380E-05	3.730E-03
Carf	calcium response factor	1.381	0.466	4.540E-05	3.820E-03
F8a1	coagulation factor VIII-associated 1	-1.313	-0.393	4.530E-05	3.820E-03
Clip2	CAP-GLY domain containing linker protein 2	-1.224	-0.292	4.630E-05	3.870E-03
Zfp407	zinc finger protein 407	1.346	0.429	4.650E-05	3.870E-03
Naa16	NMDA receptor regulated 1-like	1.492	0.577	4.760E-05	3.890E-03
Pot1	protection of telomeres 1	1.415	0.501	4.730E-05	3.890E-03
Shfm1	split hand/foot malformation (ectrodactyly) type 1	-1.359	-0.443	4.750E-05	3.890E-03
Vstm2b	V-set and transmembrane domain containing 2B	-1.378	-0.463	4.850E-05	3.940E-03
Rps7	ribosomal protein S7	-1.299	-0.377	4.940E-05	3.980E-03
Ttc37	tetratricopeptide repeat domain 37	1.404	0.490	4.960E-05	3.980E-03
Nsd1	nuclear receptor-binding SET-domain protein 1	1.268	0.343	5.000E-05	3.990E-03
Dnajc13	DnaJ (Hsp40) homolog, subfamily C, member 13	1.332	0.414	5.030E-05	4.000E-03
Mss51	MSS51 mitochondrial translational activator	1.504	0.589	5.130E-05	4.050E-03
AABR07067506.1	AABR07067506.1	-1.429	-0.515	5.160E-05	4.050E-03
Igsf6	immunoglobulin superfamily, member 6	1.502	0.587	5.230E-05	4.080E-03
Secisbp2l	SECIS binding protein 2-like	1.298	0.376	5.260E-05	4.080E-03
Mga	MAX gene associated	1.389	0.474	5.450E-05	4.200E-03
Phip	pleckstrin homology domain interacting protein	1.430	0.516	5.500E-05	4.220E-03
Arf5	ADP-ribosylation factor 5	-1.355	-0.438	5.750E-05	4.240E-03
Rps17	ribosomal protein S17	-1.412	-0.498	5.560E-05	4.240E-03
Atad2	ATPase family, AAA domain containing 2	1.494	0.579	5.710E-05	4.240E-03
Cacnb1	calcium channel, voltage-dependent, beta 1 subunit	-1.293	-0.371	5.720E-05	4.240E-03
Cnot2	CCR4-NOT transcription complex, subunit 2	1.213	0.278	5.810E-05	4.240E-03
Htt	huntingtin	1.259	0.332	5.810E-05	4.240E-03
Itch	itchy, E3 ubiquitin protein ligase	1.408	0.494	5.730E-05	4.240E-03
Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	-1.318	-0.398	5.580E-05	4.240E-03
Nfatc3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	1.345	0.428	5.810E-05	4.240E-03
Rpl41	ribosomal protein L41	-1.305	-0.384	5.830E-05	4.240E-03
Rhob	ras homolog gene family, member B	-1.376	-0.461	5.980E-05	4.320E-03
Osbpl6	oxysterol binding protein-like 6	1.320	0.401	6.320E-05	4.540E-03
Tmem87b	transmembrane protein 87B	1.371	0.455	6.350E-05	4.540E-03
Rplp2	WD repeat domain 89	-1.494	-0.579	6.670E-05	4.750E-03
Scand1	SCAN domain-containing 1	-1.396	-0.481	6.730E-05	4.770E-03
UBE2M	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	-1.328	-0.409	6.830E-05	4.810E-03
Atpif1	ATPase inhibitory factor 1	-1.327	-0.408	6.980E-05	4.840E-03
Fbxl15	F-box and leucine-rich repeat protein 15	-1.384	-0.469	7.000E-05	4.840E-03

Lvrn	laeverin	1.487	0.572	6.960E-05	4.840E-03
Mphosph9	M-phase phosphoprotein 9	1.378	0.463	6.960E-05	4.840E-03
Ddhd2	DDHD domain containing 2	1.437	0.523	7.200E-05	4.950E-03
Brwd1	bromodomain and WD repeat domain containing 1	1.354	0.437	7.420E-05	5.050E-03
Dclre1c	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae)	1.477	0.563	7.460E-05	5.050E-03
Phldb2	pleckstrin homology-like domain, family B, member 2	1.379	0.464	7.410E-05	5.050E-03
Orc2	origin recognition complex, subunit 2	1.408	0.494	7.550E-05	5.060E-03
Prr7	proline rich 7 (synaptic)	-1.434	-0.520	7.530E-05	5.060E-03
TAF9	predicted gene 12372	-1.291	-0.368	7.820E-05	5.220E-03
DMD	dystrophin, muscular dystrophy	1.339	0.421	7.920E-05	5.260E-03
Vps37d	vacuolar protein sorting 37D (yeast)	-1.312	-0.392	8.140E-05	5.380E-03
Edf1	endothelial differentiation-related factor 1	-1.380	-0.465	8.420E-05	5.470E-03
Abhd8	abhydrolase domain containing 8	-1.309	-0.389	8.350E-05	5.470E-03
Dync2h1	dynein cytoplasmic 2 heavy chain 1	1.413	0.499	8.440E-05	5.470E-03
Pikfyve	phosphoinositide kinase, FYVE finger containing	1.361	0.445	8.380E-05	5.470E-03
Zmynd19	zinc finger, MYND domain containing 19	-1.239	-0.309	8.550E-05	5.520E-03
Kif20a	kinesin family member 20A	1.366	0.450	8.690E-05	5.580E-03
Pycr2	pyrroline-5-carboxylate reductase family, member 2	-1.268	-0.343	9.040E-05	5.780E-03
Luc7l3	LUC7-like 3 pre-mRNA splicing facto	1.439	0.525	9.290E-05	5.880E-03
Unc119	unc-119 homolog (C. elegans)	-1.291	-0.368	9.260E-05	5.880E-03
Chchd10	coiled-coil-helix-coiled-coil-helix domain containing 10	-1.466	-0.552	9.440E-05	5.940E-03
Basp1	brain abundant, membrane attached signal protein 1	-1.406	-0.492	9.460E-05	5.940E-03
Papss1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	-1.170	-0.227	9.620E-05	6.010E-03
Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	-1.413	-0.499	9.760E-05	6.070E-03
Rps28	ribosomal protein S28	-1.459	-0.545	9.870E-05	6.110E-03
Apc	adenomatosis polyposis coli	1.265	0.339	1.010E-04	6.200E-03
Arf6	ADP-ribosylation factor 6	-1.236	-0.306	1.020E-04	6.220E-03
Clk4	CDC like kinase 4	1.455	0.541	1.030E-04	6.220E-03
Seh1l	SEH1-like (S. cerevisiae)	1.245	0.316	1.020E-04	6.220E-03
Zmym6	zinc finger, MYM-type 6	1.423	0.509	1.030E-04	6.220E-03
Ppdf	ancreatic progenitor cell differentiation and proliferation factor homolog (zebrafish)	-1.333	-0.415	1.050E-04	6.240E-03
Cfp	complement factor properdin	1.439	0.525	1.040E-04	6.240E-03
Epb4.115	erythrocyte protein band 4.1-like 5	1.397	0.482	1.070E-04	6.240E-03
Hnrnpa0	heterogeneous nuclear ribonucleoprotein A0	-1.343	-0.425	1.050E-04	6.240E-03
Hint1	histidine triad nucleotide binding protein 1	-1.405	-0.491	1.070E-04	6.240E-03
Phc3	polyhomeotic-like 3 (Drosophila)	1.358	0.442	1.060E-04	6.240E-03
RPL37A	ribosomal protein L37a	-1.438	-0.524	1.070E-04	6.240E-03
RGD1564420	similar to Hypothetical protein MGC31278	1.178	0.236	1.070E-04	6.240E-03
Ypel3	yippee-like 3 (Drosophila)	-1.275	-0.350	1.050E-04	6.240E-03
Rps10	ribosomal protein S10	-1.346	-0.429	1.110E-04	6.450E-03
Bnip2	BCL2/adenovirus E1B interacting protein 2	1.371	0.455	1.130E-04	6.510E-03
Zdhhc15	zinc finger, DHHC domain containing 15	1.390	0.475	1.150E-04	6.610E-03
Cox6c	cytochrome c oxidase, subunit VIc	-1.312	-0.392	1.190E-04	6.840E-03
Abca8b	ATP-binding cassette, sub-family A (ABC1), member 8b	1.399	0.484	1.230E-04	6.950E-03
Phlpp2	PH domain and leucine rich repeat protein phosphatase 2	1.328	0.409	1.230E-04	6.950E-03
Ttc14	tetratricopeptide repeat domain 14	1.466	0.552	1.220E-04	6.950E-03
H2afy2	H2A histone family, member Y2	-1.220	-0.287	1.240E-04	6.970E-03
LOC680233	hypothetical protein LOC688095	-1.382	-0.467	1.240E-04	6.970E-03
Nfrkb	nuclear factor related to kappa B binding protein	1.306	0.385	1.270E-04	7.080E-03

Cox5b	cytochrome c oxidase, subunit Vb	-1.277	-0.353	1.290E-04	7.160E-03
Rps9	ribosomal protein S9	-1.464	-0.550	1.320E-04	7.300E-03
Wdr18	WD repeat domain 18	-1.289	-0.366	1.320E-04	7.300E-03
Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	-1.469	-0.555	1.340E-04	7.360E-03
Nudc	nuclear distribution gene C homolog (Aspergillus), pseudogene 1	-1.434	-0.520	1.340E-04	7.360E-03
Rbbp8	retinoblastoma binding protein 8	1.332	0.414	1.370E-04	7.400E-03
Rnf208	ring finger protein 208	-1.336	-0.418	1.360E-04	7.400E-03
Sap30l	SAP30-like	-1.345	-0.428	1.350E-04	7.400E-03
H1fx	H1 histone family, member X	-1.453	-0.539	1.380E-04	7.420E-03
Fbll1	fibrillarin-like 1	-1.391	-0.476	1.390E-04	7.470E-03
Gadd45gip1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	-1.319	-0.399	1.390E-04	7.470E-03
ENSRNOG00000045588	ENSRNOG00000045588	-1.306	-0.385	1.410E-04	7.520E-03
Ubald2	UBA-like domain containing 2	-1.394	-0.479	1.430E-04	7.580E-03
Sepsecs	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	1.350	0.433	1.440E-04	7.610E-03
Baz2b	bromodomain adjacent to zinc finger domain, 2B	1.376	0.461	1.450E-04	7.630E-03
Rn60_14_0792.1	ENSRNOG00000029723	-1.465	-0.551	1.480E-04	7.780E-03
Hmx3	H6 homeo box 3	-1.459	-0.545	1.500E-04	7.840E-03
RPS6	ribosomal protein S6	-1.461	-0.547	1.520E-04	7.870E-03
Xpo4	exportin 4	1.398	0.483	1.510E-04	7.870E-03
ENSRNOG00000039654	ENSRNOG00000039654	-1.465	-0.551	1.530E-04	7.930E-03
Myo9a	myosin IXa	1.348	0.431	1.550E-04	7.980E-03
Mt3	metallothionein 3	-1.387	-0.472	1.580E-04	8.060E-03
Phb2	prohibitin 2	-1.235	-0.305	1.570E-04	8.060E-03
Dmc1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	1.464	0.550	1.590E-04	8.120E-03
Slc28a2	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	1.463	0.549	1.620E-04	8.210E-03
Rps16	ribosomal protein S16	-1.364	-0.448	1.670E-04	8.350E-03
Ap4e1	adaptor-related protein complex AP-4, epsilon 1	1.370	0.454	1.670E-04	8.350E-03
Etfdh	electron transferring flavoprotein, dehydrogenase	1.265	0.339	1.660E-04	8.350E-03
Rpgrip1l	Rpgrip1-like	1.359	0.443	1.670E-04	8.350E-03
Rnf126	ring finger protein 126	-1.376	-0.460	1.710E-04	8.360E-03
Btbd7	BTB (POZ) domain containing 7	1.389	0.474	1.690E-04	8.360E-03
Evi5l	ecotropic viral integration site 5-like	-1.199	-0.262	1.710E-04	8.360E-03
PCBP2	poly(rC) binding protein 2	-1.179	-0.238	1.690E-04	8.360E-03
Ppp5c	protein phosphatase 5, catalytic subunit	-1.228	-0.296	1.710E-04	8.360E-03
RGD1311899	similar to RIKEN cDNA 2210016L21 gene	-1.272	-0.347	1.720E-04	8.360E-03
Slc32a1	solute carrier family 32 (GABA vesicular transporter), member 1	-1.439	-0.525	1.680E-04	8.360E-03
Zcchc7	zinc finger, CCHC domain containing 7	1.373	0.457	1.700E-04	8.360E-03
Pap0g	poly(A) polymerase gamma	1.402	0.488	1.730E-04	8.390E-03
Cspp1	centrosome and spindle pole associated protein 1	1.370	0.454	1.750E-04	8.410E-03
Eif4h	eukaryotic translation initiation factor 4H	-1.218	-0.284	1.750E-04	8.410E-03
CCNL2	cyclin L2	1.376	0.461	1.760E-04	8.420E-03
Atp5i	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit E	-1.409	-0.495	1.780E-04	8.490E-03
Fam227a	family with sequence similarity 227, member A	1.456	0.542	1.780E-04	8.490E-03
Nup205	nucleoporin 205	1.357	0.440	1.840E-04	8.750E-03
Aip	aryl-hydrocarbon receptor-interacting protein	-1.273	-0.348	1.870E-04	8.860E-03
Gramd1c	GRAM domain containing 1C	1.431	0.517	1.890E-04	8.890E-03
Qtrtd1	queuine tRNA-ribosyltransferase domain containing 1	1.365	0.449	1.890E-04	8.890E-03

Ankle2	ankyrin repeat and LEM domain containing 2	1.324	0.405	1.900E-04	8.900E-03
Glt8d1	glycosyltransferase 8 domain containing 1	1.270	0.345	1.920E-04	8.970E-03
Aqr	aquarius	1.229	0.297	1.960E-04	9.090E-03
Fastkd3	FAST kinase domains 3	1.401	0.486	1.970E-04	9.090E-03
Lrrk2	leucine-rich repeat kinase 2	1.431	0.517	1.960E-04	9.090E-03
Cdc34	cell division cycle 34 homolog (<i>S. cerevisiae</i>)	-1.354	-0.437	1.990E-04	9.110E-03
Narg2	NMDA receptor-regulated gene 2	1.442	0.528	1.980E-04	9.110E-03
Cot11	coactosin-like 1 (<i>Dictyostelium</i>)	-1.370	-0.454	2.010E-04	9.180E-03
Rnpc3	RNA-binding region (RNP1, RRM) containing 3	1.397	0.482	2.020E-04	9.190E-03
Smarcb1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	-1.229	-0.297	2.020E-04	9.190E-03
Rbl1	retinoblastoma-like 1 (p107)	1.423	0.509	2.030E-04	9.210E-03
Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	1.355	0.438	2.060E-04	9.240E-03
Agbl3	ATP/GTP binding protein-like 3	1.445	0.531	2.060E-04	9.240E-03
Fuz	fuzzy homolog (<i>Drosophila</i>)	-1.293	-0.371	2.060E-04	9.240E-03
Snx17	sorting nexin 17	-1.236	-0.306	2.070E-04	9.240E-03
Tceal6	transcription elongation factor A (SII)-like 6	-1.299	-0.377	2.070E-04	9.240E-03
Csmd3	CUB and Sushi multiple domains 3	1.358	0.442	2.110E-04	9.360E-03
Lage3	L antigen family, member 3	-1.309	-0.389	2.110E-04	9.360E-03
Rsrp1	arginine and serine rich protein 1	1.332	0.414	2.140E-04	9.400E-03
Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	-1.319	-0.399	2.130E-04	9.400E-03
Dzf17	zinc finger protein 17	1.292	0.370	2.140E-04	9.400E-03
MBD3	methyl-CpG binding domain protein 3	-1.306	-0.385	2.150E-04	9.420E-03
Mta1	metastasis associated 1	-1.193	-0.254	2.170E-04	9.430E-03
Tbc1d4	TBC1 domain family, member 4	1.412	0.498	2.170E-04	9.430E-03
Ergic3	ERGIC and golgi 3	-1.225	-0.293	2.190E-04	9.440E-03
Osgin2	oxidative stress induced growth inhibitor family member 2	1.336	0.418	2.180E-04	9.440E-03
Pcbp4	poly(rC) binding protein 4	-1.276	-0.352	2.210E-04	9.490E-03
Irf2bp1	interferon regulatory factor 2 binding protein-like	-1.318	-0.398	2.230E-04	9.570E-03
Slc25a27	solute carrier family 25, member 27	1.237	0.307	2.250E-04	9.620E-03
Rps15	ribosomal protein S15	-1.235	-0.305	2.310E-04	9.720E-03
Rps27	ribosomal protein S27	-1.393	-0.478	2.300E-04	9.720E-03
Crebrf	CREB3 regulatory factor	1.404	0.490	2.300E-04	9.720E-03
Erc6l2	ERCC excision repair 6 like 2	1.315	0.395	2.310E-04	9.720E-03
Ipo4	importin 4	-1.193	-0.255	2.300E-04	9.720E-03
Dact3	dapper homolog 3, antagonist of beta-catenin (<i>xenopus</i>)	-1.310	-0.390	2.330E-04	9.730E-03
Gpr27	G protein-coupled receptor 27	-1.391	-0.476	2.320E-04	9.730E-03
Cntrl	centriolin	1.363	0.447	2.340E-04	9.740E-03
Grik2	glutamate receptor, ionotropic, kainate 2 (beta 2)	1.309	0.388	2.340E-04	9.740E-03
HRAS1	Harvey rat sarcoma virus oncogene 1	-1.297	-0.375	2.370E-04	9.770E-03
Sf3b5	splicing factor 3b, subunit 5	-1.308	-0.387	2.370E-04	9.770E-03
Thra	thyroid hormone receptor alpha	-1.271	-0.346	2.360E-04	9.770E-03
Maf1	MAF1 homolog (<i>S. cerevisiae</i>)	-1.158	-0.212	2.440E-04	1.000E-02
Emc6	elastin microfibril interfacier 2	-1.377	-0.462	2.500E-04	1.020E-02
Ralgapa1	GTPase activating RANGAP domain-like 1	1.293	0.371	2.520E-04	1.030E-02
Lrch3	leucine-rich repeats and calponin homology (CH) domain containing 3	1.264	0.338	2.530E-04	1.030E-02
Rnf170	ring finger protein 170	1.293	0.371	2.530E-04	1.030E-02
ENSRNOG00000029723	uncharacterized protein	1.410	0.496	2.510E-04	1.030E-02
Rnf7	ring finger protein 7	-1.392	-0.477	2.610E-04	1.040E-02
Epg5	ectopic P-granules autophagy protein 5 homolog (<i>C.</i>	1.366	0.450	2.610E-04	1.040E-02

	elegans)				
ERCC5	excision repair cross-complementing rodent repair deficiency, complementation group 5	1.306	0.385	2.570E-04	1.040E-02
Gcfc2	GC-rich sequence DNA-binding factor 2	1.404	0.490	2.590E-04	1.040E-02
Tet1	tet oncogene 1	1.431	0.517	2.590E-04	1.040E-02
Mif	macrophage migration inhibitory factor-like	-1.406	-0.492	2.650E-04	1.050E-02
Greb1l	cDNA sequence AK220484	1.424	0.510	2.660E-04	1.050E-02
Nufip2	NUFIP2, FMR1 interacting protein 2	1.369	0.453	2.650E-04	1.050E-02
Rps29	ribosomal protein S29	-1.365	-0.449	2.670E-04	1.060E-02
RPL26	ribosomal protein L26	-1.394	-0.479	2.700E-04	1.060E-02
Rpl10a	ribosomal protein L10A	-1.355	-0.438	2.760E-04	1.070E-02
C1qtnf4	C1q and tumor necrosis factor related protein 4	-1.407	-0.493	2.780E-04	1.070E-02
Eif1b	eukaryotic translation initiation factor 1B	-1.223	-0.290	2.770E-04	1.070E-02
Gpr98	G protein-coupled receptor 98	1.434	0.520	2.720E-04	1.070E-02
Lrrc4b	leucine rich repeat containing 4B	-1.279	-0.355	2.750E-04	1.070E-02
Map7d1	MAP7 domain containing 1	-1.219	-0.286	2.730E-04	1.070E-02
Pdxp	pyridoxal (pyridoxine, vitamin B6) phosphatase	-1.303	-0.382	2.740E-04	1.070E-02
Jund	Jun proto-oncogene related gene d	-1.417	-0.503	2.820E-04	1.090E-02
Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	-1.174	-0.231	2.850E-04	1.090E-02
Rpl19	ribosomal protein L19	-1.230	-0.299	2.920E-04	1.100E-02
Sf3b4	splicing factor 3b, subunit 4	-1.254	-0.327	2.930E-04	1.100E-02
Csnk1g2	casein kinase 1, gamma 2	-1.294	-0.372	2.890E-04	1.100E-02
Fam89b	family with sequence similarity 89, member B	-1.304	-0.383	2.920E-04	1.100E-02
Foxp4	forkhead box P4	-1.300	-0.378	2.900E-04	1.100E-02
Gdap2	ganglioside-induced differentiation-associated-protein 2	1.335	0.417	2.930E-04	1.100E-02
Ibtk	inhibitor of Bruton agammaglobulinemia tyrosine kinase	1.343	0.425	2.870E-04	1.100E-02
Mtus1	mitochondrial tumor suppressor 1	1.307	0.386	2.890E-04	1.100E-02
Zfp187	zinc finger protein 187	1.367	0.451	2.900E-04	1.100E-02
Cacnb2	calcium channel, voltage-dependent, beta 2 subunit	1.236	0.306	2.970E-04	1.110E-02
Mid1ip1	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish))	-1.211	-0.276	3.020E-04	1.120E-02
Wdfy2	WD repeat and FYVE domain containing 2	1.325	0.406	3.040E-04	1.130E-02
Ccser2	coiled-coil serine-rich protein 2	1.251	0.323	3.100E-04	1.140E-02
Ubn2	ubiquitin 2	1.327	0.408	3.070E-04	1.140E-02
Zfp575	zinc finger protein 575	-1.354	-0.437	3.090E-04	1.140E-02
Scn8a	sodium channel, voltage-gated, type VIII, alpha	1.289	0.366	3.130E-04	1.150E-02
Eif4ebp3	ankyrin repeat and KH domain containing 1	1.318	0.398	3.150E-04	1.160E-02
Eml4	echinoderm microtubule associated protein like 4	1.364	0.448	3.190E-04	1.170E-02
Ssr4	signal sequence receptor, delta	-1.247	-0.318	3.240E-04	1.180E-02
Atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	-1.347	-0.430	3.280E-04	1.190E-02
KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1	1.363	0.447	3.300E-04	1.190E-02
Lrrc10b	predicted gene 705	-1.422	-0.508	3.300E-04	1.190E-02
Ptov1	prostate tumor over expressed gene 1	-1.304	-0.383	3.330E-04	1.190E-02
Poglut1	protein O-glucosyltransferase 1	1.281	0.357	3.300E-04	1.190E-02
RGD1565363	similar to RIKEN cDNA 1110025L05	-1.371	-0.455	3.340E-04	1.190E-02
Zfp192	zinc finger protein 192	1.425	0.511	3.330E-04	1.190E-02
Cox6a1	cytochrome c oxidase, subunit VI a, polypeptide 1	-1.343	-0.425	3.440E-04	1.200E-02
Lrnf4	leucine rich repeat and fibronectin type III domain containing 4	-1.307	-0.386	3.370E-04	1.200E-02
Sec61b	Sec61 beta subunit	-1.290	-0.367	3.370E-04	1.200E-02
Ssbp4	single stranded DNA binding protein 4	-1.370	-0.454	3.420E-04	1.200E-02
Slc20a1	solute carrier family 20, member 1	1.249	0.321	3.410E-04	1.200E-02

Cactin	spliceosome C complex subunit	-1.251	-0.323	3.380E-04	1.200E-02
Sox12	SRY-box containing gene 12	-1.311	-0.391	3.440E-04	1.200E-02
Zfp202	zinc finger protein 202	1.336	0.418	3.440E-04	1.200E-02
Zfp428	zinc finger protein 428	-1.292	-0.370	3.410E-04	1.200E-02
Cadm4	cell adhesion molecule 4	-1.333	-0.415	3.480E-04	1.210E-02
Ddx20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	1.281	0.357	3.480E-04	1.210E-02
Nup160	nucleoporin 160	1.329	0.410	3.530E-04	1.220E-02
Ubr1	ubiquitin 1	-1.199	-0.262	3.540E-04	1.220E-02
Efcab14	EF-hand calcium binding domain 14	1.317	0.397	3.620E-04	1.230E-02
Flywch2	FLYWCH family member 2	-1.261	-0.334	3.580E-04	1.230E-02
Gnaz	guanine nucleotide binding protein, alpha z subunit	-1.263	-0.337	3.550E-04	1.230E-02
Npat	nuclear protein in the AT region	1.385	0.470	3.570E-04	1.230E-02
Stx3	syntaxin 3	1.343	0.425	3.560E-04	1.230E-02
ENSRNOG00000046381	ENSRNOG00000046381	-1.356	-0.439	3.600E-04	1.230E-02
Rac3	RAS-related C3 botulinum substrate 3	-1.344	-0.427	3.630E-04	1.240E-02
Rps12	ribosomal protein S12	-1.341	-0.423	3.670E-04	1.250E-02
Cd46	CD46 antigen, complement regulatory protein	1.432	0.518	3.720E-04	1.250E-02
Cdt1	chromatin licensing and DNA replication factor 1	-1.414	-0.500	3.760E-04	1.250E-02
Mdn1	midasin homolog (yeast)	1.431	0.517	3.680E-04	1.250E-02
Ncapg2	non-SMC condensin II complex, subunit G2	1.414	0.500	3.710E-04	1.250E-02
Sgpl1	sphingosine phosphate lyase 1	1.312	0.392	3.750E-04	1.250E-02
Ubr2	ubiquitin protein ligase E3 component n-recogin 2	1.241	0.312	3.700E-04	1.250E-02
Wsb1	WD repeat and SOCS box-containing 1	1.388	0.473	3.750E-04	1.250E-02
Uhrf2	ubiquitin-like, containing PHD and RING finger domains 2	1.334	0.416	3.800E-04	1.260E-02
Zfand3	zinc finger, AN1-type domain 3	-1.193	-0.254	3.790E-04	1.260E-02
Rps3a	ribosomal protein S3A	-1.268	-0.343	3.840E-04	1.270E-02
Bcl7c	B-cell CLL/lymphoma 7C	-1.304	-0.383	3.890E-04	1.270E-02
Hps5	Hermansky-Pudlak syndrome 5 homolog (human)	1.395	0.480	3.890E-04	1.270E-02
Hmga1	high mobility group AT-hook I, related sequence 1	-1.352	-0.435	3.900E-04	1.270E-02
Podxl2	podocalyxin-like 2	-1.255	-0.328	3.880E-04	1.270E-02
Trim5	predicted gene 4992	1.408	0.494	3.840E-04	1.270E-02
Ptprd	protein tyrosine phosphatase, receptor type, D	1.273	0.348	3.870E-04	1.270E-02
Serpinc1	serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	1.385	0.470	3.860E-04	1.270E-02
AABR07054456.3	AABR07054456.3	-1.430	-0.516	3.840E-04	1.270E-02
Fntb	farnesyltransferase, CAAX box, beta	-1.216	-0.282	3.960E-04	1.280E-02
Mysm1	myb-like, SWIRM and MPN domains 1	1.379	0.464	3.970E-04	1.280E-02
Rpl36al	ribosomal protein L36A-like	-1.290	-0.367	3.990E-04	1.280E-02
Cisd1	CDGSH iron sulfur domain 1	-1.229	-0.297	3.970E-04	1.280E-02
Cramp11	Crp, cramped-like (Drosophila)	1.326	0.407	4.000E-04	1.280E-02
Nog	noggin	-1.393	-0.478	4.000E-04	1.280E-02
Nr2f6	nuclear receptor subfamily 2, group F, member 6	-1.296	-0.374	3.990E-04	1.280E-02
Ist1	ESCRT-III associated factor	1.171	0.228	4.030E-04	1.290E-02
Cdon	cell adhesion molecule-related/down-regulated by oncogenes	1.376	0.460	4.110E-04	1.300E-02
Chd8	chromodomain helicase DNA binding protein 8	1.169	0.225	4.150E-04	1.300E-02
Map3k2	mitogen-activated protein kinase kinase kinase 2	1.352	0.435	4.150E-04	1.300E-02
Pclo	piccolo (presynaptic cytomatrix protein)	1.271	0.346	4.080E-04	1.300E-02
Ralgapa2	Ral GTPase activating protein catalytic alpha subunit 2	1.318	0.398	4.120E-04	1.300E-02
Slc7a6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	1.238	0.308	4.130E-04	1.300E-02
Tceal3	transcription elongation factor A (SII)-like 3	-1.301	-0.380	4.130E-04	1.300E-02

Tnrc6b	trinucleotide repeat containing 6b	1.327	0.408	4.150E-04	1.300E-02
Ubqln2	ubiquilin 2	-1.200	-0.263	4.090E-04	1.300E-02
Baz2a	bromodomain adjacent to zinc finger domain, 2A	1.308	0.387	4.190E-04	1.310E-02
C1qbp	complement component 1, q subcomponent binding protein	-1.246	-0.317	4.230E-04	1.310E-02
Foxo6	forkhead box O6	-1.300	-0.378	4.250E-04	1.310E-02
Ptms	parathyrosin	-1.225	-0.293	4.210E-04	1.310E-02
Phex	phosphate regulating gene with homologies to endopeptidases on the X chromosome (hypophosphatemia, vitamin D resistant rickets)	1.419	0.505	4.260E-04	1.310E-02
Zfp787	zinc finger protein 787	-1.327	-0.408	4.240E-04	1.310E-02
Gpatch8	G patch domain containing 8	1.283	0.360	4.320E-04	1.320E-02
Secisbp2	SECIS binding protein 2	1.318	0.398	4.300E-04	1.320E-02
Stard9	START domain containing 9	1.397	0.482	4.290E-04	1.320E-02
Hexim1	hexamethylene bis-acetamide inducible 1	-1.194	-0.256	4.340E-04	1.330E-02
Rps25	ribosomal protein S25	-1.328	-0.409	4.430E-04	1.350E-02
Atr	ataxia telangiectasia and Rad3 related	1.411	0.497	4.470E-04	1.350E-02
Ncapd3	non-SMC condensin II complex, subunit D3	1.281	0.357	4.440E-04	1.350E-02
Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	1.397	0.482	4.470E-04	1.350E-02
Gpr162	G protein-coupled receptor 162	-1.223	-0.291	4.540E-04	1.360E-02
Med23	mediator complex subunit 23	1.279	0.355	4.530E-04	1.360E-02
Rnf213	ring finger protein 213	1.344	0.426	4.490E-04	1.360E-02
Akt1s1	AKT1 substrate 1 (proline-rich)	-1.232	-0.301	4.580E-04	1.370E-02
Csrp2	cysteine and glycine-rich protein 2	-1.274	-0.349	4.590E-04	1.370E-02
Kans1l	KAT8 regulatory NSL complex subunit 1-like	1.393	0.478	4.560E-04	1.370E-02
Pggt1b	protein geranylgeranyltransferase type I, beta subunit	1.336	0.418	4.570E-04	1.370E-02
Vps13d	vacuolar protein sorting 13 D (yeast)	1.239	0.309	4.600E-04	1.370E-02
ENSRNOG00000049713	ENSRNOG00000049713	1.423	0.509	4.650E-04	1.380E-02
Carmil2	capping protein regulator and myosin 1 linker 2	-1.273	-0.348	4.690E-04	1.390E-02
RGD1307752	similar to RIKEN cDNA 1110008F13	-1.186	-0.246	4.750E-04	1.400E-02
Cox5a	cytochrome c oxidase, subunit Va	-1.316	-0.396	4.850E-04	1.410E-02
Kcna2	potassium voltage-gated channel, shaker-related subfamily, member 2	1.402	0.488	4.830E-04	1.410E-02
Pfn1	profilin 1	-1.283	-0.359	4.830E-04	1.410E-02
Phb	prohibitin	-1.202	-0.266	4.780E-04	1.410E-02
Prmt2	protein arginine N-methyltransferase 2	-1.225	-0.293	4.780E-04	1.410E-02
TRAPPC2	similar to Chain A, The Crystal Structure Of The Bet3-Trs31-Sedlin Complex	-1.422	-0.508	4.780E-04	1.410E-02
Zfp706	zinc finger protein 706	-1.327	-0.408	4.840E-04	1.410E-02
Mpc2	mitochondrial pyruvate carrier 2	-1.235	-0.304	4.930E-04	1.430E-02
Phactr3	phosphatase and actin regulator 3	-1.280	-0.356	4.910E-04	1.430E-02
Socs1	suppressor of cytokine signaling 1	-1.415	-0.501	4.930E-04	1.430E-02
ATG101	autophagy related 101	-1.180	-0.239	5.050E-04	1.450E-02
Rel2	RELT-like 2	-1.366	-0.450	5.010E-04	1.450E-02
Usp24	ubiquitin specific peptidase 24	1.347	0.430	5.050E-04	1.450E-02
Nek9	NIMA (never in mitosis gene a)-related expressed kinase 9	1.238	0.308	5.110E-04	1.460E-02
Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	-1.227	-0.295	5.070E-04	1.460E-02
Sumo2l	small ubiquitin-like modifier 4	-1.412	-0.498	5.080E-04	1.460E-02
Slc1a2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	1.319	0.399	5.130E-04	1.460E-02
Qser1	glutamine and serine rich 1	1.356	0.439	5.150E-04	1.470E-02
Mir186	microRNA 186	1.406	0.492	5.190E-04	1.470E-02

Fam69b	family with sequence similarity 69, member B	-1.223	-0.290	5.210E-04	1.480E-02
U2surp	U2 snRNP-associated SURP domain containing	1.343	0.425	5.240E-04	1.480E-02
ATP5G3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 3	-1.231	-0.300	5.280E-04	1.490E-02
Cygb	cytoglobin	-1.310	-0.390	5.330E-04	1.490E-02
Dock7	dedicator of cytokinesis 7	1.225	0.293	5.280E-04	1.490E-02
Ninl	ninein-like	1.329	0.410	5.330E-04	1.490E-02
Plag1	pleiomorphic adenoma gene 1	1.385	0.470	5.290E-04	1.490E-02
Psemb5	predicted gene 3375	-1.254	-0.327	5.300E-04	1.490E-02
Gfm2	G elongation factor, mitochondrial 2	1.294	0.372	5.430E-04	1.500E-02
Luzp1	leucine zipper protein 1	1.308	0.387	5.440E-04	1.500E-02
Lrp1b	low density lipoprotein-related protein 1B (deleted in tumors)	1.363	0.447	5.430E-04	1.500E-02
Nenf	neuron derived neurotrophic factor	-1.340	-0.422	5.440E-04	1.500E-02
Pgap1	post-GPI attachment to proteins 1	1.319	0.399	5.360E-04	1.500E-02
Ppp6r3	protein phosphatase 6, regulatory subunit 3	1.246	0.317	5.410E-04	1.500E-02
Ptpn9	protein tyrosine phosphatase, non-receptor type 9	1.184	0.244	5.470E-04	1.500E-02
Phtf1	putative homeodomain transcription factor 1	1.385	0.470	5.470E-04	1.500E-02
Wwc3	WWC family member 3	1.345	0.428	5.450E-04	1.500E-02
Lrrn2	leucine rich repeat protein 2, neuronal	-1.241	-0.311	5.560E-04	1.510E-02
Ranbp17	RAN binding protein 17	1.358	0.442	5.510E-04	1.510E-02
Setdb2	SET domain, bifurcated 2	1.382	0.467	5.500E-04	1.510E-02
RGD1305587	similar to RIKEN cDNA 2010107G23	-1.257	-0.330	5.550E-04	1.510E-02
Ubr5	ubiquitin protein ligase E3 component n-recognin 5	1.248	0.320	5.580E-04	1.510E-02
Zzz3	zinc finger, ZZ domain containing 3	1.330	0.411	5.520E-04	1.510E-02
Ccdc92	coiled-coil domain containing 92	-1.260	-0.333	5.700E-04	1.530E-02
Exosc5	exosome component 5	-1.288	-0.365	5.690E-04	1.530E-02
Hcfc2	host cell factor C2	1.256	0.329	5.640E-04	1.530E-02
Prr14l	proline rich 14-like	1.322	0.403	5.710E-04	1.530E-02
Serp2	stress-associated endoplasmic reticulum protein family member 2	-1.339	-0.421	5.700E-04	1.530E-02
Mff	mitochondrial fission factor	-1.415	-0.501	5.760E-04	1.540E-02
Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit 1A	-1.296	-0.374	5.730E-04	1.540E-02
Zfp612	zinc finger protein 612	1.356	0.439	5.780E-04	1.540E-02
Ddit4	DNA-damage-inducible transcript 4	-1.245	-0.316	5.800E-04	1.550E-02
Capzb	capping protein (actin filament) muscle Z-line, beta	-1.170	-0.227	5.890E-04	1.570E-02
Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)	-1.177	-0.235	5.930E-04	1.570E-02
Tmem26	transmembrane protein 26	1.398	0.483	5.910E-04	1.570E-02
UBB	ubiquitin B	-1.242	-0.313	5.980E-04	1.580E-02
Acot7	acyl-CoA thioesterase 7	-1.275	-0.351	6.010E-04	1.580E-02
Acbd6	acyl-Coenzyme A binding domain containing 6	-1.251	-0.323	6.010E-04	1.580E-02
YBX1	similar to nuclease sensitive element binding protein 1	-1.283	-0.359	6.050E-04	1.590E-02
Krit1	KRIT1, ankyrin repeat containing	1.380	0.465	6.070E-04	1.590E-02
Sycp3	synaptonemal complex protein 3	1.413	0.499	6.030E-04	1.590E-02
Zfp451	zinc finger protein 451	1.317	0.397	6.100E-04	1.590E-02
Cep290	centrosomal protein 290	1.387	0.472	6.140E-04	1.600E-02
DPF1	D4, zinc and double PHD fingers family 1	-1.228	-0.296	6.110E-04	1.600E-02
Otud4	OTU domain containing 4	1.335	0.417	6.120E-04	1.600E-02
Rab23	RAB23, member RAS oncogene family	1.180	0.239	6.240E-04	1.620E-02
Emd	echinoderm microtubule associated protein like 4	-1.231	-0.300	6.360E-04	1.650E-02
Ganc	glucosidase, alpha	1.345	0.428	6.420E-04	1.660E-02
Exosc4	exosome component 4	-1.300	-0.378	6.470E-04	1.670E-02

Hcfc1r1	host cell factor C1 regulator 1 (XPO1-dependent)	-1.408	-0.494	6.490E-04	1.670E-02
Hypk	Huntingtin interacting protein K	-1.268	-0.343	6.480E-04	1.670E-02
Mbnl1	muscleblind-like 1 (Drosophila)	1.273	0.348	6.520E-04	1.670E-02
RGD1565775	similar to RIKEN cDNA 2810403A07	1.334	0.416	6.520E-04	1.670E-02
Fam178a	family with sequence similarity 178, member A	1.348	0.431	6.580E-04	1.680E-02
Cntfr	ciliary neurotrophic factor receptor	-1.344	-0.427	6.610E-04	1.690E-02
Bms1	BMS1 homolog, ribosome assembly protein (yeast)	1.322	0.403	6.660E-04	1.700E-02
Ppia	peptidylprolyl isomerase A	-1.268	-0.342	6.740E-04	1.710E-02
Bok	BCL2-related ovarian killer protein	-1.241	-0.312	6.730E-04	1.710E-02
Cds2	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2	1.291	0.368	6.830E-04	1.720E-02
Gsk3a	glycogen synthase kinase 3 alpha	-1.253	-0.325	6.830E-04	1.720E-02
Pam16	presequence translocase-associated motor 16 homolog (S. cerevisiae)	-1.304	-0.383	6.800E-04	1.720E-02
Rc3h2	ring finger and CCCH-type zinc finger domains 2	1.322	0.403	6.810E-04	1.720E-02
Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	-1.253	-0.325	6.870E-04	1.730E-02
Med17	mediator complex subunit 17	1.355	0.438	6.960E-04	1.750E-02
Arhgap29	Rho GTPase activating protein 29	1.365	0.449	6.970E-04	1.750E-02
RGD1307100	imilar to RIKEN cDNA D630029K19	1.359	0.443	7.070E-04	1.760E-02
Ltv1	LTV1 homolog (S. cerevisiae)	1.310	0.390	7.020E-04	1.760E-02
Camk2n2	calcium/calmodulin-dependent protein kinase II inhibitor 2	-1.391	-0.476	7.160E-04	1.780E-02
RGD1308134	similar to RIKEN cDNA 1110020A23	-1.272	-0.347	7.150E-04	1.780E-02
Tomm6	translocase of outer mitochondrial membrane 6 homolog (yeast)	-1.336	-0.418	7.150E-04	1.780E-02
Dda1	DET1 and DDB1 associated 1	-1.283	-0.360	7.250E-04	1.790E-02
Fnip1	folliculin interacting protein 1	1.352	0.435	7.220E-04	1.790E-02
Snx13	sorting nexin 13	1.342	0.424	7.270E-04	1.790E-02
Wbp4	WW domain binding protein 4	1.294	0.372	7.230E-04	1.790E-02
Uba52	ubiquitin A-52 residue ribosomal protein fusion product 1	-1.286	-0.363	7.380E-04	1.810E-02
Il1rap1	interleukin 1 receptor accessory protein-like 1	1.384	0.469	7.390E-04	1.810E-02
Rrad	Ras-related associated with diabetes	-1.380	-0.465	7.340E-04	1.810E-02
Pogz	pogo transposable element with ZNF domain	1.180	0.239	7.580E-04	1.850E-02
Zfp386	zinc finger protein 386 (Kruppel-like)	1.369	0.453	7.550E-04	1.850E-02
Star	steroidogenic acute regulatory protein	1.363	0.447	7.650E-04	1.870E-02
Eml6	echinoderm microtubule associated protein like 6	1.340	0.422	7.750E-04	1.880E-02
ENSRNOG00000046986	ENSRNOG00000046986	1.287	0.364	7.730E-04	1.880E-02
Rpl13a	ribosomal protein L13A	-1.215	-0.281	7.820E-04	1.900E-02
Ly6h	lymphocyte antigen 6 complex, locus H	-1.292	-0.370	7.950E-04	1.910E-02
Rnaseh2a	ribonuclease H2, large subunit	-1.252	-0.324	7.950E-04	1.910E-02
Smc5	structural maintenance of chromosomes 5	1.367	0.451	7.980E-04	1.910E-02
Usf2	upstream transcription factor 2	-1.240	-0.310	8.040E-04	1.910E-02
Gnl1	guanine nucleotide binding protein-like 1	-1.244	-0.315	7.930E-04	1.910E-02
Med1	mediator complex subunit 1	1.256	0.329	7.890E-04	1.910E-02
Map3k11	mitogen-activated protein kinase kinase kinase 11	-1.387	-0.472	7.890E-04	1.910E-02
Ndn	neclin	-1.229	-0.297	8.020E-04	1.910E-02
Kctd17	potassium channel tetramerisation domain containing 17	-1.239	-0.309	8.000E-04	1.910E-02
Kcnmb4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	-1.274	-0.349	7.980E-04	1.910E-02
ENSRNOG00000018204	ENSRNOG00000018204	1.402	0.488	7.890E-04	1.910E-02
Cox8a	cytochrome c oxidase, subunit VIIIa	-1.346	-0.429	8.130E-04	1.920E-02
Acadsb	acyl-Coenzyme A dehydrogenase, short/branched chain	1.330	0.411	8.110E-04	1.920E-02

Mrps34	mitochondrial ribosomal protein S34	-1.270	-0.345	8.160E-04	1.920E-02
Mospd2	motile sperm domain containing 2	1.355	0.438	8.110E-04	1.920E-02
Snrpg	predicted gene 8186	-1.388	-0.473	8.070E-04	1.920E-02
Vps13a	vacuolar protein sorting 13A (yeast)	1.394	0.479	8.090E-04	1.920E-02
Clip3	CAP-GLY domain containing linker protein 3	-1.398	-0.483	8.200E-04	1.930E-02
Nabp2	nucleic acid binding protein 2	-1.242	-0.313	8.200E-04	1.930E-02
Mospd3	motile sperm domain containing 3	-1.205	-0.269	8.280E-04	1.940E-02
Samd14	sterile alpha motif domain containing 14	-1.319	-0.399	8.260E-04	1.940E-02
Arid4a	AT rich interactive domain 4A (RBP1-like)	1.327	0.408	8.340E-04	1.950E-02
Mrpl34	mitochondrial ribosomal protein L34	-1.310	-0.390	8.350E-04	1.950E-02
Ahr	aryl-hydrocarbon receptor	1.376	0.460	8.460E-04	1.960E-02
Fam35a	family with sequence similarity 35, member A	1.337	0.419	8.470E-04	1.960E-02
Msh3	mutS homolog 3 (E. coli)	1.313	0.393	8.430E-04	1.960E-02
Pebp1	phosphatidylethanolamine binding protein 1	-1.253	-0.325	8.470E-04	1.960E-02
Pfn2	profilin 2	-1.281	-0.357	8.500E-04	1.960E-02
Psm7	proteasome (prosome, macropain) subunit, alpha type 7	-1.208	-0.273	8.490E-04	1.960E-02
Ube2r2	ubiquitin-conjugating enzyme E2R 2	-1.174	-0.232	8.460E-04	1.960E-02
Vps72	vacuolar protein sorting 72 (yeast)	-1.222	-0.289	8.420E-04	1.960E-02
Gls	glutaminase	1.292	0.370	8.590E-04	1.970E-02
Ndufs5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	-1.364	-0.448	8.570E-04	1.970E-02
Vldlr	very low density lipoprotein receptor	1.317	0.397	8.660E-04	1.980E-02
Akap8	A kinase (PRKA) anchor protein 8	1.302	0.381	8.750E-04	1.990E-02
Fam73a	family with sequence similarity 73, member A	1.213	0.279	8.770E-04	1.990E-02
Pafah1b3	platelet-activating factor acetylhydrolase, isoform 1b, subunit 3	-1.276	-0.352	8.720E-04	1.990E-02
Slfn3	schlafen 3	1.398	0.483	8.690E-04	1.990E-02
Trpm3	transient receptor potential cation channel, subfamily M, member 3	1.255	0.328	8.790E-04	1.990E-02
Tmem158	transmembrane protein 158	-1.382	-0.467	8.750E-04	1.990E-02
Usp6nl	USP6 N-terminal like	1.245	0.316	8.940E-04	2.020E-02
Timm13	translocase of inner mitochondrial membrane 13 homolog (yeast)	-1.287	-0.364	9.070E-04	2.050E-02
Tpgs1	tubulin polyglutamylase complex subunit 1	-1.309	-0.388	9.090E-04	2.050E-02
Mitd1	MIT, microtubule interacting and transport, domain containing 1	1.373	0.457	9.200E-04	2.070E-02
Cdk9	cyclin-dependent kinase 9 (CDC2-related kinase)	-1.197	-0.260	9.280E-04	2.090E-02
Mrpl54	mitochondrial ribosomal protein L54	-1.333	-0.415	9.300E-04	2.090E-02
Samd1	sterile alpha motif domain containing 1	-1.249	-0.321	9.330E-04	2.090E-02
Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	-1.225	-0.293	9.380E-04	2.100E-02
Ssna1	Sjogren's syndrome nuclear autoantigen 1	-1.324	-0.405	9.370E-04	2.100E-02
BC055324	cDNA sequence BC055324	1.381	0.466	9.530E-04	2.130E-02
RGD1563834	similar to 40S ribosomal protein S16	-1.389	-0.474	9.580E-04	2.130E-02
Ubc	ubiquitin C	-1.289	-0.366	9.700E-04	2.140E-02
Dennd5b	DENN/MADD domain containing 5B	1.286	0.363	9.680E-04	2.140E-02
Nox4	NADPH oxidase 4	1.394	0.479	9.700E-04	2.140E-02
Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	1.246	0.317	9.610E-04	2.140E-02
40971		-1.227	-0.295	9.630E-04	2.140E-02
Fam127b	family with sequence similarity 127, member B	-1.237	-0.307	9.730E-04	2.150E-02
Alkbh2	alkB, alkylation repair homolog 2 (E. coli)	-1.359	-0.443	9.790E-04	2.160E-02
Kmt2a	lysine methyltransferase 2A	1.344	0.426	9.830E-04	2.160E-02
Heatr5a	HEAT repeat containing 5A	1.280	0.356	9.870E-04	2.170E-02

Plekha1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	1.319	0.399	9.890E-04	2.170E-02
Ctxn1	cortexin 1	-1.326	-0.407	1.000E-03	2.180E-02
Cyb561d2	cytochrome b-561 domain containing 2	-1.299	-0.377	1.010E-03	2.180E-02
Dzip3	DAZ interacting protein 3, zinc finger	1.294	0.372	1.010E-03	2.180E-02
Fkbp8	FK506 binding protein 8	-1.254	-0.326	9.950E-04	2.180E-02
Irf2bp2	interferon regulatory factor 2 binding protein 2	-1.336	-0.418	1.010E-03	2.180E-02
Sec61g	predicted gene 11575	-1.301	-0.380	1.010E-03	2.180E-02
Sh2d3c	SH2 domain containing 3C	-1.320	-0.400	1.010E-03	2.180E-02
RGD1559896	similar to RIKEN cDNA 2310022B05	-1.223	-0.290	1.000E-03	2.180E-02
Son	Son DNA binding protein	1.207	0.272	1.000E-03	2.180E-02
Syt3	synaptotagmin III	-1.318	-0.398	1.000E-03	2.180E-02
Trappc8	trafficking protein particle complex 8	1.259	0.332	1.000E-03	2.180E-02
Scyl3	SCY1-like 3 (S. cerevisiae)	1.335	0.417	1.020E-03	2.200E-02
Clock	circadian locomoter output cycles kaput	1.365	0.449	1.040E-03	2.230E-02
Fancd2	Fanconi anemia, complementation group D2	1.309	0.389	1.040E-03	2.230E-02
Npff	neuropeptide FF-amide peptide precursor	1.381	0.466	1.040E-03	2.230E-02
Zzef1	zinc finger, ZZ-type with EF hand domain 1	1.243	0.314	1.040E-03	2.230E-02
Ap3b1	adaptor-related protein complex 3, beta 1 subunit	1.268	0.343	1.050E-03	2.240E-02
Lypla2	lysophospholipase 2	-1.199	-0.262	1.050E-03	2.240E-02
Mcrip1	MAPK regulated co-repressor interacting protein 1	-1.236	-0.306	1.050E-03	2.240E-02
Gipc1	GIPC PDZ domain containing family, member 1	-1.223	-0.290	1.070E-03	2.250E-02
Hap1	huntingtin-associated protein 1	-1.233	-0.302	1.060E-03	2.250E-02
Paccin2	protein kinase C and casein kinase substrate in neurons 2	-1.188	-0.249	1.070E-03	2.250E-02
Rab5c	RAB5C, member RAS oncogene family	-1.184	-0.244	1.070E-03	2.250E-02
Ranbp10	RAN binding protein 10	1.259	0.332	1.070E-03	2.250E-02
RGD1559909	RGD1559909	-1.295	-0.373	1.070E-03	2.250E-02
RGD1560394	RGD1560394	-1.362	-0.446	1.060E-03	2.250E-02
Topbp1	topoisomerase (DNA) II binding protein 1	1.213	0.279	1.070E-03	2.250E-02
Ube4a	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	1.243	0.314	1.060E-03	2.250E-02
Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	-1.261	-0.335	1.090E-03	2.270E-02
Ngfrap1	nerve growth factor receptor (TNFRSF16) associated protein 1	-1.268	-0.343	1.090E-03	2.270E-02
Acap2	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	1.223	0.291	1.090E-03	2.280E-02
Limk1	LIM-domain containing, protein kinase	-1.198	-0.261	1.090E-03	2.280E-02
MP68	6.8 kDa mitochondrial proteolipid	-1.353	-0.436	1.100E-03	2.300E-02
Rpl13	ribosomal protein L13	-1.277	-0.353	1.120E-03	2.310E-02
Wrn	Werner syndrome homolog (human)	1.376	0.460	1.130E-03	2.310E-02
Cltb	clathrin, light polypeptide (Lcb)	-1.250	-0.322	1.120E-03	2.310E-02
Dusp14	dual specificity phosphatase 14	-1.379	-0.464	1.120E-03	2.310E-02
Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	-1.244	-0.315	1.120E-03	2.310E-02
Neur1a	neuralized homolog 1A (Drosophila)	-1.359	-0.443	1.120E-03	2.310E-02
Orc3	origin recognition complex, subunit 3	1.274	0.349	1.110E-03	2.310E-02
Pnn	pinin	1.337	0.419	1.110E-03	2.310E-02
Tbk1	TANK-binding kinase 1	1.307	0.386	1.120E-03	2.310E-02
Tmem245	transmembrane protein 245	1.331	0.412	1.130E-03	2.310E-02
Vegfb	vascular endothelial growth factor B	-1.357	-0.440	1.110E-03	2.310E-02
E2f3	E2F transcription factor 3	1.292	0.370	1.130E-03	2.320E-02
Lrig2	leucine-rich repeats and immunoglobulin-like domains 2	1.302	0.381	1.150E-03	2.350E-02
Stxbp5	syntaxin binding protein 5 (tomosyn)	1.198	0.261	1.160E-03	2.370E-02

Urb2	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	1.236	0.306	1.160E-03	2.370E-02
Caly	calcyon neuron-specific vesicular protein	-1.339	-0.421	1.180E-03	2.380E-02
Plekha5	pleckstrin homology domain containing, family A member 5	1.312	0.392	1.170E-03	2.380E-02
Reck	reversion-inducing-cysteine-rich protein with kazal motifs	1.330	0.411	1.170E-03	2.380E-02
Cox17	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)	-1.317	-0.397	1.180E-03	2.390E-02
Dennd1b	DENN/MADD domain containing 1B	1.364	0.448	1.180E-03	2.390E-02
Srrd	SRR1 domain containing	-1.304	-0.383	1.190E-03	2.390E-02
Nup37	nucleoporin 37	1.365	0.449	1.190E-03	2.400E-02
Zmat1	zinc finger, matrin type 1	1.317	0.397	1.200E-03	2.420E-02
Rpl36a	similar to ribosomal protein L36a	-1.257	-0.330	1.220E-03	2.450E-02
Dpp8	dipeptidylpeptidase 8	1.203	0.267	1.220E-03	2.450E-02
Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	1.368	0.452	1.230E-03	2.470E-02
Numbl	numb-like	-1.283	-0.359	1.250E-03	2.510E-02
Trmt61a	tRNA methyltransferase 61 homolog A (S. cerevisiae)	-1.237	-0.307	1.260E-03	2.520E-02
RGD1559904	similar to mKIAA1429 protein	1.318	0.398	1.260E-03	2.520E-02
Rfx7	regulatory factor X, 7	1.319	0.399	1.280E-03	2.530E-02
Fau	similar to fau	-1.272	-0.347	1.280E-03	2.530E-02
Lmtk3	emur tyrosine kinase 3	-1.291	-0.368	1.280E-03	2.530E-02
Enho	energy homeostasis associated	-1.333	-0.415	1.270E-03	2.530E-02
Gdap111	ganglioside-induced differentiation-associated protein 1-like 1	-1.247	-0.318	1.280E-03	2.530E-02
Mrp63	mitochondrial ribosomal protein 63	-1.320	-0.400	1.270E-03	2.530E-02
Tpst1	protein-tyrosine sulfotransferase 1	-1.174	-0.231	1.280E-03	2.530E-02
Sncb	synuclein, beta	-1.320	-0.401	1.270E-03	2.530E-02
Sp1	trans-acting transcription factor 1	1.280	0.356	1.270E-03	2.530E-02
Cecr2	cat eye syndrome chromosome region, candidate 2 homolog (human)	1.351	0.434	1.290E-03	2.540E-02
Pcm1	pericentriolar material 1	1.305	0.384	1.290E-03	2.540E-02
Wdr3	WD repeat domain 3	1.240	0.310	1.300E-03	2.540E-02
Zfp78	zinc finger protein 78	1.383	0.468	1.290E-03	2.540E-02
Cat	catalase	-1.189	-0.250	1.310E-03	2.560E-02
Xrn1	5'-3' exoribonuclease 1	1.339	0.421	1.310E-03	2.570E-02
Ogfr	opioid growth factor receptor	-1.240	-0.310	1.320E-03	2.570E-02
Jun	Jun oncogene	-1.374	-0.458	1.320E-03	2.580E-02
Chadl	chondroadherin-like	-1.356	-0.439	1.330E-03	2.590E-02
Nmral1	NmrA-like family domain containing 1	-1.256	-0.329	1.340E-03	2.590E-02
Cep85	centrosomal protein 85	1.302	0.381	1.350E-03	2.610E-02
Glb1l	galactosidase, beta 1-like	1.328	0.409	1.350E-03	2.610E-02
AABR07061902.1	AABR07061902.1	-1.322	-0.403	1.350E-03	2.610E-02
Camk2n1	calcium/calmodulin-dependent protein kinase II inhibitor 1	-1.324	-0.405	1.370E-03	2.630E-02
Zfp871	zinc finger protein 871	1.340	0.422	1.360E-03	2.630E-02
Imp3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	-1.240	-0.310	1.370E-03	2.640E-02
Trit1	tRNA isopentenyltransferase 1	1.291	0.368	1.370E-03	2.640E-02
Map3k10	mitogen-activated protein kinase kinase kinase 10	-1.292	-0.370	1.380E-03	2.650E-02
Col11a1	collagen, type XI, alpha 1	1.379	0.464	1.390E-03	2.660E-02
CYC1	cytochrome c-1	-1.226	-0.294	1.390E-03	2.660E-02
Kcnt2	potassium channel, subfamily T, member 2	1.274	0.349	1.390E-03	2.660E-02
Zfp286a	zinc finger protein 286A	1.299	0.377	1.390E-03	2.660E-02

Sod1	superoxide dismutase 1, soluble	-1.235	-0.304	1.400E-03	2.670E-02
Cops6	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana)	-1.194	-0.256	1.400E-03	2.670E-02
Pink1	PTEN induced putative kinase 1	-1.282	-0.358	1.410E-03	2.680E-02
Chd9	chromodomain helicase DNA binding protein 9	1.373	0.457	1.420E-03	2.690E-02
Gnai2	guanine nucleotide binding protein (G protein), alpha inhibiting 2	-1.214	-0.280	1.420E-03	2.690E-02
Kcnj8	potassium inwardly-rectifying channel, subfamily J, member 8	1.341	0.423	1.420E-03	2.690E-02
Wnk3	WNK lysine deficient protein kinase 3	1.301	0.380	1.420E-03	2.690E-02
Clcc1	chloride channel CLIC-like 1	1.198	0.261	1.430E-03	2.710E-02
Phf15	PHD finger protein 15	1.373	0.457	1.430E-03	2.710E-02
Eefsec	eukaryotic elongation factor, selenocysteine-tRNA-specific	-1.242	-0.313	1.440E-03	2.720E-02
Stub1	STIP1 homology and U-Box containing protein 1	-1.243	-0.314	1.450E-03	2.720E-02
Strn4	striatin, calmodulin binding protein 4	-1.215	-0.281	1.460E-03	2.750E-02
Gxylt1	glycosyltransferase 8 domain containing 3	1.338	0.420	1.480E-03	2.760E-02
Mir2985	microRNA 2985	1.376	0.460	1.480E-03	2.760E-02
Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	-1.235	-0.304	1.470E-03	2.760E-02
Pla2g12a	phospholipase A2, group X1IA	-1.247	-0.318	1.480E-03	2.760E-02
Slc35f5	solute carrier family 35, member F5	1.290	0.367	1.480E-03	2.760E-02
Sf3b3	splicing factor 3b, subunit 3	1.213	0.278	1.470E-03	2.760E-02
Bad	BCL2-associated agonist of cell death	-1.229	-0.298	1.490E-03	2.770E-02
B9d2	B9 protein domain 2	-1.301	-0.380	1.510E-03	2.810E-02
Morc3	microrchidia 3	1.309	0.389	1.520E-03	2.810E-02
Nup155	nucleoporin 155	1.273	0.348	1.520E-03	2.810E-02
Stk11	serine/threonine kinase 11	-1.205	-0.269	1.520E-03	2.810E-02
Snrpd3	small nuclear ribonucleoprotein D3	-1.171	-0.228	1.520E-03	2.810E-02
Eif2ak4	eukaryotic translation initiation factor 2 alpha kinase 4	1.248	0.320	1.540E-03	2.840E-02
Frs3	fibroblast growth factor receptor substrate 3	-1.268	-0.342	1.550E-03	2.840E-02
Higd2a	HIG1 domain family, member 2A	-1.319	-0.399	1.540E-03	2.840E-02
Hmgn2	high mobility group nucleosomal binding domain 4	-1.289	-0.366	1.550E-03	2.840E-02
Nup153	nucleoporin 153	1.276	0.352	1.550E-03	2.840E-02
Prrc2c	proline-rich coiled-coil 2C	1.192	0.253	1.550E-03	2.840E-02
Atp5l	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	-1.248	-0.320	1.560E-03	2.850E-02
Atp5d	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	-1.300	-0.378	1.570E-03	2.860E-02
Mrpl12	mitochondrial ribosomal protein L12	-1.212	-0.277	1.570E-03	2.860E-02
Zfp560	zinc finger protein 560	1.301	0.380	1.560E-03	2.860E-02
EIF3F	eukaryotic translation initiation factor 3, subunit F	-1.220	-0.287	1.580E-03	2.870E-02
Cdc40	cell division cycle 40 homolog (yeast)	1.318	0.398	1.590E-03	2.880E-02
Dusp26	dual specificity phosphatase 26 (putative)	-1.262	-0.336	1.580E-03	2.880E-02
Hcn2	hyperpolarization-activated, cyclic nucleotide-gated K+ 2	-1.246	-0.317	1.590E-03	2.880E-02
Prmt10	protein arginine methyltransferase 10 (putative)	1.223	0.290	1.590E-03	2.880E-02
Ppp1r9b	protein phosphatase 1, regulatory subunit 9B	-1.155	-0.208	1.590E-03	2.880E-02
Usp28	ubiquitin specific peptidase 28	1.218	0.285	1.580E-03	2.880E-02
Rpl34	ribosomal protein L34	-1.255	-0.328	1.600E-03	2.900E-02
Ppp2r5d	protein phosphatase 2, regulatory subunit B (B56), delta isoform	-1.139	-0.188	1.620E-03	2.930E-02
Arl13b	ADP-ribosylation factor-like 13B	1.318	0.398	1.630E-03	2.940E-02
Dusp7	dual specificity phosphatase 7	-1.222	-0.289	1.640E-03	2.940E-02
Efha	EF hand domain family, member B	1.373	0.457	1.640E-03	2.940E-02
Fnbp4	formin binding protein 4	1.278	0.354	1.640E-03	2.940E-02

Map1lc3a	microtubule-associated protein 1 light chain 3 alpha	-1.301	-0.380	1.640E-03	2.940E-02
Nbeal1	neurobeachin like 1	1.351	0.434	1.650E-03	2.940E-02
Rfc1	replication factor C (activator 1) 1	1.193	0.255	1.650E-03	2.940E-02
Ttll4	tubulin tyrosine ligase-like family, member 4	1.275	0.350	1.640E-03	2.940E-02
Wwc1	WW, C2 and coiled-coil domain containing 1	-1.239	-0.309	1.630E-03	2.940E-02
Slc25a1	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	-1.266	-0.340	1.660E-03	2.950E-02
Bop1	block of proliferation 1	-1.188	-0.248	1.660E-03	2.960E-02
Nek10	NIMA (never in mitosis gene a)- related kinase 10	1.325	0.406	1.670E-03	2.960E-02
Asun	asunder, spermatogenesis regulator	1.295	0.373	1.680E-03	2.970E-02
Pdlim4	PDZ and LIM domain 4	-1.329	-0.410	1.680E-03	2.970E-02
Noc3l	nucleolar complex associated 3 homolog (S. cerevisiae)	1.356	0.439	1.690E-03	2.980E-02
Pianp	PILR alpha associated neural protein	-1.253	-0.325	1.690E-03	2.980E-02
Rock2	Rho-associated coiled-coil containing protein kinase 2	1.314	0.394	1.690E-03	2.980E-02
Hspbp1	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1	-1.229	-0.297	1.710E-03	3.000E-02
Zdhhc6	zinc finger, DHHC domain containing 6	1.268	0.343	1.710E-03	3.010E-02
Preld1	PRELI domain containing 1	-1.239	-0.309	1.730E-03	3.020E-02
Pick1	protein interacting with C kinase 1	-1.209	-0.274	1.720E-03	3.020E-02
Rapgef6	Rap guanine nucleotide exchange factor (GEF) 6	1.283	0.360	1.720E-03	3.020E-02
Tmem67	transmembrane protein 67	1.284	0.361	1.730E-03	3.020E-02
Ube2d1	ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog (yeast)	-1.341	-0.423	1.730E-03	3.020E-02
Fam135a	family with sequence similarity 135, member A	1.319	0.399	1.750E-03	3.030E-02
Hecw2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	1.275	0.351	1.740E-03	3.030E-02
Lrrc73	leucine rich repeat containing 73	-1.333	-0.415	1.750E-03	3.030E-02
Pold2	polymerase (DNA directed), delta 2, regulatory subunit	-1.285	-0.362	1.740E-03	3.030E-02
Pcdh15	protocadherin 15	1.275	0.350	1.740E-03	3.030E-02
Csk	c-src tyrosine kinase	-1.117	-0.159	1.770E-03	3.040E-02
Dusp8	dual specificity phosphatase 8	-1.218	-0.284	1.750E-03	3.040E-02
Fsd1	fibronectin type 3 and SPRY domain-containing protein	-1.228	-0.296	1.750E-03	3.040E-02
Myl9	myosin, light polypeptide 9, regulatory	-1.300	-0.378	1.760E-03	3.040E-02
Slc27a4	solute carrier family 27 (fatty acid transporter), member 4	-1.198	-0.261	1.770E-03	3.040E-02
Trna1ap	tRNA selenocysteine 1 associated protein 1	-1.213	-0.279	1.760E-03	3.040E-02
Uqcrc	ubiquinol-cytochrome c reductase, complex III subunit VII	-1.276	-0.352	1.770E-03	3.040E-02
Vbp1	von Hippel-Lindau binding protein 1	-1.361	-0.445	1.770E-03	3.040E-02
Rnf219	ring finger protein 219	1.275	0.350	1.780E-03	3.060E-02
Utp14a	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	1.245	0.316	1.790E-03	3.070E-02
Atp6ap1l	ATPase, H+ transporting, lysosomal accessory protein 1-like	-1.368	-0.452	1.830E-03	3.130E-02
Dnmt3b	DNA methyltransferase 3B	1.348	0.431	1.830E-03	3.130E-02
Gnb2	guanine nucleotide binding protein (G protein), beta 2	-1.269	-0.344	1.830E-03	3.130E-02
Snhg11	small nucleolar RNA host gene 11 (non-protein coding)	1.348	0.431	1.830E-03	3.130E-02
Ubac2	ubiquitin associated domain containing 2	-1.186	-0.246	1.830E-03	3.130E-02
SCN2A1	sodium channel, voltage-gated, type II, alpha 1	1.244	0.315	1.850E-03	3.140E-02
Arpc1a	actin related protein 2/3 complex, subunit 1A	-1.285	-0.362	1.850E-03	3.150E-02
Tac3	tachykinin 3	-1.338	-0.420	1.870E-03	3.170E-02
H2afy	H2A histone family, member Y	-1.151	-0.203	1.880E-03	3.180E-02
RGD1310016	RIC1 homolog, RAB6A GEF complex partner 1	1.265	0.339	1.880E-03	3.180E-02

RGD1307704	similar to RIKEN cDNA 2410016O06	-1.269	-0.344	1.880E-03	3.180E-02
AC109096.1	AC109096.1	-1.294	-0.372	1.880E-03	3.180E-02
Orc5	origin recognition complex, subunit 5	1.249	0.321	1.890E-03	3.200E-02
Rassf1	Ras association (RalGDS/AF-6) domain family member 1	-1.207	-0.271	1.900E-03	3.200E-02
Ppp1ca	protein phosphatase 1, catalytic subunit, alpha isoform	-1.178	-0.236	1.910E-03	3.220E-02
Rpl37	ribosomal protein L37	-1.283	-0.360	1.910E-03	3.220E-02
Cutc	cutC copper transporter homolog (E.coli)	1.313	0.393	1.930E-03	3.230E-02
Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	-1.218	-0.284	1.920E-03	3.230E-02
Pnmal2	PNMA-like 2	-1.179	-0.238	1.930E-03	3.230E-02
2510002D24Rik	RIKEN cDNA 2510002D24 gene	-1.221	-0.288	1.930E-03	3.230E-02
ENSRNOG00000049932	ENSRNOG00000049932	1.360	0.444	1.930E-03	3.230E-02
Grina	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	-1.261	-0.335	1.950E-03	3.250E-02
Angel2	angel homolog 2 (Drosophila)	1.238	0.308	1.970E-03	3.280E-02
Nkx6-2	NK6 homeobox 2	-1.333	-0.415	1.990E-03	3.310E-02
Ppfibp2	protein tyrosine phosphatase, receptor-type, F interacting protein, binding protein 2	1.365	0.449	1.990E-03	3.310E-02
Rif1	Rap1 interacting factor 1 homolog (yeast)	1.347	0.430	1.990E-03	3.310E-02
Tnrc6c	trinucleotide repeat containing 6C	1.230	0.299	2.000E-03	3.320E-02
Dgcr6	DiGeorge syndrome critical region gene 6	-1.283	-0.360	2.010E-03	3.330E-02
Nhlrc2	NHL repeat containing 2	1.331	0.413	2.010E-03	3.330E-02
Smpd3	sphingomyelin phosphodiesterase 3, neutral	-1.159	-0.213	2.040E-03	3.370E-02
Tma7	translation machinery associated 7 homolog	-1.364	-0.448	2.040E-03	3.370E-02
Tmem179	transmembrane protein 179	-1.230	-0.299	2.050E-03	3.390E-02
RGD1309594	similar to RIKEN cDNA 1810043G02	-1.250	-0.322	2.060E-03	3.390E-02
Cnih2	cornichon homolog 2 (Drosophila)	-1.271	-0.346	2.070E-03	3.400E-02
Donson	downstream neighbor of SON	1.291	0.368	2.070E-03	3.400E-02
Fam189a1	family with sequence similarity 189, member A1	-1.316	-0.396	2.070E-03	3.400E-02
Ttc21b	tetratricopeptide repeat domain 21B	1.317	0.397	2.080E-03	3.410E-02
Hnrnpl	heterogeneous nuclear ribonucleoprotein L	-1.159	-0.213	2.100E-03	3.430E-02
Maz	MYC-associated zinc finger protein (purine-binding transcription factor)	-1.292	-0.370	2.100E-03	3.430E-02
Chpf	chondroitin polymerizing factor	-1.281	-0.357	2.150E-03	3.500E-02
Masp2	mannan-binding lectin serine peptidase 2	1.285	0.362	2.150E-03	3.500E-02
Tgfb1i1	transforming growth factor beta 1 induced transcript 1	-1.291	-0.368	2.150E-03	3.500E-02
AC133270.1	Rn60_14_0792.1	1.308	0.387	2.140E-03	3.500E-02
Ctnb2	cortactin binding protein 2	1.240	0.310	2.170E-03	3.510E-02
Rundc3a	RUN domain containing 3A	-1.268	-0.343	2.170E-03	3.510E-02
Ttc7b	tetratricopeptide repeat domain 7B	-1.212	-0.277	2.170E-03	3.510E-02
Rn50_X_0744.1	Rn50_X_0744.1	-1.276	-0.352	2.170E-03	3.510E-02
Mgat4b	mannoside acetylglucosaminyltransferase 4, isoenzyme B	-1.220	-0.287	2.180E-03	3.520E-02
Nmt2	N-myristoyltransferase 2	1.254	0.326	2.170E-03	3.520E-02
Ppwd1	peptidylprolyl isomerase domain and WD repeat containing 1	1.314	0.394	2.190E-03	3.530E-02
Dstyk	dual serine/threonine and tyrosine protein kinase	1.297	0.375	2.190E-03	3.540E-02
Limd2	LIM domain containing 2	-1.211	-0.276	2.210E-03	3.550E-02
Diras1	DIRAS family, GTP-binding RAS-like 1	-1.245	-0.316	2.200E-03	3.550E-02
Atg16l1	autophagy-related 16-like 1 (yeast)	1.173	0.230	2.230E-03	3.570E-02
Fancb	Fanconi anemia, complementation group B	1.361	0.445	2.230E-03	3.570E-02
Kif15	kinesin family member 15	1.323	0.404	2.230E-03	3.570E-02
Mon2	MON2 homolog (yeast)	1.268	0.342	2.220E-03	3.570E-02

Pias1	protein inhibitor of activated STAT 1	1.263	0.337	2.230E-03	3.570E-02
Trim8	tripartite motif protein 8	-1.183	-0.243	2.230E-03	3.570E-02
Fth1	ferritin heavy chain 1	-1.254	-0.326	2.240E-03	3.580E-02
Kat2b	lysine acetyltransferase 2B	1.336	0.418	2.250E-03	3.580E-02
Tdp2	tyrosyl-DNA phosphodiesterase 2	1.331	0.413	2.290E-03	3.650E-02
Csnk1g1	casein kinase 1, gamma 1	1.317	0.397	2.310E-03	3.670E-02
Dad1	defender against cell death 1	-1.268	-0.342	2.310E-03	3.670E-02
Kif21a	kinesin family member 21A	1.146	0.197	2.310E-03	3.670E-02
2410089E03Rik	RIKEN cDNA 2410089E03 gene	1.288	0.365	2.330E-03	3.690E-02
Ipo11	importin 11	1.261	0.334	2.330E-03	3.700E-02
Tubg2	tubulin, gamma 2	-1.235	-0.305	2.350E-03	3.710E-02
Chmp4b1	chromatin modifying protein 4B-like 1	-1.197	-0.259	2.360E-03	3.710E-02
Chd6	chromodomain helicase DNA binding protein 6	1.278	0.354	2.350E-03	3.710E-02
Glpr2	GLI pathogenesis-related 2	-1.333	-0.415	2.360E-03	3.710E-02
Rusc2	RUN and SH3 domain containing 2	-1.273	-0.348	2.360E-03	3.710E-02
Strip1	striatin interacting protein 1	-1.146	-0.197	2.350E-03	3.710E-02
Dusp1	dual specificity phosphatase 1	-1.265	-0.339	2.370E-03	3.720E-02
Adamts20	ADAM metalloproteinase with thrombospondin type 1 motif, 20	1.348	0.431	2.380E-03	3.730E-02
Dars2	aspartyl-tRNA synthetase 2 (mitochondrial)	1.235	0.305	2.380E-03	3.730E-02
Npdc1	neural proliferation, differentiation and control gene 1	-1.285	-0.362	2.390E-03	3.740E-02
Abhd17a	abhydrolase domain containing 17A	-1.271	-0.346	2.400E-03	3.750E-02
Cacng8	calcium channel, voltage-dependent, gamma subunit 8	-1.321	-0.402	2.400E-03	3.750E-02
Btf3	predicted gene 9308	-1.191	-0.252	2.400E-03	3.750E-02
Lrp6	low density lipoprotein receptor-related protein 6	1.261	0.334	2.410E-03	3.760E-02
Dnajb2	DnaJ (Hsp40) homolog, subfamily B, member 2	-1.138	-0.187	2.410E-03	3.760E-02
Rad50	RAD50 homolog (S. cerevisiae)	1.301	0.380	2.420E-03	3.760E-02
Clpp	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	-1.268	-0.343	2.430E-03	3.770E-02
C2cd4c	family with sequence similarity 148, member C	-1.250	-0.322	2.440E-03	3.770E-02
Iscu	IscU iron-sulfur cluster scaffold homolog (E. coli)	-1.206	-0.270	2.430E-03	3.770E-02
Usp45	ubiquitin specific peptidase 45	1.272	0.347	2.420E-03	3.770E-02
Zbtb44	zinc finger and BTB domain containing 44	1.260	0.333	2.430E-03	3.770E-02
Atp13a3	ATPase type 13A3	1.342	0.424	2.450E-03	3.780E-02
Dpy19l4	dpy-19-like 4 (C. elegans)	1.288	0.365	2.450E-03	3.780E-02
Ralgapb	Ral GTPase activating protein non-catalytic beta subunit	1.192	0.253	2.450E-03	3.780E-02
Vps54	vacuolar protein sorting 54 (yeast)	1.305	0.384	2.480E-03	3.810E-02
Mrpl20	mitochondrial ribosomal protein L20	-1.210	-0.275	2.480E-03	3.820E-02
Pvr1	poliovirus receptor-related 1	-1.276	-0.352	2.490E-03	3.830E-02
Rasa2	RAS p21 protein activator 2	1.332	0.414	2.490E-03	3.830E-02
Emilin2	echinoderm microtubule associated protein like 5	1.322	0.403	2.510E-03	3.850E-02
St6galnac6	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6	-1.233	-0.302	2.520E-03	3.860E-02
AABR06057713.1	AABR06057713.1	1.344	0.426	2.530E-03	3.860E-02
Setd2	SET domain containing 2	1.182	0.241	2.530E-03	3.870E-02
Nvl	nuclear VCP-like	1.322	0.403	2.550E-03	3.890E-02
Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	-1.328	-0.409	2.560E-03	3.900E-02
Kdm2a	lysine (K)-specific demethylase 2A	1.221	0.288	2.570E-03	3.900E-02
Pld1	phospholipase D1	1.255	0.328	2.580E-03	3.900E-02
SEC24A	Sec24 related gene family, member A (S. cerevisiae)	1.240	0.310	2.570E-03	3.900E-02
Zfp280c	zinc finger protein 280C	1.311	0.391	2.570E-03	3.900E-02
Zfp771	zinc finger protein 771	-1.266	-0.340	2.570E-03	3.900E-02

Atp5b	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	-1.164	-0.219	2.580E-03	3.910E-02
Trip12	thyroid hormone receptor interactor 12	1.270	0.345	2.580E-03	3.910E-02
Arf1	ADP-ribosylation factor 1	-1.152	-0.204	2.590E-03	3.920E-02
Eef1g	eukaryotic translation elongation factor 1 gamma	-1.129	-0.175	2.610E-03	3.930E-02
Pot1b	protection of telomeres 1B	1.324	0.405	2.610E-03	3.930E-02
Trim28	tripartite motif-containing 28	-1.131	-0.177	2.600E-03	3.930E-02
Zc3h11a	zinc finger CCCH type containing 11A	1.217	0.283	2.600E-03	3.930E-02
Cuedc1	CUE domain containing 1	-1.207	-0.272	2.640E-03	3.940E-02
Lpxn	leupaxin	1.257	0.330	2.630E-03	3.940E-02
Nrtn	neurturin	-1.354	-0.437	2.640E-03	3.940E-02
Ranbp1	RAN binding protein 1	-1.202	-0.265	2.640E-03	3.940E-02
Thoc2	THO complex 2	1.336	0.418	2.630E-03	3.940E-02
Tbcc	tubulin-specific chaperone C	-1.232	-0.301	2.640E-03	3.940E-02
AABR07045621.1	AABR07045621.1	1.350	0.433	2.630E-03	3.940E-02
Borcs6	BLOC-1 related complex subunit 6	-1.255	-0.328	2.660E-03	3.950E-02
Glce	glucuronyl C5-epimerase	1.273	0.348	2.650E-03	3.950E-02
ENSRNOG00000047147	ENSRNOG00000047147	1.353	0.436	2.650E-03	3.950E-02
Efr3a	EFR3 homolog A (S. cerevisiae)	1.329	0.410	2.670E-03	3.960E-02
Atxn10	ataxin 10	-1.152	-0.204	2.680E-03	3.970E-02
Emc10	ER membrane protein complex subunit 10	-1.237	-0.307	2.670E-03	3.970E-02
Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	-1.207	-0.271	2.680E-03	3.970E-02
Eif3i	eukaryotic translation initiation factor 3, subunit I	-1.204	-0.268	2.690E-03	3.980E-02
Mark4	MAP/microtubule affinity-regulating kinase 4	-1.267	-0.341	2.690E-03	3.980E-02
Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	-1.213	-0.278	2.690E-03	3.980E-02
Prkd3	protein kinase D3	1.319	0.399	2.700E-03	3.980E-02
Rilpl2	Rab interacting lysosomal protein-like 2	-1.220	-0.287	2.710E-03	3.990E-02
Kat2a	K(lysine) acetyltransferase 2A	-1.193	-0.254	2.720E-03	4.000E-02
Zfp608	zinc finger protein 608	1.201	0.264	2.730E-03	4.000E-02
40976		-1.247	-0.318	2.720E-03	4.000E-02
Med16	mediator complex subunit 16	-1.254	-0.327	2.740E-03	4.020E-02
Nsun3	NOL1/NOP2/Sun domain family member 3	1.353	0.436	2.740E-03	4.020E-02
Uba6	ubiquitin-like modifier activating enzyme 6	1.319	0.399	2.740E-03	4.020E-02
Med25	mediator of RNA polymerase II transcription, subunit 25 homolog (yeast)	-1.266	-0.340	2.770E-03	4.040E-02
Mccc1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	1.268	0.342	2.760E-03	4.040E-02
Mrpl37	mitochondrial ribosomal protein L37	-1.210	-0.275	2.760E-03	4.040E-02
Zgrf1	zinc finger, GRF-type containing 1	1.344	0.426	2.770E-03	4.040E-02
AABR07057678.1	AABR07057678.1	1.293	0.371	2.770E-03	4.040E-02
Atp9b	ATPase, class II, type 9B	1.149	0.201	2.800E-03	4.070E-02
Nav2	neuron navigator 2	1.197	0.259	2.810E-03	4.070E-02
Pkd2	polycystic kidney disease 2	1.269	0.344	2.810E-03	4.070E-02
Tstd1	predicted gene 4848	1.351	0.434	2.800E-03	4.070E-02
Trnp1	TMF1-regulated nuclear protein 1	-1.347	-0.430	2.810E-03	4.070E-02
Tmem132e	transmembrane protein 132E	-1.280	-0.356	2.810E-03	4.070E-02
Tkt	transketolase	-1.236	-0.306	2.820E-03	4.080E-02
Nme2	similar to Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (P18)	-1.246	-0.317	2.840E-03	4.100E-02
Suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	1.250	0.322	2.840E-03	4.100E-02
Ubl5	predicted gene 5955	-1.197	-0.259	2.870E-03	4.130E-02
Tbc1d32	TBC1 domain family, member 32	1.292	0.370	2.860E-03	4.130E-02

Hars2	histidyl-tRNA synthetase 2, mitochondrial (putative)	1.247	0.318	2.890E-03	4.150E-02
Pim3	proviral integration site 3	-1.228	-0.296	2.890E-03	4.150E-02
RGD1560775	similar to RIKEN cDNA 4930579C12 gene	1.276	0.352	2.900E-03	4.160E-02
Brcc3	BRCA1/BRCA2-containing complex, subunit 3	-1.235	-0.304	2.930E-03	4.200E-02
Xrcc6	X-ray repair complementing defective repair in Chinese hamster cells 6	1.268	0.342	2.930E-03	4.200E-02
41160		-1.210	-0.275	2.930E-03	4.200E-02
Thap7	THAP domain containing 7	-1.291	-0.369	2.960E-03	4.230E-02
Rps20	ribosomal protein S20	-1.235	-0.305	2.980E-03	4.250E-02
Dmx1	Dmx-like 1	1.300	0.378	2.980E-03	4.250E-02
Shprh	SNF2 histone linker PHD RING helicase	1.306	0.385	2.980E-03	4.250E-02
Tnip1	TNFAIP3 interacting protein 1	-1.258	-0.331	2.970E-03	4.250E-02
RGD1304704	similar to Hypothetical protein CGI-99	-1.205	-0.269	3.000E-03	4.260E-02
Rpl29	ribosomal protein L29	-1.247	-0.319	3.010E-03	4.270E-02
40969		-1.239	-0.309	3.010E-03	4.270E-02
Aatk	apoptosis-associated tyrosine kinase	-1.189	-0.250	3.050E-03	4.280E-02
Dnajc15	DnaJ (Hsp40) homolog, subfamily C, member 15	-1.202	-0.266	3.050E-03	4.280E-02
Emc4	emerin	-1.191	-0.252	3.040E-03	4.280E-02
Fbxo31	F-box protein 31	-1.220	-0.287	3.050E-03	4.280E-02
G2E3	G2/M-phase specific E3 ubiquitin ligase	1.328	0.409	3.040E-03	4.280E-02
Mtpap	mitochondrial poly(A) polymerase	1.220	0.287	3.030E-03	4.280E-02
Rassf6	Ras association (RalGDS/AF-6) domain family member 6	1.341	0.423	3.030E-03	4.280E-02
Rps11	ribosomal protein S11	-1.143	-0.193	3.020E-03	4.280E-02
Zfp580	zinc finger protein 580	-1.336	-0.418	3.020E-03	4.280E-02
RGD1562484	RGD1562484	-1.342	-0.424	3.020E-03	4.280E-02
B3gat3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	-1.240	-0.310	3.070E-03	4.290E-02
Fam131c	family with sequence similarity 131, member C	-1.338	-0.420	3.070E-03	4.290E-02
Fam216a	family with sequence similarity 216, member A	-1.176	-0.234	3.070E-03	4.290E-02
Myo3a	myosin IIIA	1.336	0.418	3.060E-03	4.290E-02
Ckb	similar to creatine kinase, brain	-1.253	-0.325	3.070E-03	4.290E-02
Fndc10	fibronectin type III domain containing 10	-1.334	-0.416	3.060E-03	4.290E-02
Farp2	FERM, RhoGEF and pleckstrin domain protein 2	1.235	0.304	3.100E-03	4.320E-02
Dlg4	discs, large homolog 4 (Drosophila)	-1.246	-0.317	3.120E-03	4.350E-02
Arpp21	cyclic AMP-regulated phosphoprotein, 21	1.324	0.405	3.140E-03	4.360E-02
Isyna1	myo-inositol 1-phosphate synthase A1	-1.297	-0.375	3.140E-03	4.360E-02
Ranbp2	RAN binding protein 2	1.332	0.414	3.130E-03	4.360E-02
Rpl35	ribosomal protein L35	-1.274	-0.349	3.150E-03	4.360E-02
RGD1306746	similar to Hypothetical protein MGC25529	1.210	0.275	3.140E-03	4.360E-02
Zbtb25	zinc finger and BTB domain containing 25	1.292	0.370	3.130E-03	4.360E-02
Aldh1a1	aldehyde dehydrogenase family 1, subfamily A1	1.342	0.424	3.170E-03	4.390E-02
Ccdc97	coiled-coil domain containing 97	-1.220	-0.287	3.190E-03	4.400E-02
Dcun1d2	DCN1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae)	1.242	0.313	3.190E-03	4.400E-02
Tmem240	transmembrane protein 240	-1.307	-0.386	3.190E-03	4.400E-02
Zfp949	zinc finger protein 949	1.286	0.363	3.200E-03	4.410E-02
Mtx3	metaxin 3	1.319	0.399	3.220E-03	4.430E-02
Ppil1	peptidylprolyl isomerase (cyclophilin)-like 1	-1.207	-0.272	3.230E-03	4.440E-02
Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	1.311	0.391	3.240E-03	4.440E-02
Fbn1	fibrillin 1	1.306	0.385	3.230E-03	4.440E-02
Fyn	Fyn proto-oncogene	-1.164	-0.219	3.240E-03	4.440E-02
Kif5b	kinesin family member 5B	1.229	0.297	3.240E-03	4.440E-02

Comt	catechol-O-methyltransferase	-1.245	-0.316	3.280E-03	4.450E-02
Fam171a2	family with sequence similarity 171, member A2	-1.288	-0.365	3.280E-03	4.450E-02
Gosr1	golgi SNAP receptor complex member 1	1.189	0.250	3.280E-03	4.450E-02
Mfsd8	major facilitator superfamily domain containing 8	1.300	0.378	3.290E-03	4.450E-02
Mesdc1	mesoderm development candidate 1	-1.286	-0.363	3.260E-03	4.450E-02
Rnf5	ring finger protein 5	-1.194	-0.256	3.270E-03	4.450E-02
Sh3rf3	SH3 domain containing ring finger 3	-1.300	-0.379	3.290E-03	4.450E-02
RGD1305464	similar to human chromosome 15 open reading frame 39	-1.315	-0.395	3.270E-03	4.450E-02
Sgta	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	-1.235	-0.305	3.270E-03	4.450E-02
Srcap	Snf2-related CREBBP activator protein	1.268	0.343	3.250E-03	4.450E-02
Sra1	steroid receptor RNA activator 1	1.170	0.226	3.260E-03	4.450E-02
Tubgcp5	tubulin, gamma complex associated protein 5	1.344	0.426	3.270E-03	4.450E-02
ATL3	atlastin GTPase 3	1.309	0.388	3.300E-03	4.470E-02
Eri3	exoribonuclease 3	-1.172	-0.229	3.320E-03	4.480E-02
Kdm5a	lysine (K)-specific demethylase 5A	1.317	0.397	3.330E-03	4.490E-02
ENSRNOG00000049316	ENSRNOG00000049316	-1.340	-0.422	3.340E-03	4.500E-02
Rbm42	RNA binding motif protein 42	-1.251	-0.323	3.370E-03	4.540E-02
Atp5g2	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	-1.177	-0.235	3.380E-03	4.550E-02
Atf7	activating transcription factor 7	1.330	0.411	3.380E-03	4.550E-02
Arhgap17	Rho GTPase activating protein 17	1.291	0.369	3.390E-03	4.550E-02
Rnasek	ribonuclease, RNase K	-1.236	-0.306	3.380E-03	4.550E-02
Tpr	translocated promoter region	1.146	0.196	3.430E-03	4.560E-02
Ap2s1	adaptor-related protein complex 2, sigma 1 subunit	-1.272	-0.347	3.420E-03	4.560E-02
Aes	amino-terminal enhancer of split	-1.260	-0.333	3.410E-03	4.560E-02
Ccdc39	coiled-coil domain containing 39	1.296	0.374	3.430E-03	4.560E-02
Dleu7	deleted in lymphocytic leukemia, 7	-1.300	-0.379	3.410E-03	4.560E-02
Hectd2	HECT domain containing 2	1.296	0.374	3.410E-03	4.560E-02
Mapk8ip1	mitogen-activated protein kinase 8 interacting protein 1	-1.218	-0.285	3.420E-03	4.560E-02
Txndc15	thioredoxin domain containing 15	-1.174	-0.231	3.420E-03	4.560E-02
Ube2v1	ubiquitin-conjugating enzyme E2 variant 1	-1.268	-0.343	3.430E-03	4.560E-02
SCAI	suppressor of cancer cell invasion	1.269	0.344	3.440E-03	4.570E-02
Wibg	within bgcn homolog (Drosophila)	-1.241	-0.311	3.450E-03	4.580E-02
Dsn1	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	1.324	0.405	3.460E-03	4.590E-02
Mtbp	Mdm2, transformed 3T3 cell double minute p53 binding protein	1.317	0.397	3.460E-03	4.590E-02
Ago3	argonaute 3, RISC catalytic component	1.339	0.421	3.490E-03	4.610E-02
Dhrs13	dehydrogenase/reductase 13	-1.263	-0.337	3.490E-03	4.620E-02
Mlf2	myeloid leukemia factor 2	-1.211	-0.276	3.500E-03	4.630E-02
RGD1560398	RGD1560398	-1.321	-0.402	3.520E-03	4.630E-02
Sf3b2	splicing factor 3b, subunit 2	-1.124	-0.169	3.510E-03	4.630E-02
Trmt112	tRNA methyltransferase 11-2 homolog (S. cerevisiae)	-1.241	-0.311	3.510E-03	4.630E-02
Wnk1	WNK lysine deficient protein kinase 1	1.235	0.305	3.520E-03	4.630E-02
Mir3064	microRNA 3064	1.292	0.370	3.510E-03	4.630E-02
Cited4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	-1.340	-0.422	3.530E-03	4.640E-02
Tmem64	transmembrane protein 64	-1.302	-0.381	3.530E-03	4.640E-02
Asna1	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	-1.188	-0.248	3.570E-03	4.680E-02
Eif5a	eukaryotic translation initiation factor 5A	-1.180	-0.239	3.580E-03	4.680E-02
Trip11	thyroid hormone receptor interactor 11	1.267	0.341	3.570E-03	4.680E-02

Fryl	furry homolog-like (Drosophila)	1.270	0.345	3.590E-03	4.690E-02
Pcgf6	polycomb group ring finger 6	1.268	0.342	3.600E-03	4.700E-02
Rtn2	reticulon 2 (Z-band associated protein)	-1.224	-0.292	3.600E-03	4.700E-02
Tspan15	tetraspanin 15	-1.224	-0.292	3.600E-03	4.700E-02
NNAT	neuronatin	-1.233	-0.302	3.620E-03	4.710E-02
RGD1566239	similar to RIKEN cDNA 2810428115	-1.278	-0.354	3.630E-03	4.720E-02
ANAPC11	anaphase promoting complex subunit 11	-1.200	-0.263	3.650E-03	4.730E-02
Psmb4	proteasome (prosome, macropain) subunit, beta type 4	-1.203	-0.267	3.650E-03	4.730E-02
Zfp182	zinc finger protein 182	1.300	0.379	3.640E-03	4.730E-02
Eif6	eukaryotic translation initiation factor 6	-1.137	-0.185	3.660E-03	4.740E-02
Rbm28	RNA binding motif protein 28	1.238	0.308	3.650E-03	4.740E-02
Akt1	similar to serine/threonine protein kinase	-1.200	-0.263	3.670E-03	4.750E-02
Stmn3	stathmin-like 3	-1.272	-0.347	3.670E-03	4.750E-02
Ninj1	ninjurin 1	-1.296	-0.374	3.720E-03	4.800E-02
Rtn	rotatin	1.309	0.388	3.720E-03	4.800E-02
Smim18	small integral membrane protein 18	-1.260	-0.333	3.720E-03	4.800E-02
Pram1	PML-RAR alpha-regulated adaptor molecule 1	1.333	0.415	3.740E-03	4.820E-02
Sipa1l3	signal-induced proliferation-associated 1 like 3	-1.223	-0.290	3.750E-03	4.830E-02
Trim24	tripartite motif-containing 24	1.139	0.188	3.760E-03	4.830E-02
Mef2a	myocyte enhancer factor 2A	1.265	0.339	3.780E-03	4.840E-02
Rpl11	ribosomal protein L11	-1.166	-0.221	3.790E-03	4.840E-02
Top3a	topoisomerase (DNA) III alpha	1.286	0.363	3.810E-03	4.840E-02
Bax	BCL2-associated X protein	-1.204	-0.268	3.770E-03	4.840E-02
Gzf1	GDNF-inducible zinc finger protein 1	1.260	0.333	3.780E-03	4.840E-02
Hipk3	homeodomain interacting protein kinase 3	1.188	0.249	3.770E-03	4.840E-02
Itga6	integrin alpha 6	1.217	0.283	3.790E-03	4.840E-02
Psen2	presenilin 2	-1.241	-0.312	3.780E-03	4.840E-02
Spag9	sperm associated antigen 9	1.223	0.290	3.800E-03	4.840E-02
TMEM11	transmembrane protein 11	-1.179	-0.237	3.780E-03	4.840E-02
Vcan	versican	1.254	0.327	3.800E-03	4.840E-02
Efhd2	EF hand domain containing 2	-1.215	-0.281	3.820E-03	4.860E-02
Galk1	galactokinase 1	-1.257	-0.330	3.830E-03	4.860E-02
Osbp19	oxysterol binding protein-like 9	1.204	0.268	3.820E-03	4.860E-02
CK137956	cDNA sequence CK137956	-1.333	-0.415	3.870E-03	4.880E-02
Dolk	dolichol kinase	-1.221	-0.288	3.850E-03	4.880E-02
Fam173b	family with sequence similarity 173, member B	1.199	0.262	3.860E-03	4.880E-02
Psmc3	proteasome (prosome, macropain) 26S subunit, ATPase 3	-1.155	-0.208	3.860E-03	4.880E-02
Ssx1	SSX family member 1	1.328	0.409	3.860E-03	4.880E-02
RGD1562469	RGD1562469	-1.207	-0.271	3.860E-03	4.880E-02
Abhd17c	abhydrolase domain containing 17C	-1.177	-0.235	3.890E-03	4.900E-02
ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	1.290	0.367	3.890E-03	4.900E-02
Lrfn3	leucine rich repeat and fibronectin type III domain containing 3	-1.243	-0.314	3.890E-03	4.900E-02
Dnajb11	DnaJ (Hsp40) homolog, subfamily B, member 11	-1.175	-0.233	3.910E-03	4.910E-02
Spint2	serine protease inhibitor, Kunitz type 2	-1.247	-0.318	3.910E-03	4.910E-02
Taf2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.262	0.336	3.900E-03	4.910E-02
Ubn1	ubiquitin 1	1.235	0.304	3.920E-03	4.920E-02
Stx7	syntaxin 7	-1.250	-0.322	3.940E-03	4.930E-02
Vprbp	Vpr (HIV-1) binding protein	1.232	0.301	3.940E-03	4.930E-02
Dnajc30	DnaJ (Hsp40) homolog, subfamily C, member 30	-1.303	-0.382	3.960E-03	4.950E-02

Kcnc4	potassium voltage gated channel, Shaw-related subfamily, member 4	-1.258	-0.331	3.960E-03	4.950E-02
Lfng	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-1.236	-0.306	4.000E-03	4.990E-02
Slc39a7	solute carrier family 39 (zinc transporter), member 7	-1.168	-0.224	3.990E-03	4.990E-02

Supplemental Table 4. RNA seq analysis of sexually dimorphic hippocampal and hypothalamic gene expression

Supplemental Table 4a. Significantly ($padj \leq 0.05$) altered hippocampal genes in Control ♂ vs Control ♀					
Gene Symbol	Description	Fold Change	log2FC	p value	padj
Car2	carbonic anhydrase 2	-1.861	-0.896	5.000E-05	2.481E-02
Ccnl1	cyclin L1	-1.822	-0.865	5.000E-05	2.481E-02
Ccnl2	cyclin L2	-1.953	-0.966	5.000E-05	2.481E-02
Ccnt2	cyclin T2	-1.676	-0.745	5.000E-05	2.481E-02
Cdon	cell adhesion associated, oncogene regulated	-1.925	-0.945	5.000E-05	2.481E-02
Col1a1	collagen, type I, alpha 1	-7.346	-2.877	5.000E-05	2.481E-02
Crabp1	cellular retinoic acid binding protein 1	-2.179	-1.124	5.000E-05	2.481E-02
Eif2s3y	eukaryotic translation initiation factor 2, subunit 3, structural, Y-linked	1.620	0.696	5.000E-05	2.481E-02
Fam227a	family with sequence similarity 227, member A	-2.006	-1.004	5.000E-05	2.481E-02
Lace1	lactation elevated 1	-13.851	-3.792	5.000E-05	2.481E-02
Leng8	leukocyte receptor cluster (LRC) member 8	-1.846	-0.884	5.000E-05	2.481E-02
Leprel2	leprecan-like protein 2	-1.833	-0.874	5.000E-05	2.481E-02
Luc7l3	LUC7-like 3 pre-mRNA splicing factor	-1.804	-0.851	5.000E-05	2.481E-02
Npy1r	neuropeptide Y receptor Y1	2.155	1.108	5.000E-05	2.481E-02
Nrp2	neuropilin 2	1.865	0.899	5.000E-05	2.481E-02
Nts	neurotensin	-2.024	-1.017	5.000E-05	2.481E-02
Paxbp1	PAX3 and PAX7 binding protein 1	-1.904	-0.929	5.000E-05	2.481E-02
Pdyn	prodynorphin	-3.582	-1.841	5.000E-05	2.481E-02
Pnlsr	PNN-interacting serine/arginine-rich protein	-2.104	-1.073	5.000E-05	2.481E-02
RGD1561931	similar to KIAA2022 protein	1.788	0.838	5.000E-05	2.481E-02
Rock1	Rho-associated coil containing protein kinase 1	-1.791	-0.841	5.000E-05	2.481E-02
Rpl30	ribosomal protein L30	-1.783	-0.834	5.000E-05	2.481E-02
Rsrp1	arginine/serine-rich protein 1	-1.658	-0.730	5.000E-05	2.481E-02
Spp1	secreted phosphoprotein 1	2.057	1.041	5.000E-05	2.481E-02
Tac1	tachykinin, precursor 1	-3.520	-1.816	5.000E-05	2.481E-02
Uhrf2	ubiquitin-like with PHD and ring finger domains 2	-1.783	-0.834	5.000E-05	2.481E-02
Csp1	centrosome and spindle pole associated protein 1	-1.981	-0.987	1.000E-04	4.300E-02
Fam111a	family with sequence similarity 111, member A	1.708	0.772	1.000E-04	4.300E-02
Nktr	natural killer cell triggering receptor	-1.611	-0.688	1.000E-04	4.300E-02

Supplemental Table 4b. Significantly ($padj \leq 0.05$) altered hypothalamic genes in Control ♂ vs. Control ♀					
Gene Symbol	Description	Fold Change	log2FC	p value	padj
AABR06042582.1	AABR06042582.1	-1.857	-0.893	5.000E-05	7.773E-03
AABR06078887.1	AABR06078887.1	-1.825	-0.868	5.000E-05	7.773E-03
Abca8a	ATP-binding cassette, subfamily A (ABC1), member 8a	2.339	1.226	5.000E-05	7.773E-03

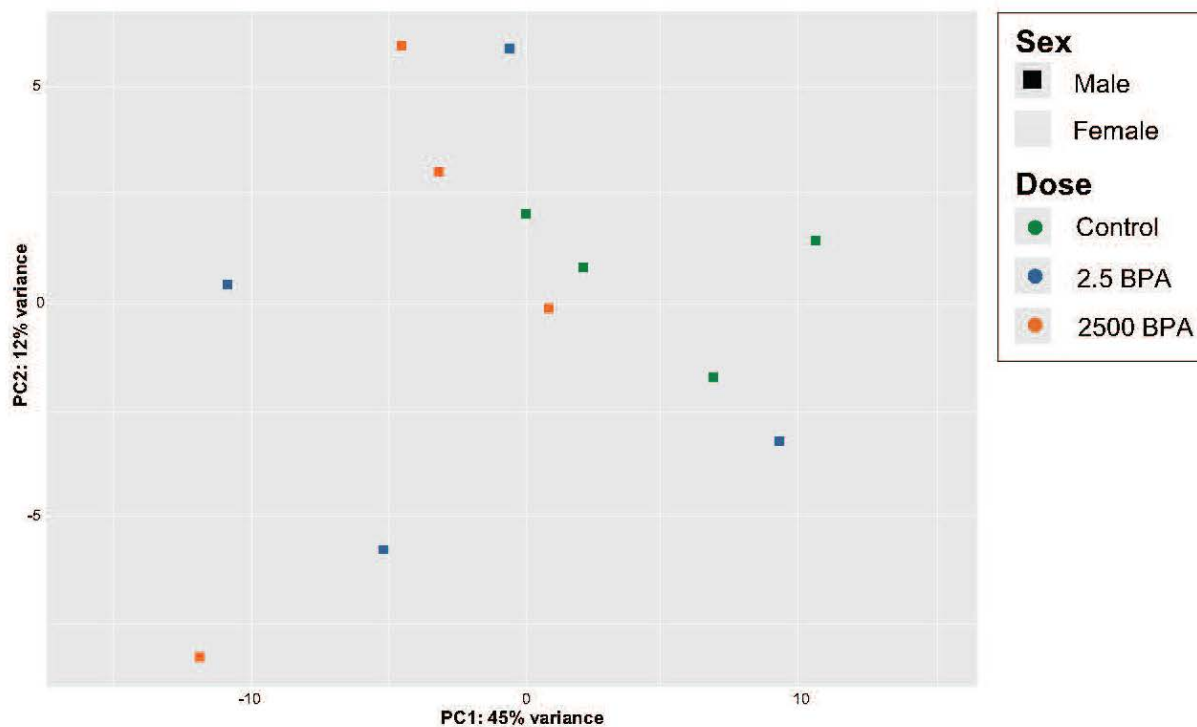
Acp5	acid phosphatase 5, tartrate resistant	7.290	2.866	5.000E-05	7.773E-03
Adams12	ADAM metallopeptidase with thrombospondin type 1 motif, 12	1.899	0.925	5.000E-05	7.773E-03
Aebp1	AE binding protein 1	2.651	1.407	5.000E-05	7.773E-03
Ahnak	AHNAK nucleoprotein	1.840	0.879	5.000E-05	7.773E-03
Arpp21	cAMP-regulated phosphoprotein 21	1.993	0.995	5.000E-05	7.773E-03
Birc6	baculoviral IAP repeat-containing 6	1.672	0.741	5.000E-05	7.773E-03
Cdkn1c	cyclin-dependent kinase inhibitor 1C	1.940	0.956	5.000E-05	7.773E-03
Cenpf	centromere protein F	1.611	0.688	5.000E-05	7.773E-03
Cfh	complement factor H	2.376	1.248	5.000E-05	7.773E-03
Col11a1	collagen, type XI, alpha 1	2.285	1.192	5.000E-05	7.773E-03
Col12a1	collagen, type XII, alpha 1	2.987	1.579	5.000E-05	7.773E-03
Col1a1	collagen, type I, alpha 1	30.730	4.942	5.000E-05	7.773E-03
Col1a2	collagen, type I, alpha 2	5.458	2.448	5.000E-05	7.773E-03
Col3a1	collagen, type III, alpha 1	4.247	2.087	5.000E-05	7.773E-03
Col6a1	collagen, type VI, alpha 1	2.234	1.159	5.000E-05	7.773E-03
Cp	ceruloplasmin (ferroxidase)	2.106	1.074	5.000E-05	7.773E-03
Ctsk	cathepsin K	4.696	2.232	5.000E-05	7.773E-03
Dab2	disabled 2, mitogen-responsive phosphoprotein	2.144	1.100	5.000E-05	7.773E-03
Dcn	decorin	8.857	3.147	5.000E-05	7.773E-03
Dlx1	distal-less homeobox 1	-1.632	-0.707	5.000E-05	7.773E-03
Dmrta2	DMRT-like family A2	3.909	1.967	5.000E-05	7.773E-03
Ebf2	early B-cell factor 2	2.938	1.555	5.000E-05	7.773E-03
Ebf3	early B-cell factor 3	2.654	1.408	5.000E-05	7.773E-03
Fam111a	amily with sequence similarity 111, member A	2.187	1.129	5.000E-05	7.773E-03
Fam227a	family with sequence similarity 227, member A	2.072	1.051	5.000E-05	7.773E-03
Fat3	FAT atypical cadherin 3	1.894	0.922	5.000E-05	7.773E-03
Foxa1	forkhead box A1	4.423	2.145	5.000E-05	7.773E-03
Foxb1	forkhead box B1	8.063	3.011	5.000E-05	7.773E-03
Frzb	frizzled-related protein	2.528	1.338	5.000E-05	7.773E-03
Gad1	glutamate decarboxylase 1	-1.548	-0.630	5.000E-05	7.773E-03
Gfap	glial fibrillary acidic protein	2.404	1.265	5.000E-05	7.773E-03
Gjb2	gap junction protein, beta 2	3.680	1.880	5.000E-05	7.773E-03
Gjb6	gap junction protein, beta 6	4.793	2.261	5.000E-05	7.773E-03
Gpr50	G protein-coupled receptor 50	-1.856	-0.892	5.000E-05	7.773E-03
Hba2	hemoglobin alpha, adult chain 2	1.807	0.853	5.000E-05	7.773E-03
Hmgcs2	3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)	1.769	0.823	5.000E-05	7.773E-03
Hopx	HOP homeobox	2.102	1.072	5.000E-05	7.773E-03
Ibsp	integrin-binding sialoprotein	12.109	3.598	5.000E-05	7.773E-03
Id3	inhibitor of DNA binding 3	2.242	1.165	5.000E-05	7.773E-03
Igf2	insulin-like growth factor 2	3.139	1.651	5.000E-05	7.773E-03
Itgb4	integrin subunit beta 4	3.862	1.949	5.000E-05	7.773E-03
Leng8	leukocyte receptor cluster (LRC) member 8	1.724	0.786	5.000E-05	7.773E-03
Lmx1a	LIM homeobox transcription factor 1 alpha	4.842	2.276	5.000E-05	7.773E-03
LOC100360841	ribosomal protein L37-like	-1.786	-0.837	5.000E-05	7.773E-03
LOC100909555	uncharacterized LOC100909555	-2.271	-1.183	5.000E-05	7.773E-03
LOC100910017	60S ribosomal protein L31-like	-1.715	-0.778	5.000E-05	7.773E-03
LOC100910855	mimscan-like	8.758	3.131	5.000E-05	7.773E-03
LOC257642	rRNA promoter binding protein	-1.894	-0.921	5.000E-05	7.773E-03
Luc7l3	LUC7-like 3 pre-mRNA splicing factor	1.693	0.760	5.000E-05	7.773E-03
Lum	lumican	29.349	4.875	5.000E-05	7.773E-03
Meis2	Meis homeobox 2	-3.710	-1.891	5.000E-05	7.773E-03
Mki67	marker of proliferation Ki-67	1.736	0.796	5.000E-05	7.773E-03

Neurod6	neuronal differentiation 6	2.958	1.565	5.000E-05	7.773E-03
Nme2-ps1	non-metastatic cells 2, protein (NM23B) expressed in, pseudogene 1	-1.890	-0.918	5.000E-05	7.773E-03
Notch2	notch 2	2.026	1.019	5.000E-05	7.773E-03
Oxt	oxytocin/neurophysin 1 prepropeptide	-8.031	-3.006	5.000E-05	7.773E-03
Pitx2	paired-like homeodomain 2	5.430	2.441	5.000E-05	7.773E-03
Pnlsr	PNN-interacting serine/arginine-rich protein	1.639	0.713	5.000E-05	7.773E-03
Pomc	proopiomelanocortin	1.949	0.963	5.000E-05	7.773E-03
Postn	periostin, osteoblast specific factor	14.096	3.817	5.000E-05	7.773E-03
Prpf4b	pre-mRNA processing factor 4B	1.549	0.631	5.000E-05	7.773E-03
Ptgds	prostaglandin D2 synthase	9.303	3.218	5.000E-05	7.773E-03
Rbm5	RNA binding motif protein 5	1.627	0.702	5.000E-05	7.773E-03
RGD1311723	centrosomal protein 295	1.834	0.875	5.000E-05	7.773E-03
Rn50_10_0291.1	Rn50_10_0291.1	-1.636	-0.710	5.000E-05	7.773E-03
Rpl30	ribosomal protein L30	-2.087	-1.062	5.000E-05	7.773E-03
Rps29	ribosomal protein S29	-1.591	-0.670	5.000E-05	7.773E-03
Ryr3	ryanodine receptor 3	2.138	1.097	5.000E-05	7.773E-03
Sacs	sacsin molecular chaperone	1.718	0.781	5.000E-05	7.773E-03
Scn7a	sodium channel, voltage-gated, type VII, alpha	2.450	1.293	5.000E-05	7.773E-03
Scn9a	sodium channel, voltage-gated, type IX, alpha subunit	1.666	0.736	5.000E-05	7.773E-03
Serp2	stress-associated endoplasmic reticulum protein family member 2	-1.583	-0.662	5.000E-05	7.773E-03
Slc32a1	solute carrier family 32 (GABA vesicular transporter), member 1	-1.737	-0.797	5.000E-05	7.773E-03
Smg1	SMG1 phosphatidylinositol 3-kinase-related kinase	1.713	0.776	5.000E-05	7.773E-03
Sncb	synuclein, beta	-1.546	-0.629	5.000E-05	7.773E-03
Sned1	sushi, nidogen and EGF-like domains 1	2.354	1.235	5.000E-05	7.773E-03
Spp1	secreted phosphoprotein 1	13.844	3.791	5.000E-05	7.773E-03
Thbs2	thrombospondin 2	2.528	1.338	5.000E-05	7.773E-03
Tnc	tenascin C	2.068	1.048	5.000E-05	7.773E-03
Trpm7	transient receptor potential cation channel, subfamily M, member 7	1.638	0.712	5.000E-05	7.773E-03
Ttc14	tetratricopeptide repeat domain 14	1.772	0.825	5.000E-05	7.773E-03
Vip	vasoactive intestinal peptide	2.228	1.156	5.000E-05	7.773E-03
Wsb1	WD repeat and SOCS box-containing 1	1.506	0.591	5.000E-05	7.773E-03
Zfp192	zinc finger protein 192	1.693	0.759	5.000E-05	7.773E-03
Atr	ATR serine/threonine kinase	1.758	0.814	1.000E-04	1.416E-02
C7	complement component 7	2.864	1.518	1.000E-04	1.416E-02
Cyp7b1	cytochrome P450, family 7, subfamily b, 1	2.048	1.034	1.000E-04	1.416E-02
LOC100360154	ribosomal protein S21-like	-1.850	-0.887	1.000E-04	1.416E-02
Mbp	myelin basic protein	1.703	0.768	1.000E-04	1.416E-02
Rps2712	ribosomal protein S27-like 2	-1.626	-0.701	1.000E-04	1.416E-02
Setx	senataxin	1.546	0.629	1.000E-04	1.416E-02
Sparcl1	SPARC like 1	1.473	0.559	1.000E-04	1.416E-02
Tbc1d4	TBC1 domain family, member 4	2.739	1.453	1.000E-04	1.416E-02
AABR06028164.1	AABR06028164.1	-2.043	-1.031	1.500E-04	1.803E-02
AABR06098740.1	AABR06098740.1	-1.490	-0.575	1.500E-04	1.803E-02
Anln1	anillin, actin binding protein-like 1	2.687	1.426	1.500E-04	1.803E-02
Bag3	Bcl2-associated athanogene 3	2.390	1.257	1.500E-04	1.803E-02
Ccnt2	cyclin T2	1.563	0.644	1.500E-04	1.803E-02
Clk1	CDC-like kinase 1	1.561	0.642	1.500E-04	1.803E-02
Col5a2	collagen, type V, alpha 2	1.646	0.719	1.500E-04	1.803E-02
Cycs	cytochrome c, somatic	-1.547	-0.629	1.500E-04	1.803E-02
Emx2	empty spiracles homeobox 2	2.308	1.206	1.500E-04	1.803E-02
Fgl2	fibrinogen-like 2	2.702	1.434	1.500E-04	1.803E-02
Lpar1	lysophosphatidic acid receptor 1	1.597	0.676	1.500E-04	1.803E-02

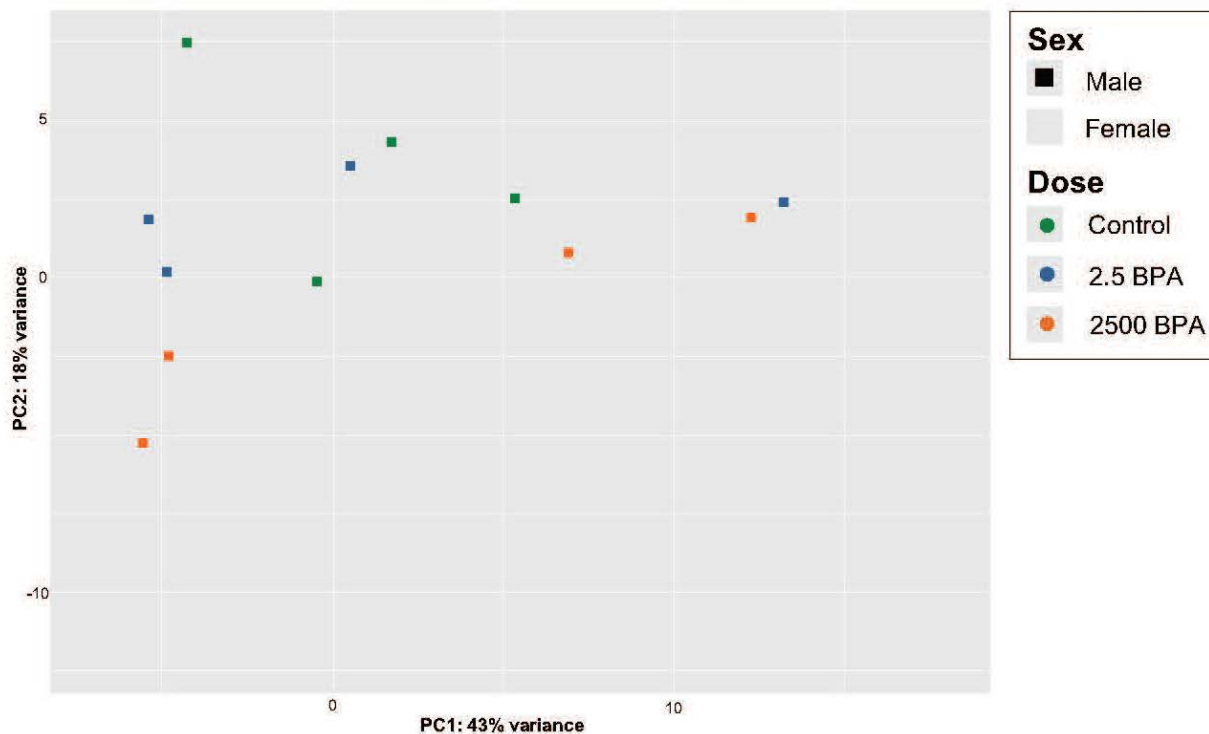
Onecut3	one cut homeobox 3	-2.987	-1.579	1.500E-04	1.803E-02
Ppic	peptidylprolyl isomerase C	1.736	0.795	1.500E-04	1.803E-02
Reck	reversion-inducing-cysteine-rich protein with kazal motifs	1.826	0.868	1.500E-04	1.803E-02
Slc13a4	solute carrier family 13 (sodium/sulfate symporter), member 4	7.313	2.870	1.500E-04	1.803E-02
Sst	somatostatin	-1.569	-0.650	1.500E-04	1.803E-02
Tet1	tet methylcytosine dioxygenase 1	1.829	0.871	1.500E-04	1.803E-02
Zfp483	zinc finger protein 483	1.702	0.767	1.500E-04	1.803E-02
Aspm	abnormal spindle microtubule assembly	1.744	0.802	2.000E-04	2.270E-02
Hba1	uncharacterized protein	1.559	0.640	2.000E-04	2.270E-02
LOC688684	similar to 60S ribosomal protein L32	-1.586	-0.666	2.000E-04	2.270E-02
Mmp9	matrix metalloproteinase 9	16.267	4.024	2.000E-04	2.270E-02
Sp8	Sp8 transcription factor	-3.827	-1.936	2.000E-04	2.270E-02
Tbca	tubulin folding cofactor A	-1.599	-0.677	2.000E-04	2.270E-02
Tgds	TDP-glucose 4,6-dehydratase	1.776	0.829	2.000E-04	2.270E-02
AABR06037143.1	AABR06037143.1	-1.580	-0.660	2.500E-04	2.572E-02
AABR06057457.1	AABR06057457.1	-1.547	-0.629	2.500E-04	2.572E-02
Adamts1	ADAM metalloproteinase with thrombospondin type 1 motif, 1	2.130	1.091	2.500E-04	2.572E-02
Aldh1a2	aldehyde dehydrogenase 1 family, member A2	4.214	2.075	2.500E-04	2.572E-02
Ankhd1	ankyrin repeat and KH domain containing 1	1.548	0.631	2.500E-04	2.572E-02
Antxr1	anthrax toxin receptor 1	1.762	0.817	2.500E-04	2.572E-02
Barhl1	BarH-like homeobox 1	2.974	1.572	2.500E-04	2.572E-02
Lgals1	lectin, galactoside-binding, soluble, 1	2.239	1.163	2.500E-04	2.572E-02
LOC100363012	ribosomal protein S21, pseudogene 1	-1.492	-0.577	2.500E-04	2.572E-02
Nfat5	nuclear factor of activated T-cells 5, tonicity-responsive	1.502	0.587	2.500E-04	2.572E-02
Slc6a20	solute carrier family 6 (proline IMINO transporter), member 20	3.278	1.713	2.500E-04	2.572E-02
Trim5	tripartite motif-containing 5	1.960	0.971	2.500E-04	2.572E-02
Vps13a	vacuolar protein sorting 13 homolog A (S. cerevisiae)	1.796	0.845	2.500E-04	2.572E-02
AABR06013961.1	AABR06013961.1	-1.734	-0.794	3.000E-04	2.899E-02
Capg	capping protein (actin filament), gelsolin-like	2.108	1.076	3.000E-04	2.899E-02
Casp2	caspase 2	1.590	0.669	3.000E-04	2.899E-02
Cldn11	claudin 11	1.936	0.953	3.000E-04	2.899E-02
LOC100362583	ribosomal protein L13a-like	-1.477	-0.563	3.000E-04	2.899E-02
Lypd6b	LY6/PLAUR domain containing 6B	-1.691	-0.758	3.000E-04	2.899E-02
Mdm4	MDM4, p53 regulator	1.637	0.711	3.000E-04	2.899E-02
Nr2f2	Nr2f2	-1.515	-0.599	3.000E-04	2.899E-02
Prkd3	protein kinase D3	1.726	0.788	3.000E-04	2.899E-02
AABR06014093.1	AABR06014093.1	-1.459	-0.545	3.500E-04	3.109E-02
AABR06027146.1	AABR06027146.1	-1.672	-0.742	3.500E-04	3.109E-02
Bgn	biglycan	1.956	0.968	3.500E-04	3.109E-02
Chrm5	cholinergic receptor, muscarinic 5	1.843	0.882	3.500E-04	3.109E-02
Dopey1	dopey family member 1	1.583	0.662	3.500E-04	3.109E-02
Esyt2	extended synaptotagmin-like protein 2	1.767	0.822	3.500E-04	3.109E-02
Fam135b	family with sequence similarity 135, member B	2.086	1.061	3.500E-04	3.109E-02
Jund	jun D proto-oncogene	-1.449	-0.535	3.500E-04	3.109E-02
LOC680227	LRRGT00193	126.396	6.982	3.500E-04	3.109E-02
Panx3	pannexin 3	13.884	3.795	3.500E-04	3.109E-02
RGD1565131	similar to ribosomal protein L15	-1.684	-0.752	3.500E-04	3.109E-02
Strip2	striatin interacting protein 2	3.123	1.643	3.500E-04	3.109E-02
Vipr2	vasoactive intestinal peptide receptor 2	1.887	0.916	3.500E-04	3.109E-02
AABR06087647.1	AABR06087647.1	-1.506	-0.591	4.000E-04	3.467E-02
Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	-1.886	-0.916	4.000E-04	3.467E-02
RGD2320734	cytochrome b-c1 complex subunit 9-like	-1.506	-0.591	4.000E-04	3.467E-02

Vstm2l	V-set and transmembrane domain containing 2 like	-1.956	-0.968	4.000E-04	3.467E-02
Islr	immunoglobulin superfamily containing leucine-rich repeat	2.510	1.328	4.500E-04	3.786E-02
LOC679894	similar to THO complex subunit 2 (Tho2)	1.586	0.665	4.500E-04	3.786E-02
Nup62cl	Nup62cl	-1.653	-0.725	4.500E-04	3.786E-02
Rasgrf2	RAS protein-specific guanine nucleotide-releasing factor 2	1.845	0.883	4.500E-04	3.786E-02
Srek1	splicing regulatory glutamine/lysine-rich protein 1	1.593	0.672	4.500E-04	3.786E-02
AABR06009564.1	AABR06009564.1	-1.525	-0.609	5.000E-04	4.110E-02
LOC100911545	alpha-2-macroglobulin-like	2.130	1.091	5.000E-04	4.110E-02
Mrs2	MRS2 magnesium transporter	1.696	0.762	5.000E-04	4.110E-02
Timm8b	translocase of inner mitochondrial membrane 8 homolog b	-1.459	-0.545	5.000E-04	4.110E-02
Dlx2	distal-less homeobox 2	-1.685	-0.753	5.500E-04	4.346E-02
Dnah9	dynein, axonemal, heavy chain 9	1.609	0.687	5.500E-04	4.346E-02
Fam214a	family with sequence similarity 214, member A	1.516	0.600	5.500E-04	4.346E-02
LOC100362685	up-regulated during skeletal muscle growth protein 5 pseudogene	-1.620	-0.696	5.500E-04	4.346E-02
LOC100911178	uncharacterized protein	1.434	0.520	5.500E-04	4.346E-02
Prrt1	proline-rich transmembrane protein 1	-1.519	-0.603	5.500E-04	4.346E-02
Vsn1	visinin-like 1	-1.448	-0.534	5.500E-04	4.346E-02
Cst6	cystatin E/M	-1.647	-0.720	6.000E-04	4.589E-02
Kif20b	kinesin family member 20B	2.037	1.026	6.000E-04	4.589E-02
Krit1	KRIT1, ankyrin repeat containing	1.542	0.625	6.000E-04	4.589E-02
Nktr	natural killer cell triggering receptor	1.479	0.564	6.000E-04	4.589E-02
Thoc1	THO complex 1	1.733	0.793	6.000E-04	4.589E-02
Zmym6	zinc finger, MYM-type 6	1.581	0.661	6.000E-04	4.589E-02
AABR06062966.1	AABR06062966.1	-1.472	-0.558	6.500E-04	4.602E-02
C1qc	complement component 1, q subcomponent, C chain	1.783	0.834	6.500E-04	4.602E-02
Crabp1	cellular retinoic acid binding protein 1	-2.249	-1.169	6.500E-04	4.602E-02
Dlx5	distal-less homeobox 5	-1.622	-0.698	6.500E-04	4.602E-02
Emp1	epithelial membrane protein 1	1.992	0.994	6.500E-04	4.602E-02
Fabp7	fatty acid binding protein 7, brain	-1.428	-0.514	6.500E-04	4.602E-02
LOC100911902	cellular retinoic acid-binding protein 2-like	2.034	1.025	6.500E-04	4.602E-02
LOC306079	similar to RIKEN cDNA 3100001N19	-1.526	-0.610	6.500E-04	4.602E-02
Man2a1	mannosidase, alpha, class 2A, member 1	1.584	0.664	6.500E-04	4.602E-02
Mgp	matrix Gla protein	2.823	1.497	6.500E-04	4.602E-02
Prp2l1	proline rich protein 2-like 1	1.927	0.947	6.500E-04	4.602E-02
Rpl18a	ribosomal protein L18A	-1.441	-0.527	6.500E-04	4.602E-02
Tbc1d31	TBC1 domain family, member 31	1.824	0.867	6.500E-04	4.602E-02
Top2a	topoisomerase (DNA) II alpha	1.632	0.706	6.500E-04	4.602E-02
Utm	utrophin	1.670	0.740	6.500E-04	4.602E-02
Atad5	ATPase family, AAA domain containing 5	1.720	0.783	7.000E-04	4.836E-02
Ddr2	discoidin domain receptor tyrosine kinase 2	2.302	1.203	7.000E-04	4.836E-02
LOC100363048	rCG47273-like	-1.801	-0.849	7.000E-04	4.836E-02
Otp	orthopedia homeobox	-1.520	-0.604	7.000E-04	4.836E-02
Penk	proenkephalin	-1.549	-0.631	7.000E-04	4.836E-02
Atm	ATM serine/threonine kinase	1.696	0.762	7.500E-04	4.989E-02
Cttna1	catenin alpha-like 1	1.594	0.672	7.500E-04	4.989E-02
Gng2	guanine nucleotide binding protein (G protein), gamma 2	-1.620	-0.696	7.500E-04	4.989E-02
Kdm6a	lysine (K)-specific demethylase 6A	1.640	0.713	7.500E-04	4.989E-02
Kmt2c	lysine (K)-specific methyltransferase 2C	1.483	0.569	7.500E-04	4.989E-02
LOC102557074	uncharacterized LOC102557074	-1.839	-0.879	7.500E-04	4.989E-02
Psme4	proteasome activator subunit 4	1.466	0.552	7.500E-04	4.989E-02
RGD1308544	LOC361192	-1.728	-0.789	7.500E-04	4.989E-02

A Unsupervised PCA of hippocampus RNAseq dataset



B Unsupervised PCA of hypothalamus RNAseq dataset



Supplemental Figure 1: Unsupervised principal component analyses (PCA) of (A) hippocampal and (B) hypothalamic RNA-seq data did not indicate clear clustering. The data did not group by exposure or sex. PCA was run on the entire data set, not just the subset genes identified as differentially expressed (by sex or BPA exposure).