

Table S2 - Information about DEGs showing the gene name and Ensembl ID, description of annotated gene, LogFoldChange, logCPM, LR, Pvalue and FDR

Gene name	Gene synonym	Gene stable ID	Gene description	log2FC	logCPM	LR	PValue	FDR
LOC107049387		-----	coiled-coil domain-containing protein 81-like	5.46	1.97062	40.28884	2.19E-10	3.03E-08
LOC107049379		-----	coiled-coil domain-containing protein 81-like	4.84	3.65201	52.31400	4.73E-13	1.28E-10
BTN3A2	-----	ENSGALG00010006046	butyrophilin, subfamily 3, member A2	4.59	-0.54104	96.64486	8.29E-23	8.53E-20
LOC107052718		-----	endogenous retrovirus group K member 11 Pol protein	4.02	4.49362	478.12181	5.48E-106	9.01E-102
LOC107052719	gag; SE21Q1b	-----	uncharacterized LOC107052719	3.31	3.31605	205.06580	1.64E-46	1.35E-42
GBP	-----	ENSGALG00010028163	guanylate binding protein	2.35	1.72085	22.23495	2.41E-06	9.92E-05
HEATR7B2L2	MROH2B; HEATR7B2L	-----	maestro heat-like repeat-containing protein family member 2B	2.33	0.28425	42.36640	7.57E-11	1.17E-08
MOGL4	MOGL; BG4	-----	myelin oligodendrocyte glycoprotein like	2.33	1.48422	59.72453	1.09E-14	4.08E-12
LOC112531062		-----	zinc finger protein 519-like	2.30	-0.21369	24.70611	6.68E-07	3.47E-05
LOC428505		ENSGALG00000046353	SUN domain-containing protein 3-like	2.20	-0.64518	28.24581	1.07E-07	7.17E-06
OR11A1	-----	ENSGALG00000041229	olfactory receptor 1020-like	2.19	0.50449	12.06927	5.13E-04	7.39E-03
BTN3A3L1	BG2	-----	butyrophilin subfamily 3 member A3-like 1	2.17	1.81418	32.06362	1.49E-08	1.25E-06
LOC107056757		-----	uncharacterized LOC107056757	2.16	0.65034	53.72986	2.30E-13	7.42E-11
LOC112532660		-----	monocarboxylate transporter 9-like	2.15	1.38082	89.29726	3.40E-21	3.29E-18
LOC101749199		-----	uncharacterized LOC101749199	2.07	0.00455	40.87006	1.63E-10	2.36E-08
LOC101751234		-----	uncharacterized LOC101751234	2.06	-0.25751	21.52971	3.48E-06	1.36E-04
LOC101747302		-----	uncharacterized LOC101747302	2.02	5.83788	119.07181	1.01E-27	1.66E-24
C4	C4-2	ENSGALG00000032231	complement 4	2.02	2.73485	62.11648	3.24E-15	1.30E-12
LOC107054918		-----	uncharacterized LOC107054918	1.95	-0.34757	29.00461	7.22E-08	5.10E-06
LOC107050939		-----	zinc finger protein 135-like	1.94	1.47057	11.92164	5.55E-04	7.86E-03
MHCIA9	MHCY6	-----	major histocompatibility complex Y, class I heavy chain 6	1.88	3.28359	28.77669	8.12E-08	5.59E-06
LOC107051303		-----	zinc finger protein 160-like	1.84	1.78809	55.81257	7.97E-14	2.68E-11
ACKR1	-----	-----	atypical chemokine receptor 1 (Duffy blood group)	1.84	0.66674	63.10464	1.96E-15	8.72E-13
ADCY8	-----	ENSGALG00000030251	adenylate cyclase 8	1.82	1.24948	43.00156	5.47E-11	8.65E-09
LOC101750974		-----	uncharacterized LOC101750974	1.77	-0.68164	21.92255	2.84E-06	1.14E-04
COLEC10	CL-1	ENSGALG00000033144	collectin subfamily member 10	1.77	3.52940	10.69550	1.07E-03	1.26E-02
C2orf50	-----	-----	chromosome 2 open reading frame 50	1.76	-0.63290	22.80235	1.80E-06	7.73E-05
LOC112531790		-----	uncharacterized LOC112531790	1.75	-0.39584	15.17031	9.82E-05	2.04E-03
LOC112533394		-----	protocadherin beta-15-like	1.70	-0.51149	14.10428	1.73E-04	3.19E-03
OR52R1L2	-----	ENSGALG00000053623	olfactory receptor 52R1-like	1.67	0.06438	30.25804	3.78E-08	2.87E-06
GM2A	-----	ENSGALG00000027534	GM2 ganglioside activator	1.65	4.44794	135.27486	2.87E-31	6.76E-28
ADGRG5	-----	ENSGALG00000001149	adhesion G protein-coupled receptor G5	1.64	-0.58325	25.77582	3.83E-07	2.16E-05
LOC107051154		-----	protocadherin beta-8-like	1.60	0.72921	18.54055	1.66E-05	4.88E-04
LYG2	LYG1	ENSGALG00000016761	lysozyme g2	1.60	-0.21761	15.95552	6.48E-05	1.48E-03
AKR1B1L	AKR1E2	ENSGALG00000053854	aldo-keto reductase family 1 member E2	1.59	3.23802	12.89178	3.30E-04	5.28E-03
MROH2B1	-----	-----	maestro heat-like repeat family member 2B 1	1.59	-0.74565	19.18100	1.19E-05	3.74E-04
VSIG1	CHT1	ENSGALG00000008290	V-set and immunoglobulin domain containing 1	1.58	-0.64250	14.28824	1.57E-04	2.93E-03
LOC100859910		-----	uncharacterized LOC100859910	1.51	2.19170	49.91625	1.60E-12	3.83E-10
BF2	B-F	ENSGALG00000041380	Major histocompatibility complex class I antigen BF2	1.48	2.53136	62.62506	2.50E-15	1.03E-12
DHRS13	-----	ENSGALG00000004009	dehydrogenase/reductase 13	1.48	1.97704	68.54611	1.24E-16	6.37E-14
LOC107053759		-----	uncharacterized LOC107053759	1.47	1.17686	28.35526	1.01E-07	6.84E-06
LOC100858315	ARHGAP33L1	-----	Rho GTPase-activating protein 33 like 1	1.47	0.09050	16.14343	5.87E-05	1.36E-03

LOC112533400		-----	uncharacterized LOC112533400	1.45	-0.99113	12.94309	3.21E-04	5.19E-03
BTN3A3L2	B-G; BG5; BG11	-----	butyrophilin subfamily 3 member A3-like 2	1.43	4.68356	29.09217	6.90E-08	4.92E-06
SAMD7	-----	ENSGALG00000009383	sterile alpha motif domain containing 7	1.40	1.89607	13.13568	2.90E-04	4.80E-03
LOC107052398		-----	uncharacterized LOC107052398	1.39	0.77701	37.73894	8.09E-10	9.31E-08
OR5AS1	-----	ENSGALG00000043910	olfactory receptor family 5 subfamily AS member 1	1.37	0.10685	15.34482	8.96E-05	1.90E-03
BF1	B-F	ENSGALG00000033932	MHC BF1 class I	1.37	2.63024	36.19169	1.79E-09	1.89E-07
LOC107053999		-----	uncharacterized LOC107053999	1.36	1.03996	32.25657	1.35E-08	1.15E-06
LOC112531075		-----	zinc finger protein 501-like	1.36	0.45089	17.17720	3.40E-05	8.67E-04
LOC112533561		-----	uncharacterized LOC112533561	1.33	1.10952	18.17183	2.02E-05	5.68E-04
LOC101748371		-----	uncharacterized LOC101748371	1.33	2.62172	21.03708	4.50E-06	1.69E-04
LOC107053444		-----	uncharacterized LOC107053444	1.33	0.89736	30.94816	2.65E-08	2.09E-06
LOC112530181		-----	uncharacterized LOC112530181	1.33	1.79082	10.78328	1.02E-03	1.22E-02
LOC107053612		-----	translation initiation factor IF-2-like	1.32	-0.81959	12.30254	4.52E-04	6.72E-03
LOC107054467		-----	protocadherin beta-15-like	1.31	0.21127	9.74161	1.80E-03	1.86E-02
LOC112532499		-----	uncharacterized LOC112532499	1.30	0.32758	20.44867	6.13E-06	2.20E-04
SLC2A2	GLUT2	ENSGALG00000009306	solute carrier family 2 member 2	1.30	1.34307	8.41145	3.73E-03	3.10E-02
LOC112529957		-----	sperm acrosome membrane-associated protein 6	1.30	3.17608	77.79166	1.15E-18	7.85E-16
TTR	-----	ENSGALG00000015143	transthyretin	1.29	3.12347	7.22748	7.18E-03	4.91E-02
LOC107054533		-----	uncharacterized LOC107054533	1.29	-0.15858	10.78192	1.02E-03	1.22E-02
LOC101749307		-----	uncharacterized LOC101749307	1.28	-0.35228	8.51975	3.51E-03	2.96E-02
CDHR1	PCDH21	ENSGALG00000002314	cadherin related family member 1	1.28	-0.66578	10.56603	1.15E-03	1.33E-02
LOC107054129		-----	uncharacterized LOC107054129	1.27	-0.32016	14.97645	1.09E-04	2.18E-03
LOC101750503		-----	uncharacterized LOC101750503	1.27	1.53048	40.86040	1.64E-10	2.36E-08
TAP2	-----	-----	transporter 2, ATP binding cassette subfamily B	1.26	2.05204	53.40004	2.72E-13	8.45E-11
PECAM1	-----	ENSGALG00000046125	platelet and endothelial cell adhesion molecule 1	1.25	5.77834	75.13973	4.39E-18	2.58E-15
SYPL1	-----	ENSGALG00000029006	synaptophysin like 1	1.24	-0.02826	19.70023	9.06E-06	2.99E-04
SH2D1B	-----	ENSGALG00000028448	SH2 domain containing 1B	1.24	0.74777	10.95612	9.33E-04	1.14E-02
LOC431499	ARHGAP33L2	-----	Rho GTPase activating protein 33 like 2	1.24	2.78730	37.71847	8.17E-10	9.34E-08
CRP	APCS	ENSGALG00000022137	C-reactive protein, pentraxin-related	1.22	-0.38563	16.73408	4.30E-05	1.06E-03
LOC107050915		-----	uncharacterized LOC107050915	1.22	1.38717	10.98934	9.16E-04	1.13E-02
MUC4	-----	ENSGALG00000048048	mucin 4, cell surface associated	1.21	-0.36391	7.96281	4.77E-03	3.71E-02
LOC112533543		-----	zinc finger protein 135-like	1.20	3.97705	46.62441	8.60E-12	1.68E-09
LOC776376	CRPL2	-----	C-reactive protein like 2	1.20	0.91163	31.38050	2.12E-08	1.73E-06
WNT11B	cWnt11b	ENSGALG00000004401	wingless-type MMTV integration site family, member 11b	1.20	-0.49402	10.28950	1.34E-03	1.48E-02
VWA5A	-----	ENSGALG00000028815	von Willebrand factor A domain containing 5A	1.19	0.21225	23.45323	1.28E-06	5.84E-05
LOC101749621		-----	uncharacterized LOC101749621	1.16	-0.65184	10.34655	1.30E-03	1.45E-02
NKX2-1	NKX2.1	ENSGALG00000037632	NK2 homeobox 1	1.16	-0.23795	11.92039	5.55E-04	7.86E-03
LOC107050034		-----	uncharacterized LOC107050034	1.16	1.65606	38.42395	5.69E-10	6.69E-08
CNGA2	-----	ENSGALG00000007282	cyclic nucleotide gated channel alpha 2	1.16	0.06504	14.29413	1.56E-04	2.93E-03
LOC101747293		-----	PHD finger protein 7-like	1.15	-0.36903	9.57152	1.98E-03	2.00E-02
LOC107051395		-----	uncharacterized threonine-rich GPI-anchored glycoprotein PJ4664.02-like	1.14	0.34103	14.16702	1.67E-04	3.10E-03
DPF1	-----	ENSGALG00000052924	D4, zinc and double PHD fingers family 1	1.13	0.68293	15.74443	7.25E-05	1.62E-03
MC3R	-----	ENSGALG00000027260	melanocortin 3 receptor	1.12	-0.95275	9.20962	2.41E-03	2.27E-02
HS3ST4	-----	ENSGALG00000006290	heparan sulfate-glucosamine 3-sulfotransferase 4	1.10	0.71301	9.28501	2.31E-03	2.21E-02

LOC101750341		-----	uncharacterized LOC101750341	1.10	2.66444	47.13346	6.63E-12	1.36E-09
ALPI	ALPP	ENSGALG00000007814	alkaline phosphatase, placental	1.09	1.40649	22.69775	1.90E-06	8.04E-05
TRNP1	-----	-----	TMF1-regulated nuclear protein	1.08	-0.48361	12.13908	4.94E-04	7.20E-03
ACSBG1	-----	ENSGALG00000003286	acyl-CoA synthetase bubblegum family member 1	1.08	2.08165	36.96110	1.21E-09	1.35E-07
GIMAP8L1	-----	-----	GTPase IMAP family member 7-like 5	1.08	-0.39483	8.95774	2.76E-03	2.49E-02
CFAP161	-----	ENSGALG00000021183	cilia and flagella associated protein 161	1.08	-0.71654	9.03625	2.65E-03	2.42E-02
MIR1748	-----	ENSGALG00000025323	gga-mir-1748	1.07	-0.89483	8.37801	3.80E-03	3.13E-02
LOC112531929		-----	uncharacterized LOC112531929	1.06	1.01669	15.56254	7.98E-05	1.75E-03
MCCC2L	-----	ENSGALG00000011255	methylcrotonoyl-Coenzyme A carboxylase 2-like	1.05	3.81776	40.13540	2.37E-10	3.21E-08
OTX5	CRX	ENSGALG00000039336	orthodenticle-related homeobox 5	1.05	2.13916	7.55699	5.98E-03	4.33E-02
LOC107055278		-----	uncharacterized LOC107055278	1.05	1.42381	24.98955	5.76E-07	3.03E-05
RBM11	-----	ENSGALG00000044391	RNA binding motif protein 11	1.04	1.15019	21.15159	4.24E-06	1.61E-04
COMTD1	-----	ENSGALG00000005000	catechol-O-methyltransferase domain containing 1	1.04	4.20873	36.10497	1.87E-09	1.93E-07
TDRD6	-----	ENSGALG00000044279	tudor domain containing 6	1.02	0.52122	11.85547	5.75E-04	8.05E-03
LOC107053729		-----	uncharacterized LOC107053729	1.02	-0.00903	7.40616	6.50E-03	4.60E-02
LOC107050073		-----	uncharacterized LOC107050073	1.02	2.85859	34.60588	4.04E-09	3.93E-07
NKX2-8	-----	ENSGALG00000028483	NK2 homeobox 8	1.02	2.23816	31.14889	2.39E-08	1.90E-06
LCAT	-----	ENSGALG00000028928	lecithin-cholesterol acyltransferase	1.01	1.51001	21.26947	3.99E-06	1.53E-04
LOC107049645		-----	uncharacterized LOC107049645	1.01	1.52053	18.61441	1.60E-05	4.74E-04
GALNT15	-----	ENSGALG00000011235	polypeptide N-acetylgalactosaminyltransferase 15	1.00	2.11982	23.66561	1.15E-06	5.31E-05
SP7	-----	ENSGALG000000050811	Sp7 transcription factor	1.00	1.14687	11.27482	7.86E-04	1.01E-02
LOC419830		-----	uncharacterized LOC419830	0.99	1.73168	24.87850	6.11E-07	3.19E-05
LOC101747645		-----	translation initiation factor IF-2-like	0.99	-0.43579	9.01145	2.68E-03	2.44E-02
SPATA17	-----	ENSGALG00000009616	spermatogenesis associated 17	0.99	2.34282	39.69025	2.98E-10	3.83E-08
APOA5	-----	ENSGALG00010024749	apolipoprotein A5	0.98	1.48780	28.78212	8.10E-08	5.59E-06
RASGRF1	-----	ENSGALG00000008262	Ras protein specific guanine nucleotide releasing factor 1	0.98	0.00922	12.29136	4.55E-04	6.74E-03
APOA1	-----	ENSGALG00000007114	apolipoprotein A1	0.98	6.15499	22.21712	2.43E-06	9.99E-05
CKMT2	MIBCK	ENSGALG00000015602	creatine kinase, mitochondrial 2	0.98	-0.12810	12.23836	4.68E-04	6.89E-03
LOC112531211		-----	rho GTPase-activating protein 33-like	0.97	1.49540	15.03944	1.05E-04	2.15E-03
TGM6	-----	ENSGALG00000021232	transglutaminase 6	0.97	0.84085	16.18187	5.75E-05	1.34E-03
TAP1	-----	ENSGALG00000035075	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0.96	1.77047	16.58600	4.65E-05	1.12E-03
LOC107054756		-----	uncharacterized LOC107054756	0.96	0.44852	16.49028	4.89E-05	1.17E-03
LOC112530484		-----	uncharacterized LOC112530484	0.96	-0.32230	9.51867	2.03E-03	2.04E-02
CENPQ	-----	ENSGALG00000016692	centromere protein Q	0.96	5.89574	180.13785	4.52E-41	2.48E-37
LOC100859067		-----	uncharacterized LOC100859067	0.96	2.18051	16.04494	6.19E-05	1.43E-03
LOC112529979		-----	uncharacterized LOC112529979	0.96	1.10623	12.31106	4.50E-04	6.70E-03
LOC112532478		-----	uncharacterized LOC112532478	0.96	2.10645	21.99277	2.74E-06	1.10E-04
ACOT12	-----	ENSGALG00000015616	acyl-CoA thioesterase 12	0.96	-0.18415	9.93247	1.62E-03	1.72E-02
UCP3	UCP	ENSGALG00000017316	uncoupling protein 3	0.95	1.24409	15.72881	7.31E-05	1.63E-03
AGBL2	-----	ENSGALG00010021737	ATP/GTP binding protein like 2	0.95	1.61916	13.31954	2.63E-04	4.47E-03
LOC107050476		-----	uncharacterized LOC107050476	0.95	-0.27192	8.04157	4.57E-03	3.58E-02
F8	-----	ENSGALG00000005077	coagulation factor VIII	0.95	1.64998	15.47932	8.34E-05	1.80E-03
HAO1	-----	ENSGALG00000008845	hydroxyacid oxidase 1	0.94	0.08315	13.23276	2.75E-04	4.61E-03
AKR1B10L4	-----	-----	discontued	0.94	2.61349	12.50507	4.06E-04	6.19E-03

SPAG16	-----	ENSGALG00000003148	sperm associated antigen 16	0.94	2.90366	38.94855	4.35E-10	5.30E-08
GEM	-----	ENSGALG000000032506	GTP binding protein overexpressed in skeletal muscle	0.94	1.03292	14.42113	1.46E-04	2.78E-03
LOC112533263	-----	-----	uncharacterized LOC112533263	0.93	1.62725	7.25074	7.09E-03	4.86E-02
LOC101747452	-----	-----	serine/arginine repetitive matrix protein 2-like	0.93	-0.03893	11.08424	8.71E-04	1.08E-02
AvBD14	DEFB1	ENSGALG000000052020	avian beta-defensin 14	0.93	-0.19083	11.80476	5.91E-04	8.18E-03
NT5DC4	-----	ENSGALG000000041161	5'-nucleotidase domain containing 4	0.93	2.55384	17.89435	2.34E-05	6.41E-04
LOC107049688	-----	-----	uncharacterized LOC107049688	0.92	2.79743	27.47352	1.59E-07	1.02E-05
LOC101750700	-----	-----	uncharacterized LOC101750700	0.92	5.03911	51.73216	6.36E-13	1.59E-10
KCNK4	-----	ENSGALG000000012021	potassium channel, subfamily K, member 4	0.91	-0.29429	7.63746	5.72E-03	4.19E-02
LOC101748003	-----	-----	uncharacterized LOC101748003	0.91	0.39861	12.78459	3.49E-04	5.51E-03
FBXL13	-----	-----	F-box and leucine rich repeat protein 13	0.90	1.16175	14.71798	1.25E-04	2.45E-03
NTRK1	CTRKA	ENSGALG000000019019	neurotrophic receptor tyrosine kinase 1	0.90	0.33692	11.69628	6.26E-04	8.54E-03
LOC107054526	-----	-----	uncharacterized LOC107054526	0.90	-0.56038	9.03437	2.65E-03	2.42E-02
CPLX1	-----	ENSGALG000000015332	complexin 1	0.90	4.09625	23.05199	1.58E-06	6.92E-05
LOC101748847	-----	-----	uncharacterized LOC101748847	0.90	-0.06386	7.76404	5.33E-03	3.99E-02
DNAJC28	-----	ENSGALG000000037414	DnaJ heat shock protein family (Hsp40) member C28	0.90	2.22270	34.77439	3.70E-09	3.65E-07
LOC101751275	-----	-----	uncharacterized LOC101751275	0.90	0.19475	8.76005	3.08E-03	2.69E-02
LOC112530112	-----	-----	uncharacterized LOC112530112	0.90	1.01634	10.71463	1.06E-03	1.26E-02
LOC107049643	-----	-----	uncharacterized LOC107049643	0.89	0.57253	11.70873	6.22E-04	8.51E-03
AASDHPPT	-----	ENSGALG000000027981	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	0.89	2.04872	31.66932	1.83E-08	1.52E-06
LOC107055878	-----	-----	acid-sensing ion channel 1-like	0.89	1.37386	12.61670	3.82E-04	5.91E-03
CD79B	-----	ENSGALG000000000251	CD79b molecule	0.89	-0.18686	8.87250	2.89E-03	2.58E-02
LOC112530977	-----	-----	fibrinogen alpha-1 chain-like	0.89	1.32634	15.07318	1.03E-04	2.12E-03
LOC112532935	-----	-----	uncharacterized LOC112532935	0.89	1.49744	22.53652	2.06E-06	8.70E-05
LOC107050328	-----	-----	uncharacterized LOC107050328	0.88	2.30709	8.33768	3.88E-03	3.18E-02
LY9	-----	-----	-----	0.88	0.55941	9.03211	2.65E-03	2.42E-02
LOC112532241	-----	-----	small nucleolar RNA SNORA33	0.88	0.20526	15.65747	7.59E-05	1.68E-03
LOC107053429	-----	-----	uncharacterized LOC107053429	0.87	1.11474	22.44910	2.16E-06	9.01E-05
LOXHD1	-----	ENSGALG000000037829	lipoxygenase homology domains 1	0.87	-0.12773	7.47385	6.26E-03	4.49E-02
EPB42	-----	ENSGALG000000021230	erythrocyte membrane protein band 4.2	0.87	1.92796	7.69826	5.53E-03	4.09E-02
LOC107055363	-----	-----	uncharacterized LOC107055363	0.86	-0.47308	8.00882	4.66E-03	3.63E-02
LOC107051705	-----	-----	uncharacterized LOC107051705	0.85	4.46738	37.43035	9.47E-10	1.07E-07
KCTD16	-----	ENSGALG000000012322	potassium channel tetramerization domain containing 16	0.85	0.78043	15.92212	6.60E-05	1.50E-03
PIH1D3	DNAAF6	ENSGALG000000004870	PIH1 domain containing 3	0.85	4.65772	115.29342	6.79E-27	9.31E-24
LOC107051973	-----	-----	uncharacterized LOC107051973	0.85	-0.10831	8.96095	2.76E-03	2.49E-02
IFT81	CDV1	ENSGALG000000003854	intraflagellar transport 81	0.84	4.81819	104.60862	1.49E-24	1.63E-21
KCNE4	-----	ENSGALG000000031350	potassium voltage-gated channel subfamily E regulatory subunit 4	0.84	1.29570	12.82156	3.43E-04	5.44E-03
ULK4	-----	-----	unc-51 like kinase 4	0.84	3.65895	43.54491	4.14E-11	6.82E-09
LOC107050901	-----	-----	keratin-associated protein 10-7-like	0.84	3.45449	23.59477	1.19E-06	5.48E-05
LOC107053559	-----	-----	uncharacterized LOC107053559	0.83	0.29674	11.71815	6.19E-04	8.49E-03
HSP90AA1	-----	ENSGALG000000033212	heat shock protein 90 alpha family class A member 1	0.83	10.68309	19.27042	1.13E-05	3.61E-04
TDRKH	-----	ENSGALG000000031812	tudor and KH domain containing	0.83	3.39539	26.74730	2.32E-07	1.37E-05
BBOX1	-----	ENSGALG000000013297	gamma-butyrobetaine hydroxylase 1	0.83	4.92430	20.58288	5.71E-06	2.07E-04
IMPG2	-----	ENSGALG000000015322	interphotoreceptor matrix proteoglycan 2	0.83	1.25076	10.81653	1.01E-03	1.21E-02

SLC27A6	-----	ENSGALG00000000184	solute carrier family 27 (fatty acid transporter), member 6	0.82	1.09356	18.24623	1.94E-05	5.52E-04
RMI2	BLAP18	ENSGALG00000007155	RecQ mediated genome instability 2	0.82	4.31898	53.04169	3.27E-13	9.60E-11
RXFP2	-----	ENSGALG00000029764	relaxin/insulin-like family peptide receptor 2	0.82	2.58674	12.98660	3.14E-04	5.11E-03
AOX2	-----	ENSGALG00000020876	aldehyde oxidase 2	0.82	1.91706	24.18121	8.77E-07	4.32E-05
HIST1H4B	-----	-----	histone cluster 1, H4b	0.82	0.27428	9.78427	1.76E-03	1.83E-02
SPHKAP	4930544G21RIK	ENSGALG00000002974	SPHK1 interactor, AKAP domain containing	0.81	2.18268	14.90971	1.13E-04	2.25E-03
LOC101751352	-----	-----	translation initiation factor IF-2-like	0.81	2.35421	23.76012	1.09E-06	5.09E-05
LOC101750502	-----	-----	uncharacterized LOC101750502	0.81	4.06218	21.55026	3.45E-06	1.35E-04
LOC107054466	-----	-----	protocadherin beta-15-like	0.80	0.15285	7.37822	6.60E-03	4.65E-02
LOC107054904	-----	-----	uncharacterized LOC107054904	0.80	0.26599	10.42163	1.25E-03	1.40E-02
LOC112530086	-----	-----	fibrinogen-like protein 1-like protein	0.80	2.21999	11.75936	6.05E-04	8.34E-03
LOC112533519	-----	-----	uncharacterized LOC112533519	0.80	0.73163	12.33210	4.45E-04	6.64E-03
GP1BA	-----	-----	-----	0.80	1.58181	14.60382	1.33E-04	2.57E-03
LOC112530939	-----	-----	uncharacterized LOC112530939	0.80	0.91143	9.62481	1.92E-03	1.96E-02
LYGL	-----	ENSGALG00000043257	lysozyme g-like	0.79	3.02916	13.24720	2.73E-04	4.59E-03
TKFC	-----	ENSGALG00000037854	triokinase and FMN cyclase	0.79	4.90513	23.80200	1.07E-06	5.01E-05
DAW1	-----	ENSGALG00000002992	dynein assembly factor with WD repeats 1	0.79	0.54092	14.55476	1.36E-04	2.62E-03
LOC101749472	-----	-----	uncharacterized LOC101749472	0.78	-0.04365	7.45340	6.33E-03	4.53E-02
LOC107052084	-----	-----	uncharacterized LOC107052084	0.78	0.14793	11.72186	6.18E-04	8.48E-03
LOC112530017	-----	-----	uncharacterized LOC112530017	0.77	1.52450	7.60983	5.81E-03	4.23E-02
LOC112533567	-----	-----	myelin-oligodendrocyte glycoprotein-like	0.77	0.34967	8.05651	4.53E-03	3.56E-02
CCNO	-----	ENSGALG00000028595	cyclin O	0.77	-0.23339	8.67088	3.23E-03	2.79E-02
TMEM178B	-----	ENSGALG00000028444	transmembrane protein 178B	0.77	1.83884	21.99521	2.73E-06	1.10E-04
OTOP1	-----	ENSGALG00000030356	otopetirin 1	0.77	0.54405	7.72480	5.45E-03	4.05E-02
WNT2B	-----	ENSGALG00000034196	Wnt family member 2B	0.76	2.19330	9.94965	1.61E-03	1.71E-02
LOC418114	-----	-----	pseudouridine-5'-phosphate glycosidase-like	0.76	3.24680	38.09977	6.72E-10	7.79E-08
CYR61	CCN1	ENSGALG00000008661	cysteine rich angiogenic inducer 61	0.76	4.71668	23.34345	1.36E-06	6.11E-05
LOC107049250	-----	-----	inhibin beta C chain-like	0.76	0.37779	9.05921	2.61E-03	2.40E-02
LOC112532772	-----	-----	uncharacterized LOC112532772	0.76	0.12690	9.28508	2.31E-03	2.21E-02
INSC	-----	ENSGALG00000032558	inscuteable homolog (Drosophila)	0.76	0.23172	9.29322	2.30E-03	2.21E-02
GBP4L	-----	ENSGALG00000026152	guanylate-binding protein 4-like	0.75	1.96365	10.87515	9.75E-04	1.18E-02
NTHL1	CHNTHL1	ENSGALG00000005617	nth like DNA glycosylase 1	0.75	4.07337	41.82734	9.97E-11	1.51E-08
LOC107054327	-----	-----	uncharacterized LOC107054327	0.75	-0.15975	7.49760	6.18E-03	4.44E-02
LOC107050538	MHCY11	-----	major histocompatibility complex Y, class I heavy chain 11	0.75	0.23562	7.27512	6.99E-03	4.82E-02
FAM161A	-----	ENSGALG00000008810	family with sequence similarity 161 member A	0.75	2.14563	17.10501	3.54E-05	8.98E-04
LOC101752186	-----	-----	uncharacterized LOC101752186	0.75	0.92036	9.24568	2.36E-03	2.25E-02
LOC112532059	-----	-----	uncharacterized LOC112532059	0.75	2.22683	11.19059	8.22E-04	1.04E-02
LOC107050418	-----	-----	uncharacterized LOC107050418	0.74	0.88404	8.65688	3.26E-03	2.81E-02
FAM132A	-----	ENSGALG00000001857	family with sequence similarity 132 member A	0.74	2.85385	9.16953	2.46E-03	2.30E-02
ASTL	-----	ENSGALG00000037220	astacin like metalloendopeptidase	0.74	4.00195	11.99072	5.35E-04	7.62E-03
LOC101751045	-----	-----	uncharacterized LOC101751045	0.74	0.22711	7.18602	7.35E-03	5.00E-02
LMOD2	C-LMOD	ENSGALG00000008805	leiomodoin 2	0.73	1.27139	7.64537	5.69E-03	4.18E-02
STC2	-----	ENSGALG00000002893	stanniocalcin 2	0.73	4.92372	13.77931	2.06E-04	3.65E-03
LOC107054649	-----	-----	uncharacterized LOC107054649	0.73	1.57897	9.77790	1.77E-03	1.83E-02

LOC112533499		-----	2-acylglycerol O-acyltransferase 2-like	0.73	0.83955	9.69241	1.85E-03	1.90E-02
OXNAD1	-----	ENSGALG00000011239	oxidoreductase NAD binding domain containing 1	0.73	4.28702	50.10715	1.46E-12	3.52E-10
NHEJ1	-----	ENSGALG00000011335	non-homologous end joining factor 1	0.72	2.19453	20.72699	5.30E-06	1.95E-04
HLX	-----	ENSGALG00000037257	H2.0 like homeobox	0.72	3.18949	12.81210	3.44E-04	5.46E-03
CFAP70	-----	ENSGALG00000002551	cilia and flagella associated protein 70	0.72	2.10334	20.27949	6.69E-06	2.34E-04
MFSD2B	-----	ENSGALG00000016498	major facilitator superfamily domain containing 2B	0.72	1.95886	8.31922	3.92E-03	3.21E-02
SAMD15	-----	-----	sterile alpha motif domain containing 15	0.72	0.70312	9.22364	2.39E-03	2.26E-02
GTSF1	-----	ENSGALG00000001109	gametocyte specific factor 1	0.72	3.88663	13.34087	2.60E-04	4.43E-03
LOC107052732		-----	uncharacterized LOC107052732	0.71	0.46855	9.18362	2.44E-03	2.29E-02
LOC771917		-----	uncharacterized LOC771917	0.71	0.64828	10.53516	1.17E-03	1.34E-02
LOC107052318		-----	uncharacterized LOC107052318	0.71	1.52420	8.00297	4.67E-03	3.64E-02
LOC107055288		-----	uncharacterized LOC107055288	0.71	3.45704	23.30045	1.39E-06	6.21E-05
SLC17A9	C20orf59	ENSGALG00000028225	solute carrier family 17 member 9	0.71	2.57672	23.92389	1.00E-06	4.79E-05
NOXA1	-----	ENSGALG00000008952	NADPH oxidase activator 1	0.70	1.97992	12.20246	4.77E-04	6.99E-03
VWA5B1	-----	-----	von Willebrand factor A domain containing 5B1	0.70	4.43046	38.65580	5.06E-10	6.07E-08
LOC100857609		-----	phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-1-like	0.70	2.75183	18.13278	2.06E-05	5.78E-04
LOC101747364		-----	uncharacterized LOC101747364	0.70	1.84240	14.02125	1.81E-04	3.29E-03
SLC6A4	SERT	ENSGALG00000004246	solute carrier family 6 member 4	0.70	3.76234	13.26270	2.71E-04	4.58E-03
IL18	ChIL-18	ENSGALG00000007874	interleukin 18	0.70	3.63024	44.26565	2.87E-11	4.97E-09
MAK	-----	-----	male germ cell associated kinase	0.70	2.03241	16.91418	3.91E-05	9.77E-04
ADORA2B	A2B-AR	ENSGALG00000014182	adenosine A2b receptor	0.69	1.62156	10.14597	1.45E-03	1.57E-02
LOC101748818		-----	uncharacterized LOC101748818	0.69	0.95049	10.41983	1.25E-03	1.40E-02
SCO2	-----	ENSGALG00000046885	SCO2, cytochrome c oxidase assembly protein	0.69	3.59986	31.09835	2.45E-08	1.94E-06
SULT1E1	-----	ENSGALG00000011812	sulfotransferase family 1E member 1	0.69	1.50363	12.06869	5.13E-04	7.39E-03
DNAJC24	DPH4	ENSGALG00000012130	DnaJ heat shock protein family (Hsp40) member C24	0.69	3.10272	29.10887	6.84E-08	4.90E-06
LOC107052946		-----	uncharacterized LOC107052946	0.68	0.63573	10.65933	1.10E-03	1.28E-02
DNAJA1	-----	ENSGALG00000023066	DnaJ heat shock protein family (Hsp40) member A1	0.68	7.38649	21.42789	3.67E-06	1.42E-04
MANBAL7	-----	-----	-----	0.68	5.18503	11.29648	7.77E-04	9.98E-03
SLC39A8	-----	ENSGALG00000012298	solute carrier family 39 member 8	0.68	3.97478	13.63476	2.22E-04	3.90E-03
LOC107057116	ZNFY4	-----	MHCY region zinc finger protein 4	0.68	3.04191	11.42903	7.23E-04	9.50E-03
LOC418108		-----	poly	0.67	1.90963	10.67551	1.09E-03	1.27E-02
DNAJA4	-----	ENSGALG00000036850	DnaJ heat shock protein family (Hsp40) member A4	0.67	6.16564	29.47627	5.66E-08	4.14E-06
TMEM109	-----	-----	transmembrane protein 109	0.67	2.67533	16.42898	5.05E-05	1.20E-03
LOC112531022		-----	uncharacterized LOC112531022	0.67	0.21959	8.80203	3.01E-03	2.65E-02
VWC2L	-----	ENSGALG00000003472	von Willebrand factor C domain containing protein 2 like	0.67	3.56223	25.86107	3.67E-07	2.09E-05
LYPD6	-----	ENSGALG00000012470	LY6/PLAUR domain containing 6	0.67	1.32156	8.87688	2.89E-03	2.58E-02
CALCB	-----	-----	-----	0.67	4.57919	24.49675	7.44E-07	3.75E-05
ENKUR	-----	ENSGALG00000007680	enkurin, TRPC channel interacting protein	0.67	1.93364	10.15902	1.44E-03	1.57E-02
TMEM59L	-----	ENSGALG00000021620	transmembrane protein 59 like	0.67	1.98147	12.78525	3.49E-04	5.51E-03
LOC100857706		-----	uncharacterized LOC100857706	0.67	2.61569	13.39398	2.52E-04	4.33E-03
SLC18A2	-----	ENSGALG00000009289	solute carrier family 18 member A2	0.67	1.51114	10.47368	1.21E-03	1.38E-02
KIFC1L	-----	-----	-----	0.67	7.45576	43.02052	5.42E-11	8.65E-09
CFAP58	-----	ENSGALG00000008417	cilia and flagella associated protein 58	0.67	0.93828	11.75720	6.06E-04	8.34E-03
STN1	-----	ENSGALG00000008304	STN1, CST complex subunit	0.66	5.29576	52.66869	3.95E-13	1.08E-10

ST6GALNAC2L	-----	-----	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 2 like	0.66	2.38842	14.82561	1.18E-04	2.34E-03
VWA3A	-----	ENSGALG00000049654	von Willebrand factor A domain containing 3A	0.65	1.09276	12.83956	3.39E-04	5.41E-03
LOC112529982		-----	syntaxin-4-like	0.65	2.71443	17.91028	2.32E-05	6.37E-04
RAB19	-----	ENSGALG00000012850	RAB19, member RAS oncogene family	0.65	1.27640	11.17244	8.30E-04	1.05E-02
CRYGN	-----	ENSGALG00000006189	crystallin gamma N	0.65	1.12924	10.27383	1.35E-03	1.49E-02
GIMAP5L	-----	-----	-----	0.65	2.57118	9.82575	1.72E-03	1.79E-02
NUP210L	-----	-----	nucleoporin 210 like	0.65	2.44187	15.27203	9.31E-05	1.96E-03
LAMC3	-----	-----	laminin subunit gamma 3	0.65	4.04705	19.87715	8.26E-06	2.82E-04
LOC100857928		-----	uncharacterized LOC100857928	0.65	1.51683	11.92288	5.54E-04	7.86E-03
LDHA	-----	ENSGALG00000006300	lactate dehydrogenase A	0.64	6.34999	9.52652	2.03E-03	2.03E-02
ALG14	-----	ENSGALG00000005583	ALG14, UDP-N-acetylglucosaminyltransferase subunit	0.64	2.89310	25.75054	3.89E-07	2.18E-05
LOC107050412		-----	uncharacterized LOC107050412	0.64	1.62295	13.72154	2.12E-04	3.75E-03
MPL	c-mpl	ENSGALG00000009965	MPL proto-oncogene, thrombopoietin receptor	0.64	2.76289	13.81857	2.01E-04	3.60E-03
LYPD1	-----	ENSGALG00000050403	LY6/PLAUR domain containing 1	0.64	0.96712	7.25767	7.06E-03	4.85E-02
POLG2	-----	ENSGALG00000003520	DNA polymerase gamma 2, accessory subunit	0.63	3.48036	24.57094	7.16E-07	3.65E-05
CCDC27	-----	ENSGALG00000043926	coiled-coil domain containing 27	0.63	2.30130	16.30740	5.39E-05	1.27E-03
SLC13A3	-----	ENSGALG00000054473	solute carrier family 13 member 3	0.63	3.21238	26.06317	3.30E-07	1.90E-05
TLR4	-----	ENSGALG00000007001	toll like receptor 4	0.63	1.28219	7.28828	6.94E-03	4.80E-02
FOXF1	-----	ENSGALG00000034111	forkhead box F1	0.63	4.40096	18.56196	1.64E-05	4.84E-04
CASP7	-----	ENSGALG00000008933	caspase 7	0.63	1.86049	12.53488	3.99E-04	6.13E-03
NR2C1	-----	ENSGALG00000011327	nuclear receptor subfamily 2, group C, member 1	0.63	4.90645	36.29898	1.69E-09	1.80E-07
FAIM	-----	ENSGALG00000012082	Fas apoptotic inhibitory molecule	0.63	4.63998	34.91467	3.44E-09	3.44E-07
VSNL1	-----	ENSGALG00000016464	visinin like 1	0.63	2.28756	10.46173	1.22E-03	1.38E-02
LOC112530784		-----	small nucleolar RNA SNORD58	0.62	0.79690	7.49955	6.17E-03	4.44E-02
LOC107052236		-----	uncharacterized LOC107052236	0.62	1.28724	10.06027	1.52E-03	1.63E-02
MATK	-----	ENSGALG00000000736	megakaryocyte-associated tyrosine kinase	0.62	1.56424	10.95737	9.32E-04	1.14E-02
BMP3	-----	ENSGALG00000035052	bone morphogenetic protein 3	0.61	2.29164	7.21704	7.22E-03	4.93E-02
LOC101750197		-----	uncharacterized LOC101750197	0.61	0.59503	8.11375	4.39E-03	3.48E-02
LOC112532382		-----	uncharacterized LOC112532382	0.61	1.05164	9.00756	2.69E-03	2.44E-02
LOC112532614		-----	uncharacterized LOC112532614	0.61	4.13200	15.04094	1.05E-04	2.15E-03
FIBCD1	-----	ENSGALG00000003866	ficolin 3	0.60	1.46701	8.22506	4.13E-03	3.33E-02
COL2A1L	-----	-----	-----	0.60	5.53957	12.45309	4.17E-04	6.31E-03
HTR2B	-----	ENSGALG00000007681	5-hydroxytryptamine receptor 2B	0.60	1.07254	8.48864	3.57E-03	3.00E-02
EGLN3	-----	ENSGALG00000010001	egl-9 family hypoxia inducible factor 3	0.60	2.97052	12.12140	4.98E-04	7.24E-03
LOC107056270		-----	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3-like	0.60	3.11793	10.35408	1.29E-03	1.44E-02
LOC107054458		-----	PHD finger protein 7-like	0.60	2.03444	13.91955	1.91E-04	3.44E-03
MDH1B	-----	ENSGALG00000008548	malate dehydrogenase 1B	0.60	1.85184	13.02038	3.08E-04	5.04E-03
CYP26B1	-----	ENSGALG00000016102	cytochrome P450 family 26 subfamily B member 1	0.60	4.99141	26.98388	2.05E-07	1.25E-05
HSPA8	HSC70	ENSGALG00000006512	heat shock 70kDa protein 8	0.59	10.88731	18.49837	1.70E-05	4.93E-04
FSIP1	-----	ENSGALG00000009624	fibrous sheath interacting protein 1	0.59	1.82442	12.33437	4.45E-04	6.64E-03
LOC112532778		-----	uncharacterized LOC112532778	0.59	1.00040	9.19169	2.43E-03	2.28E-02
PLPP4	-----	ENSGALG00000029020	phospholipid phosphatase 4	0.59	5.04021	27.09565	1.94E-07	1.19E-05
PBLD	-----	ENSGALG00000003935	phenazine biosynthesis like protein domain containing	0.59	3.27521	27.57730	1.51E-07	9.74E-06
ZFPM2	-----	ENSGALG00000040079	zinc finger protein, FOG family member 2	0.59	3.07736	8.85605	2.92E-03	2.59E-02

PEX6	-----	ENSGALG00000045514	peroxisomal biogenesis factor 6	0.58	5.75744	40.03471	2.49E-10	3.34E-08
VPS41	-----	ENSGALG00000031635	VPS41, HOPS complex subunit	0.58	5.63370	52.79102	3.71E-13	1.03E-10
LOC107050006	-----	-----	uncharacterized LOC107050006	0.58	2.02232	12.14186	4.93E-04	7.20E-03
LOC421506	-----	-----	uncharacterized LOC421506	0.58	2.97125	11.04376	8.90E-04	1.10E-02
SHC4	-----	-----	SHC adaptor protein 4	0.58	3.53231	27.34973	1.70E-07	1.07E-05
PYCR1	PYCR2	ENSGALG00000007300	pyrroline-5-carboxylate reductase 1	0.57	6.86296	45.37152	1.63E-11	3.01E-09
RRP8	-----	-----	ribosomal RNA processing 8, methyltransferase, homolog (yeast)	0.57	4.54959	27.95926	1.24E-07	8.19E-06
PMFBP1	-----	-----	polyamine modulated factor 1 binding protein 1	0.57	3.08059	19.25710	1.14E-05	3.63E-04
RBFA	C18orf22	ENSGALG00000036067	ribosome binding factor A (putative)	0.57	4.60691	48.83635	2.78E-12	6.27E-10
SERPINH1	HSP47	ENSGALG00000011214	serpin family H member 1	0.57	8.19946	10.06362	1.51E-03	1.63E-02
LOC101749936	-----	-----	uncharacterized LOC101749936	0.57	1.36136	8.99986	2.70E-03	2.45E-02
RCAN2	-----	ENSGALG00000016709	regulator of calcineurin 2	0.57	6.33603	36.37279	1.63E-09	1.75E-07
CARD8	-----	ENSGALG00000007698	caspase recruitment domain family, member 8	0.57	1.01472	10.13266	1.46E-03	1.58E-02
LOC107054051	-----	-----	uncharacterized LOC107054051	0.56	2.24173	12.86856	3.34E-04	5.33E-03
RNF207	-----	ENSGALG00000050086	ring finger protein 207	0.56	4.71911	27.59626	1.49E-07	9.68E-06
TRIM63	-----	ENSGALG00000034107	tripartite motif containing 63	0.56	3.52746	10.83191	9.98E-04	1.20E-02
LOC770653	-----	-----	uncharacterized LOC770653	0.56	3.41825	10.78700	1.02E-03	1.22E-02
UCKL1	ZFP	ENSGALG00000006040	uridine-cytidine kinase 1 like 1	0.56	3.21778	12.12063	4.99E-04	7.24E-03
SPTBN4L	-----	-----	-----	0.55	3.07086	8.55723	3.44E-03	2.91E-02
RSPH14	-----	ENSGALG00000006712	radial spoke head 14 homolog	0.55	2.79561	12.22336	4.72E-04	6.93E-03
KLHL6	-----	ENSGALG00000002263	kelch like family member 6	0.55	1.69701	8.78373	3.04E-03	2.66E-02
OTOG	-----	-----	otogelin	0.55	3.19016	7.90105	4.94E-03	3.80E-02
IKBKAP	-----	ENSGALG00000001947	inhibitor of kappa light polypeptide gene enhancer in B-cells	0.55	7.01423	28.80138	8.02E-08	5.57E-06
MYH7	AMHC1	ENSGALG00000035594	myosin, heavy chain 7, cardiac muscle, beta	0.55	2.72866	7.49301	6.19E-03	4.45E-02
UGT8	-----	ENSGALG00000012018	UDP glycosyltransferase 8	0.55	2.16468	7.63432	5.73E-03	4.19E-02
MILR1	-----	ENSGALG00000046212	mast cell immunoglobulin like receptor 1	0.55	1.36625	7.94021	4.83E-03	3.74E-02
LOC107052132	-----	-----	uncharacterized LOC107052132	0.54	2.07725	10.56459	1.15E-03	1.33E-02
CBLN1	-----	ENSGALG00000042664	cerebellin 1 precursor	0.54	3.47299	7.28504	6.95E-03	4.80E-02
NOM1	-----	ENSGALG00000006437	nucleolar protein with MIF4G domain 1	0.54	4.68894	40.50798	1.96E-10	2.77E-08
SIM1	-----	ENSGALG00000015466	SIM bHLH transcription factor 1	0.54	4.92844	24.05842	9.35E-07	4.55E-05
DAO	-----	ENSGALG00000043053	D-amino acid oxidase	0.54	3.35977	23.41805	1.30E-06	5.93E-05
ASCC1	-----	ENSGALG00000026019	activating signal cointegrator 1 complex subunit 1	0.54	5.38196	27.25840	1.78E-07	1.11E-05
LOC112533544	-----	-----	E3 ubiquitin-protein ligase TRIM7-like	0.53	5.22062	48.46844	3.36E-12	7.46E-10
MISP	-----	ENSGALG00000044985	mitotic spindle positioning	0.53	2.47867	13.13857	2.89E-04	4.80E-03
VRTN	-----	ENSGALG00000010232	vertebrae development associated	0.53	2.96244	18.12469	2.07E-05	5.78E-04
SLC3A1	-----	ENSGALG00000009973	solute carrier family 3 member 1	0.53	1.38265	7.82584	5.15E-03	3.89E-02
ACOX3	-----	ENSGALG00000015591	acyl-CoA oxidase 3, pristanoyl	0.53	3.39689	14.90141	1.13E-04	2.26E-03
DNAH12	-----	ENSGALG00000005601	dynein, axonemal, heavy chain 12	0.53	1.93993	9.08794	2.57E-03	2.37E-02
PROCA1	-----	ENSGALG00000030512	protein interacting with cyclin A1	0.53	4.17809	31.39498	2.11E-08	1.72E-06
LOC107056831	-----	-----	uncharacterized LOC107056831	0.53	1.30912	7.31890	6.82E-03	4.74E-02
C26H1orf74	-----	-----	-----	0.53	2.50791	10.71670	1.06E-03	1.26E-02
GAA	-----	ENSGALG00000038853	alpha glucosidase	0.53	4.10108	12.99324	3.13E-04	5.10E-03
LOC112533501	-----	-----	protein NDRG2-like	0.52	1.24904	7.74832	5.38E-03	4.02E-02
LOC426385	-----	ENSGALG00000026301	serine/threonine kinase 35-like	0.52	4.78196	34.63907	3.97E-09	3.89E-07

HOXB1	Ghox-lab	ENSGALG00000013454	homeobox B1	0.52	6.67587	28.50349	9.35E-08	6.36E-06
AAREL	-----	ENSGALG00000033303	acylamino-acid-releasing enzyme-like	0.52	2.65371	8.01666	4.63E-03	3.62E-02
TRPV1	-----	ENSGALG00000004649	transient receptor potential cation channel subfamily V member 1	0.52	2.74528	7.51332	6.12E-03	4.41E-02
ST8SIA1	SIAL-T2	ENSGALG00000013211	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	0.52	3.86006	16.72555	4.32E-05	1.06E-03
COLEC11	-----	ENSGALG00000050002	collectin subfamily member 11	0.52	3.58007	12.68368	3.69E-04	5.75E-03
LOC100858737		-----	uncharacterized LOC100858737	0.52	1.88723	10.52930	1.17E-03	1.35E-02
SEMA3BL	-----	-----	-----	0.52	4.90530	13.88518	1.94E-04	3.49E-03
LIN28A	LIN28	ENSGALG00000036022	lin-28 homolog A	0.52	6.70121	8.26578	4.04E-03	3.27E-02
GSTK1	-----	ENSGALG00000014708	glutathione S-transferase kappa 1	0.52	5.31156	53.21372	2.99E-13	9.12E-11
IKBKE	-----	ENSGALG00000013356	inhibitor of kappa light polypeptide gene enhancer in B-cells	0.52	2.45355	9.94483	1.61E-03	1.71E-02
TRIM45	-----	ENSGALG00000014818	tripartite motif containing 45	0.51	3.52653	19.71437	8.99E-06	2.99E-04
BCO2	-----	ENSGALG00000007868	beta-carotene oxygenase 2	0.51	2.47314	11.03559	8.94E-04	1.10E-02
LOC107053557		-----	uncharacterized LOC107053557	0.51	2.59617	10.56924	1.15E-03	1.33E-02
LSM10	-----	ENSGALG00000002127	LSM10, U7 small nuclear RNA associated	0.51	2.09851	10.27309	1.35E-03	1.49E-02
LOC112532559		-----	translation initiation factor IF-2-like	0.51	3.19000	21.61043	3.34E-06	1.31E-04
HSPA5	GRP78	ENSGALG00000001000	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	0.51	9.20858	25.37409	4.72E-07	2.56E-05
LOC101750998		-----	uncharacterized LOC101750998	0.51	6.41239	9.45598	2.10E-03	2.09E-02
GCNT7	-----	ENSGALG00000007717	glucosaminyl (N-acetyl) transferase family member 7	0.50	2.26302	9.44583	2.12E-03	2.09E-02
LOC101749541		-----	translation initiation factor IF-2-like	0.50	2.16796	7.22148	7.20E-03	4.92E-02
RSPH10B	-----	-----	radial spoke head 10 homolog B	0.50	3.66384	17.03584	3.67E-05	9.30E-04
2KTGRL	-----	ENSGALG00000046360	probable 2-ketogluconate reductase-like	0.50	3.39609	16.99252	3.75E-05	9.44E-04
HLCS	-----	ENSGALG00000016047	holocarboxylase synthetase	0.50	6.00153	43.10292	5.19E-11	8.38E-09
CYP46A1	-----	ENSGALG00000011162	cytochrome P450 family 46 subfamily A member 1	0.50	4.24970	23.11713	1.52E-06	6.74E-05
FRMD5	-----	ENSGALG00000030858	FERM domain containing 5	0.50	4.16972	15.79369	7.06E-05	1.59E-03
SNAP47	-----	ENSGALG00000005412	synaptosome associated protein 47	0.50	4.65215	30.27263	3.75E-08	2.86E-06
SPTBN2	-----	-----	spectrin beta, non-erythrocytic 2	0.50	5.64761	17.87283	2.36E-05	6.48E-04
FUT10	-----	ENSGALG00000015399	fucosyltransferase 10	0.49	2.72276	9.27511	2.32E-03	2.22E-02
ADCY5	ADCY6	ENSGALG00000031244	adenylate cyclase 6	0.49	4.99531	27.03729	2.00E-07	1.22E-05
NABP1	-----	ENSGALG00000025884	nucleic acid binding protein 1	0.49	6.64157	45.11202	1.86E-11	3.40E-09
C20H20orf96	-----	-----	-----	0.49	1.88788	7.89605	4.95E-03	3.80E-02
MUT	-----	ENSGALG00000016697	methylmalonyl-CoA mutase	0.49	4.87546	20.99622	4.60E-06	1.72E-04
LOC768735	CTC-575C13.4	-----	uncharacterized protein LOC768735	0.49	2.70950	9.12314	2.52E-03	2.34E-02
SIK1	SIK2	ENSGALG00000041988	salt inducible kinase 1	0.49	6.17899	27.44546	1.62E-07	1.03E-05
LOC101747556		-----	uncharacterized LOC101747556	0.49	4.53877	19.41025	1.05E-05	3.40E-04
LOC101747742		-----	uncharacterized LOC101747742	0.48	2.90483	17.56204	2.78E-05	7.34E-04
SMC2	SCII	ENSGALG00000015691	structural maintenance of chromosomes 2	0.48	8.87683	28.52460	9.25E-08	6.32E-06
N4BP2L1	-----	ENSGALG00000017072	NEDD4 binding protein 2 like 1	0.48	3.98943	12.42733	4.23E-04	6.38E-03
LOC424430		-----	quinone oxidoreductase-like 2	0.48	2.65388	12.63342	3.79E-04	5.88E-03
PDE1C	-----	ENSGALG00000039935	phosphodiesterase 1C	0.48	4.06600	19.89312	8.19E-06	2.80E-04
LOC101747934		-----	uncharacterized LOC101747934	0.48	3.28191	14.60282	1.33E-04	2.57E-03
MAOB	-----	ENSGALG00000032836	monoamine oxidase B	0.48	3.43523	8.94008	2.79E-03	2.51E-02
PLCD3	-----	ENSGALG00000045212	phospholipase C delta 3	0.48	3.17572	13.62375	2.23E-04	3.91E-03
ATP2A3	SERCA	ENSGALG00000001564	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 3	0.47	4.71583	14.63372	1.31E-04	2.55E-03
GRHPR	-----	ENSGALG00000005423	glyoxylate and hydroxypyruvate reductase	0.47	3.38355	14.02218	1.81E-04	3.29E-03

SOCS2	-----	ENSGALG00000050619	suppressor of cytokine signaling 2	0.47	4.14594	10.65962	1.09E-03	1.28E-02
LOC101747310	-----	-----	uncharacterized LOC101747310	0.47	1.31047	7.39135	6.55E-03	4.62E-02
KLF4	-----	-----	Kruppel like factor 4	0.47	2.34432	9.94298	1.61E-03	1.71E-02
CTNNAL1	-----	ENSGALG00000013207	catenin alpha like 1	0.47	6.17645	47.33226	5.99E-12	1.28E-09
TRAPPC12	-----	ENSGALG00000016387	trafficking protein particle complex 12	0.47	4.88611	18.38055	1.81E-05	5.19E-04
CERS4	-----	ENSGALG00000043352	ceramide synthase 4	0.46	5.51261	29.00829	7.21E-08	5.10E-06
LOC107051305	-----	-----	sodium channel subunit beta-1-like	0.46	3.59859	11.83074	5.83E-04	8.11E-03
EDEM2	-----	ENSGALG00000003128	ER degradation enhancing alpha-mannosidase like protein 2	0.46	5.27678	43.29733	4.70E-11	7.66E-09
LOC112533506	-----	-----	uncharacterized LOC112533506	0.46	5.04495	25.49525	4.43E-07	2.43E-05
LOC112533366	-----	-----	uncharacterized LOC112533366	0.46	2.86910	15.16406	9.86E-05	2.04E-03
TTC32	-----	ENSGALG00000016476	tetratricopeptide repeat domain 32	0.46	3.01363	8.54752	3.46E-03	2.92E-02
LRRC75A	-----	ENSGALG00000002631	leucine rich repeat containing 75A	0.45	3.85241	12.38095	4.34E-04	6.51E-03
STRADB	-----	ENSGALG00000008373	STE20-related kinase adaptor beta	0.45	5.51091	28.88958	7.66E-08	5.39E-06
GLB1L2	-----	ENSGALG00000001604	galactosidase beta 1 like 2	0.45	5.75462	46.32640	1.00E-11	1.94E-09
DTD2	-----	ENSGALG00000009978	D-tyrosyl-tRNA deacylase 2 (putative)	0.45	3.06930	12.50638	4.06E-04	6.19E-03
ASL2	ASL	ENSGALG00000002576	argininosuccinate lyase 2	0.45	2.03955	10.62732	1.11E-03	1.30E-02
BTD	-----	ENSGALG00000011216	biotinidase	0.45	3.02549	8.79793	3.02E-03	2.65E-02
PARP14	-----	ENSGALG00000026422	poly(ADP-ribose) polymerase family member 14	0.45	2.61485	9.16801	2.46E-03	2.30E-02
VDAC1	-----	ENSGALG00000006503	voltage dependent anion channel 1	0.45	3.78611	10.81799	1.01E-03	1.21E-02
SLC16A3	MCT4	ENSGALG00000002728	solute carrier family 16 member 3	0.45	5.24705	10.65672	1.10E-03	1.28E-02
PTGR2	ZADH1	ENSGALG00000009269	prostaglandin reductase 2	0.45	5.36727	24.48681	7.48E-07	3.75E-05
ACYP2	acylphosphatase-2	ENSGALG00000027632	acylphosphatase 2	0.44	3.46013	14.23317	1.61E-04	3.00E-03
GDF10	-----	ENSGALG00000005985	growth differentiation factor 10	0.44	4.45645	8.30699	3.95E-03	3.22E-02
PAX2	PAX-2	ENSGALG00000005689	paired box 2	0.44	5.66638	11.17293	8.30E-04	1.05E-02
LOC107053581	-----	-----	uncharacterized LOC107053581	0.44	2.82782	11.40726	7.32E-04	9.55E-03
METTL25	-----	ENSGALG00000042269	methyltransferase like 25	0.44	3.07185	9.53150	2.02E-03	2.03E-02
HSD11B1L	11-BETA-HSD3	ENSGALG00000012860	hydroxysteroid 11-beta dehydrogenase 1 like	0.44	4.77915	29.69965	5.04E-08	3.74E-06
FAM13AL	-----	-----	----	0.44	3.07443	8.71579	3.15E-03	2.74E-02
TMEM116	-----	ENSGALG00000004760	transmembrane protein 116	0.44	1.51957	7.27106	7.01E-03	4.83E-02
TMEM35B	-----	ENSGALG00000002517	transmembrane protein 35B	0.44	3.44676	8.03220	4.60E-03	3.60E-02
ALDH1A2	RALDH2	ENSGALG00000004270	aldehyde dehydrogenase 1 family member A2	0.44	8.41806	31.17865	2.35E-08	1.89E-06
OLIG3	-----	-----	oligodendrocyte transcription factor 3	0.44	2.83127	7.78109	5.28E-03	3.97E-02
PCCA	-----	ENSGALG00000016872	propionyl-CoA carboxylase alpha subunit	0.44	5.54662	46.88072	7.54E-12	1.50E-09
LOC107049075	DNAJB1	-----	DnaJ heat shock protein family (Hsp40) member B1	0.44	5.95855	17.52910	2.83E-05	7.45E-04
ACOT9	-----	ENSGALG00000016351	acyl-CoA thioesterase 9	0.43	5.90691	39.31192	3.61E-10	4.54E-08
GREM2	-----	ENSGALG00000055021	gremlin 2, DAN family BMP antagonist	0.43	3.80495	11.41089	7.30E-04	9.54E-03
DMGDH	-----	ENSGALG00000004491	dimethylglycine dehydrogenase	0.43	3.58406	8.78358	3.04E-03	2.66E-02
PIGC	-----	ENSGALG00000027608	phosphatidylinositol glycan anchor biosynthesis class C	0.43	3.84211	14.98598	1.08E-04	2.18E-03
C4H4orf33	-----	-----	----	0.43	3.44109	9.94042	1.62E-03	1.71E-02
PHKB	-----	ENSGALG00000004004	phosphorylase kinase regulatory subunit beta	0.43	6.35085	19.73415	8.90E-06	2.98E-04
NANS	-----	ENSGALG00000015320	N-acetylneuraminate synthase	0.43	6.13424	35.32014	2.80E-09	2.82E-07
MUS81	-----	-----	----	0.43	3.76691	18.90877	1.37E-05	4.18E-04
WDR90	-----	ENSGALG00000028172	WD repeat domain 90	0.43	6.46628	39.52833	3.23E-10	4.12E-08
RACGAP1L	-----	-----	----	0.43	5.40665	21.24319	4.05E-06	1.54E-04

BCAT1	-----	ENSGALG00000013177	branched chain amino acid transaminase 1	0.43	6.93915	30.24282	3.81E-08	2.88E-06
CPPED1	-----	ENSGALG00000040854	calcineurin like phosphoesterase domain containing 1	0.43	5.55259	30.38603	3.54E-08	2.71E-06
DPF2	-----	-----	double PHD fingers 2	0.43	2.67743	10.15178	1.44E-03	1.57E-02
C20orf196	-----	-----	-----	0.43	2.74769	9.57720	1.97E-03	1.99E-02
LOC101750925	-----	-----	mucin-5AC-like	0.43	3.29281	7.41225	6.48E-03	4.60E-02
NPTX2	-----	ENSGALG00000003562	neuronal pentraxin 2	0.43	1.95819	8.14313	4.32E-03	3.43E-02
ZBTB46	-----	ENSGALG00000006062	zinc finger and BTB domain containing 46	0.43	6.32650	27.37041	1.68E-07	1.06E-05
LRIG1	-----	ENSGALG00000007483	leucine rich repeats and immunoglobulin like domains 1	0.43	8.00362	12.33197	4.45E-04	6.64E-03
LOC422171	ARHGAP20B	-----	Rho GTPase activating protein 20B	0.42	4.91541	19.86641	8.30E-06	2.82E-04
SMOC2	-----	ENSGALG00000011205	SPARC related modular calcium binding 2	0.42	6.15762	19.87544	8.27E-06	2.82E-04
COX17	-----	ENSGALG00000014981	COX17, cytochrome c oxidase copper chaperone	0.42	4.00233	16.70557	4.37E-05	1.07E-03
LMBR1L	-----	ENSGALG00000037665	limb development membrane protein 1 like	0.42	4.62112	26.47824	2.67E-07	1.54E-05
GFM2	-----	ENSGALG00000014939	G elongation factor mitochondrial 2	0.42	5.22475	16.42403	5.06E-05	1.21E-03
NME7	-----	ENSGALG00000015230	NME/NM23 family member 7	0.42	4.13936	15.13342	1.00E-04	2.07E-03
LOC107051884	-----	-----	uncharacterized LOC107051884	0.42	1.98471	7.87139	5.02E-03	3.83E-02
ATL1	-----	ENSGALG00000012339	atlastin GTPase 1	0.42	4.93239	28.12102	1.14E-07	7.59E-06
ADAM22	-----	ENSGALG00000008976	ADAM metallopeptidase domain 22	0.42	4.44794	16.40470	5.12E-05	1.21E-03
NKX3-2	BAPX1	ENSGALG00000031859	NK3 homeobox 2	0.42	5.87746	13.26351	2.71E-04	4.58E-03
LRRC4C	-----	ENSGALG00000007948	leucine rich repeat containing 4C	0.42	3.70878	8.74055	3.11E-03	2.71E-02
NPR3	-----	ENSGALG00000017405	natriuretic peptide receptor 3	0.42	7.02366	8.64019	3.29E-03	2.82E-02
CTGF	CCN2	ENSGALG00010004251	cellular communication network factor 2	0.42	6.05696	22.04502	2.66E-06	1.08E-04
TLE4Z1	-----	-----	-----	0.42	5.35651	17.84292	2.40E-05	6.55E-04
CPZ	-----	ENSGALG00000030209	carboxypeptidase Z	0.42	6.13455	17.29712	3.20E-05	8.22E-04
LRRC46	-----	-----	leucine rich repeat containing 46	0.42	1.79293	8.54770	3.46E-03	2.92E-02
CDH7	cadherin-7	ENSGALG00000013782	cadherin 7	0.41	4.39787	14.76364	1.22E-04	2.40E-03
LOC407092	-----	-----	ubiquitin associated protein 2	0.41	7.26531	19.71362	9.00E-06	2.99E-04
LOC101752064	-----	-----	uncharacterized LOC101752064	0.41	2.44896	7.87445	5.01E-03	3.83E-02
XPO1	exportin-1	ENSGALG00000029476	exportin 1	0.41	8.72432	33.67099	6.53E-09	5.97E-07
ARHGAP39L	-----	ENSGALG00000001536	Rho GTPase activating protein 39	0.41	4.81529	18.39244	1.80E-05	5.17E-04
KLF9	-----	ENSGALG00000027374	Kruppel like factor 9	0.41	2.64361	7.45681	6.32E-03	4.52E-02
THY1	-----	ENSGALG00000006751	Thy-1 cell surface antigen	0.41	2.09143	7.55679	5.98E-03	4.33E-02
LOC107053100	-----	-----	basic proline-rich protein-like	0.41	3.46959	10.94497	9.39E-04	1.15E-02
EPHX2	-----	ENSGALG00000016567	epoxide hydrolase 2	0.41	4.78213	19.12484	1.22E-05	3.80E-04
TOP3A	-----	ENSGALG00000005028	topoisomerase (DNA) III alpha	0.41	5.88343	12.32344	4.47E-04	6.67E-03
ITGB3BP	CENP-R	ENSGALG00000010995	integrin subunit beta 3 binding protein	0.41	5.28617	25.50565	4.41E-07	2.43E-05
ADCY2	-----	ENSGALG00000013060	adenylate cyclase 2	0.40	2.93028	7.87730	5.01E-03	3.83E-02
LOC107051471	-----	-----	fermitin family homolog 3-like	0.40	5.15465	9.36962	2.21E-03	2.15E-02
TPK1	-----	ENSGALG00000040298	thiamin pyrophosphokinase 1	0.40	4.67878	18.66951	1.55E-05	4.64E-04
STK10	-----	ENSGALG00000002816	serine/threonine kinase 10	0.40	4.34186	11.38747	7.39E-04	9.65E-03
RRP36	-----	ENSGALG00000028056	ribosomal RNA processing 36	0.40	6.23017	13.24827	2.73E-04	4.59E-03
DERL3	-----	ENSGALG00000005994	derlin 3	0.40	3.80814	11.11914	8.54E-04	1.07E-02
LOC428824	-----	-----	SITS-binding protein-like	0.40	2.94977	9.74368	1.80E-03	1.86E-02
RUVBL1	-----	ENSGALG00000005931	RuvB like AAA ATPase 1	0.40	7.44605	24.43298	7.69E-07	3.84E-05
HSPH1	-----	ENSGALG00000017077	heat shock protein family H (Hsp110) member 1	0.40	7.27078	15.38299	8.78E-05	1.87E-03

LOC107054036		-----	endogenous retrovirus group K member 9 Pol protein-like	0.40	3.61008	11.32776	7.64E-04	9.85E-03
LOC112532692		-----	uncharacterized LOC112532692	0.40	2.75564	9.22109	2.39E-03	2.26E-02
HAUS1	CCDC5	ENSGALG00000040397	HAUS augmin like complex subunit 1	0.40	4.88655	10.64963	1.10E-03	1.29E-02
DHTKD1	-----	ENSGALG00000003674	dehydrogenase E1 and transketolase domain containing 1	0.40	5.54329	12.44709	4.19E-04	6.33E-03
SYVN1	-----	-----	synoviolin 1	0.40	5.57380	13.71345	2.13E-04	3.76E-03
P2RX4	-----	ENSGALG00000003901	purinergic receptor P2X 4	0.40	3.59149	17.57099	2.77E-05	7.33E-04
GFRA2	NTNRLPHA	ENSGALG00000032856	GDNF family receptor alpha 2	0.40	4.90299	9.21209	2.40E-03	2.27E-02
RARRES1	OCX32	ENSGALG00000009594	retinoic acid receptor responder 1	0.40	4.19737	7.26996	7.01E-03	4.83E-02
SOX3	CH3	ENSGALG00000054923	SRY-box 3	0.39	4.74932	8.50563	3.54E-03	2.98E-02
CIART	-----	-----	circadian associated repressor of transcription	0.39	2.57972	7.93921	4.84E-03	3.74E-02
ZWILCH	-----	ENSGALG00000007736	zwilch kinetochore protein	0.39	6.29913	32.45825	1.22E-08	1.04E-06
TRIM47	-----	ENSGALG00000028301	tripartite motif containing 47	0.39	3.23443	7.40997	6.49E-03	4.60E-02
SDHAF1	-----	-----	succinate dehydrogenase complex assembly factor 1	0.39	5.07331	22.70151	1.89E-06	8.04E-05
LOC112530910		-----	REST corepressor 2-like	0.39	5.28041	12.71877	3.62E-04	5.67E-03
RPS6KB2	-----	ENSGALG00000031629	ribosomal protein S6 kinase B2	0.39	5.38109	24.84482	6.21E-07	3.24E-05
CFAP43	-----	ENSGALG00000036896	cilia and flagella associated protein 43	0.39	4.06222	9.45765	2.10E-03	2.09E-02
IRAK2	-----	ENSGALG00000008407	interleukin 1 receptor associated kinase 2	0.39	5.73068	33.83440	6.00E-09	5.58E-07
ENOX1	-----	ENSGALG00000016967	ecto-NOX disulfide-thiol exchanger 1	0.39	4.42873	8.38293	3.79E-03	3.13E-02
PSTK	-----	ENSGALG00000009610	phosphoseryl-tRNA kinase	0.39	3.95351	10.28026	1.34E-03	1.49E-02
PDE6G	-----	ENSGALG00000004514	phosphodiesterase 6G	0.39	3.98057	13.88633	1.94E-04	3.49E-03
BCCIP	-----	ENSGALG00000006617	BRCA2 and CDKN1A interacting protein	0.39	5.70840	40.59414	1.87E-10	2.68E-08
PUDP	-----	ENSGALG00000040388	pseudouridine 5'-phosphatase	0.38	3.05320	8.36926	3.82E-03	3.14E-02
LOC426743		-----	probable beta-D-xylosidase 5-like	0.38	3.57174	12.59570	3.87E-04	5.97E-03
LOC419584		-----	discoidin, CUB and LCCL domain-containing protein 1-like	0.38	3.87216	9.06319	2.61E-03	2.39E-02
IFT22	-----	ENSGALG00000021653	intraflagellar transport 22	0.38	4.02489	16.87648	3.99E-05	9.93E-04
IVD	-----	ENSGALG00000040267	isovaleryl-CoA dehydrogenase	0.38	5.28536	29.37212	5.97E-08	4.33E-06
EIF4A2	EIF4A1	ENSGALG00000008684	eukaryotic translation initiation factor 4A2	0.38	9.20421	12.92457	3.24E-04	5.21E-03
NDRG1	-----	ENSGALG00000054783	N-myc downstream regulated 1	0.38	5.28635	19.23987	1.15E-05	3.65E-04
KIF15	-----	ENSGALG00000036645	kinesin family member 15	0.38	7.70225	29.75511	4.90E-08	3.66E-06
APTX	FHA-HIT	ENSGALG00000001954	aprataxin	0.38	4.71755	9.34086	2.24E-03	2.17E-02
C1H11ORF70	C11orf70	ENSGALG00000017189	chromosome 1 open reading frame, human C11orf70	0.38	2.02884	8.37166	3.81E-03	3.14E-02
ARG2	-----	ENSGALG00000009519	arginase 2	0.38	6.38596	33.32830	7.78E-09	6.95E-07
POLE4	-----	ENSGALG00000031679	DNA polymerase epsilon 4, accessory subunit	0.38	5.25114	24.69622	6.71E-07	3.47E-05
ZNF624	-----	-----	zinc finger protein 624	0.38	4.20296	10.52695	1.18E-03	1.35E-02
ERN2	-----	ENSGALG00000027592	endoplasmic reticulum to nucleus signaling 2	0.38	3.48310	11.77936	5.99E-04	8.27E-03
SOX1	-----	ENSGALG00000030353	SRY-box 1	0.38	4.02537	7.58830	5.87E-03	4.27E-02
ABCB6	-----	ENSGALG00000029672	ATP binding cassette subfamily B member 6 (Langereis blood group)	0.38	4.22938	12.20211	4.77E-04	6.99E-03
HYLS1	-----	ENSGALG00000036796	HYLS1, centriolar and ciliogenesis associated	0.37	3.80127	12.74268	3.57E-04	5.60E-03
NPC2	-----	ENSGALG00000010237	Niemann-Pick disease, type C2	0.37	5.52158	9.47869	2.08E-03	2.07E-02
MRPS34	-----	ENSGALG00000001792	mitochondrial ribosomal protein S34	0.37	6.31722	39.01502	4.21E-10	5.16E-08
NR2F1	-----	ENSGALG00000027907	nuclear receptor subfamily 2 group F member 1	0.37	7.13256	18.36275	1.83E-05	5.23E-04
FOXO6	-----	ENSGALG00000026153	forkhead box O6	0.37	5.09217	17.40343	3.02E-05	7.89E-04
SLC26A8	-----	ENSGALG00000040498	solute carrier family 26 member 8	0.37	3.19351	10.43476	1.24E-03	1.40E-02
RDH5	-----	ENSGALG00000034988	retinol dehydrogenase 5	0.37	3.71502	13.67097	2.18E-04	3.84E-03

MATN2	-----	ENSGALG00000044675	matrilin 2	0.37	3.65444	10.27089	1.35E-03	1.49E-02
PIF1	-----	ENSGALG00000009032	PIF1 5'-to-3' DNA helicase	0.37	4.89973	9.28543	2.31E-03	2.21E-02
FAM177A1	-----	ENSGALG00000010046	family with sequence similarity 177 member A1	0.37	5.40244	35.62676	2.39E-09	2.44E-07
RNF32	-----	ENSGALG00000006387	ring finger protein 32	0.37	5.84118	26.82280	2.23E-07	1.33E-05
KIF26A	-----	ENSGALG00000011581	kinesin family member 26A	0.37	7.50441	11.73045	6.15E-04	8.45E-03
LPAR2	EDG4	ENSGALG00000042767	lysophosphatidic acid receptor 2	0.37	4.74568	12.69078	3.67E-04	5.74E-03
CLN5	-----	ENSGALG00000016917	ceroid-lipofuscinosis, neuronal 5	0.36	3.52719	10.16593	1.43E-03	1.56E-02
WDR24	-----	ENSGALG00000002450	WD repeat domain 24	0.36	5.89105	24.10637	9.12E-07	4.45E-05
TDRD7	-----	ENSGALG00000012350	tudor domain containing 7	0.36	4.10349	10.86841	9.78E-04	1.19E-02
WDR70	-----	ENSGALG00000003708	WD repeat domain 70	0.36	5.95855	13.62900	2.23E-04	3.90E-03
RHBDD1	-----	ENSGALG00000004957	rhomboid domain containing 1	0.36	3.51853	9.10744	2.55E-03	2.36E-02
FOXC1	CFKH-1	ENSGALG00000030442	forkhead box C1	0.36	4.32065	8.34429	3.87E-03	3.17E-02
CDH6	c-cad6B	ENSGALG00000012917	cadherin 6	0.36	5.76672	11.76177	6.05E-04	8.34E-03
ENTPD2	-----	ENSGALG00000039696	ectonucleoside triphosphate diphosphohydrolase 2	0.36	3.64873	8.16501	4.27E-03	3.40E-02
SMCO4	C11ORF75	ENSGALG00000026639	single-pass membrane protein with coiled-coil domains 4	0.36	3.88423	11.82136	5.86E-04	8.12E-03
PRSS35	-----	ENSGALG00000055053	serine protease 35	0.36	4.77094	8.41002	3.73E-03	3.10E-02
COPS9	MYEOV2	ENSGALG00000052051	COP9 signalosome subunit 9	0.36	5.31211	26.86142	2.19E-07	1.32E-05
JUN	-----	ENSGALG00000010870	Jun proto-oncogene, AP-1 transcription factor subunit	0.36	6.42953	9.39030	2.18E-03	2.14E-02
LOC107051855	-----		uncharacterized LOC107051855	0.36	4.39049	8.72816	3.13E-03	2.72E-02
SLC22A23	-----	ENSGALG00000012816	solute carrier family 22 member 23	0.36	4.83495	16.40440	5.12E-05	1.21E-03
KANSL2	-----	ENSGALG00000033877	KAT8 regulatory NSL complex subunit 2	0.36	6.60512	26.74517	2.32E-07	1.37E-05
LOC100858388	-----		78 kDa glucose-regulated protein-like	0.36	5.61814	7.64871	5.68E-03	4.18E-02
TEX2L	-----	-----	testis expressed 2	0.36	2.28410	7.19154	7.32E-03	4.98E-02
RNF213	-----	ENSGALG00000039269	ring finger protein 213	0.36	3.21741	8.14427	4.32E-03	3.43E-02
TSEN15	-----	ENSGALG00000004782	tRNA splicing endonuclease subunit 15	0.36	2.64495	7.94237	4.83E-03	3.74E-02
LOC107053815	-----		uncharacterized LOC107053815	0.36	3.53029	8.00443	4.67E-03	3.64E-02
COQ2	-----	ENSGALG00000041294	coenzyme Q2, polyprenyltransferase	0.36	2.95418	8.18851	4.22E-03	3.38E-02
MUTYH	-----	ENSGALG00000010226	mutY DNA glycosylase	0.35	5.32423	15.20812	9.63E-05	2.01E-03
HOXD4	Chox-a	ENSGALG00000023419	homeobox D4	0.35	6.02453	12.98056	3.15E-04	5.11E-03
LHFPL4	-----	ENSGALG00000048164	lipoma HMGIC fusion partner-like 4	0.35	3.13048	9.46303	2.10E-03	2.08E-02
PKDCCA	-----	ENSGALG00000042511	protein kinase domain containing, cytoplasmic A	0.35	6.21057	11.34096	7.58E-04	9.81E-03
CRYL1	-----	ENSGALG00000017135	crystallin lambda 1	0.35	3.49866	11.11022	8.59E-04	1.07E-02
ACSF2	-----	ENSGALG00000019768	acyl-CoA synthetase family member 2	0.35	5.59660	25.35484	4.77E-07	2.57E-05
MYO19	-----	ENSGALG00000005374	myosin XIX	0.35	5.36976	16.58873	4.64E-05	1.12E-03
RCCD1	-----	-----	RCC1 domain containing 1	0.35	3.40229	9.45119	2.11E-03	2.09E-02
C1HXORF36	-----	-----	-----	0.35	4.41523	13.08025	2.98E-04	4.91E-03
LOC101748153	-----		laminin subunit beta-2-like	0.35	5.42171	9.73861	1.80E-03	1.86E-02
BRIP1	-----	ENSGALG00000005279	BRCA1 interacting protein C-terminal helicase 1	0.35	4.57509	16.73027	4.31E-05	1.06E-03
NDUFA5	-----	ENSGALG00000008821	NADH:ubiquinone oxidoreductase subunit A5	0.35	5.79627	16.48855	4.89E-05	1.17E-03
LYRM7	-----	ENSGALG00000037299	LYR motif containing 7	0.35	3.70271	8.35611	3.84E-03	3.15E-02
RASL11AL	-----	ENSGALG00000007710	ras-like protein family member 11A-like	0.35	3.34609	8.40235	3.75E-03	3.10E-02
GALNT2	-----	ENSGALG00000011106	polypeptide N-acetylgalactosaminyltransferase 2	0.35	6.09882	30.77469	2.90E-08	2.26E-06
CNP	-----	ENSGALG00000003457	2',3'-cyclic nucleotide 3' phosphodiesterase	0.35	4.70616	15.03148	1.06E-04	2.15E-03
LOC107050163	-----		probable very-long-chain enoyl-CoA reductase art-1	0.35	7.23556	20.34898	6.45E-06	2.28E-04

LOC107055019		-----	uncharacterized LOC107055019	0.35	4.64229	9.18885	2.43E-03	2.29E-02
EFHD2	-----	ENSGALG00000038313	EF-hand domain family member D2	0.35	3.71877	7.65465	5.66E-03	4.17E-02
C14H7orf50	-----	ENSGALG00000004055	chromosome 14 C7orf50 homolog	0.35	5.61980	22.24157	2.40E-06	9.91E-05
HR	-----	-----	----	0.34	3.75471	11.21321	8.12E-04	1.03E-02
TUBB6	-----	ENSGALG00000031275	tubulin beta 6 class V	0.34	6.55392	10.59775	1.13E-03	1.32E-02
C25H1ORF43	C1orf43	ENSGALG00000034258	chromosome 25 open reading frame, human C1orf43	0.34	5.70825	23.02032	1.60E-06	7.00E-05
SLC41A2	-----	ENSGALG00000012697	solute carrier family 41 member 2	0.34	3.71809	8.18363	4.23E-03	3.38E-02
DYNC2LI1	-----	ENSGALG00000009954	dynein cytoplasmic 2 light intermediate chain 1	0.34	4.50562	13.38529	2.54E-04	4.35E-03
TRAPPC2	-----	ENSGALG00000016578	trafficking protein particle complex 2	0.34	5.96655	25.15805	5.28E-07	2.82E-05
ORAOV1	LTO1	ENSGALG00000007556	oral cancer overexpressed 1	0.34	6.29519	24.10758	9.11E-07	4.45E-05
MRPL49	-----	-----	mitochondrial ribosomal protein L49	0.34	4.75569	16.33090	5.32E-05	1.26E-03
KIAA1210	-----	ENSGALG00000013771	KIAA1210	0.34	4.67725	12.24603	4.66E-04	6.87E-03
BRK1	-----	-----	BRICK1, SCAR/WAVE actin nucleating complex subunit	0.34	3.93947	11.30780	7.72E-04	9.92E-03
KAT5	-----	-----	lysine acetyltransferase 5	0.34	5.57935	34.56113	4.13E-09	4.00E-07
PNPLA3	-----	ENSGALG00000029308	patatin like phospholipase domain containing 3	0.34	6.02791	12.66205	3.73E-04	5.80E-03
H1FX	-----	-----	H1 histone family member X	0.34	8.49696	14.84147	1.17E-04	2.32E-03
PEX11B	-----	ENSGALG00000052329	peroxisomal biogenesis factor 11 beta	0.34	2.95346	9.00077	2.70E-03	2.45E-02
GLIPR2	-----	ENSGALG00000028821	GLI pathogenesis related 2	0.34	5.60762	19.17631	1.19E-05	3.74E-04
GMNN	-----	ENSGALG00000013626	geminin, DNA replication inhibitor	0.34	5.87868	17.32179	3.16E-05	8.16E-04
MTHFD2	-----	ENSGALG00000034344	methylenetetrahydrofolate dehydrogenase 2, cyclohydrolase	0.34	4.99082	13.17540	2.84E-04	4.72E-03
CENPK	CENP-K	ENSGALG00000014753	centromere protein K	0.34	5.78669	11.28427	7.82E-04	1.00E-02
LOC101748987		-----	FCH domain only protein 1-like	0.34	3.96389	9.27201	2.33E-03	2.22E-02
HOXB4	Chox-Z	ENSGALG00000000284	homeobox B4	0.34	7.42851	12.70386	3.65E-04	5.71E-03
SCO1	-----	ENSGALG00000030475	SCO1, cytochrome c oxidase assembly protein	0.34	5.68592	16.79272	4.17E-05	1.03E-03
ZNF414	-----	ENSGALG00000024378	zinc finger protein 414	0.34	3.99504	8.90065	2.85E-03	2.55E-02
YWHAH	-----	ENSGALG00000006743	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta	0.34	7.81414	24.55201	7.23E-07	3.67E-05
MRPS24	-----	ENSGALG00000052064	mitochondrial ribosomal protein S24	0.33	4.33327	11.55702	6.75E-04	9.05E-03
LOC770165		-----	BUD13 homolog	0.33	3.98230	12.21358	4.74E-04	6.96E-03
NFKB1	NF-KB1	ENSGALG00000012304	nuclear factor kappa B subunit 1	0.33	4.98983	18.44768	1.75E-05	5.04E-04
ANKLE1	-----	ENSGALG00000051336	ankyrin repeat and LEM domain containing 1	0.33	5.65795	10.56754	1.15E-03	1.33E-02
HOXB2	-----	ENSGALG00000025774	homeobox B2	0.33	5.32757	14.71410	1.25E-04	2.45E-03
TGFBR2	-----	ENSGALG00000011442	transforming growth factor beta receptor 2	0.33	4.78532	14.42067	1.46E-04	2.78E-03
VEGFC	-----	ENSGALG00000010847	vascular endothelial growth factor C	0.33	4.22964	11.67180	6.35E-04	8.62E-03
SPATA20	-----	ENSGALG00000006857	spermatogenesis associated 20	0.33	5.57901	18.23008	1.96E-05	5.55E-04
TMEM132B	-----	ENSGALG00000002742	transmembrane protein 132B	0.33	4.36156	8.23207	4.12E-03	3.31E-02
N4BP2	-----	-----	NEDD4 binding protein 2	0.33	5.99959	15.93591	6.55E-05	1.49E-03
TBC1D2	-----	ENSGALG00000001944	TBC1 domain family member 2	0.33	4.12846	7.57728	5.91E-03	4.29E-02
ARL14EP	ARF7EP	ENSGALG00000012139	ADP ribosylation factor like GTPase 14 effector protein	0.33	5.18156	15.37501	8.81E-05	1.88E-03
PLA2R1	-----	ENSGALG00000011149	phospholipase A2 receptor 1	0.33	5.48317	9.27855	2.32E-03	2.22E-02
FRS3	-----	ENSGALG00000003447	fibroblast growth factor receptor substrate 3	0.33	6.19706	19.70765	9.02E-06	2.99E-04
ZNF252L	-----	-----	----	0.33	4.60149	9.89162	1.66E-03	1.74E-02
RAD50	-----	ENSGALG00000006794	RAD50 double strand break repair protein	0.33	6.44237	18.51562	1.69E-05	4.90E-04
LOC101752260		-----	uncharacterized LOC101752260	0.33	5.52499	20.67906	5.43E-06	1.99E-04
TMEM106C	-----	ENSGALG00000034069	transmembrane protein 106C	0.33	3.80079	11.51181	6.92E-04	9.19E-03

HSP90B1	hsp108	ENSGALG00000033789	heat shock protein 90 beta family member 1	0.33	9.79887	11.59500	6.61E-04	8.92E-03
GPR155	-----	ENSGALG00000014209	G protein-coupled receptor 155	0.33	5.15871	24.45376	7.61E-07	3.81E-05
LOC101750687	-----	-----	uncharacterized LOC101750687	0.33	5.86846	17.98886	2.22E-05	6.15E-04
HIBADH	-----	ENSGALG00000033207	3-hydroxyisobutyrate dehydrogenase	0.32	5.10040	19.67409	9.18E-06	3.03E-04
NDUFAF4	-----	ENSGALG00000019921	NADH:ubiquinone oxidoreductase complex assembly factor 4	0.32	4.95405	12.30541	4.52E-04	6.71E-03
LMCD1	-----	ENSGALG00000008349	LIM and cysteine rich domains 1	0.32	5.44100	9.31629	2.27E-03	2.19E-02
VASP	-----	-----	vasodilator-stimulated phosphoprotein	0.32	4.07252	9.08617	2.58E-03	2.37E-02
BUD13	-----	ENSGALG00000025882	BUD13 homolog	0.32	5.73986	26.70938	2.36E-07	1.39E-05
SHCBP1	-----	ENSGALG00000004444	SHC binding and spindle associated 1	0.32	5.34029	18.18546	2.00E-05	5.65E-04
COA5	-----	ENSGALG00000036791	cytochrome c oxidase assembly factor 5	0.32	5.49248	23.57878	1.20E-06	5.51E-05
EXOG	-----	ENSGALG00000006153	exo/endonuclease G	0.32	6.73897	26.77364	2.29E-07	1.36E-05
FAM43A	-----	ENSGALG00000041898	family with sequence similarity 43 member A	0.32	5.71185	12.93953	3.22E-04	5.19E-03
PITPNM2	-----	-----	phosphatidylinositol transfer protein membrane associated 2	0.32	5.05450	15.27229	9.31E-05	1.96E-03
SHC2	-----	ENSGALG00000001289	SHC (Src homology 2 domain containing) transforming protein 2	0.32	4.74605	8.08370	4.47E-03	3.52E-02
TMEM177	-----	ENSGALG00000011593	transmembrane protein 177	0.32	4.62737	15.62560	7.72E-05	1.70E-03
LOC107052842	-----	-----	uncharacterized LOC107052842	0.32	4.52545	12.78823	3.49E-04	5.51E-03
CAMK4L	-----	-----	calcium/calmodulin-dependent protein kinase IV-like	0.32	4.49034	10.01079	1.56E-03	1.66E-02
NFYA	-----	ENSGALG00000003247	nuclear transcription factor Y subunit alpha	0.32	7.16913	19.23455	1.16E-05	3.66E-04
MRPL55	-----	ENSGALG00000038820	mitochondrial ribosomal protein L55	0.32	4.08981	7.47926	6.24E-03	4.48E-02
TTC30B	TTC30A	ENSGALG00000009224	tetratricopeptide repeat domain 30B	0.32	4.92755	11.67842	6.32E-04	8.59E-03
ZYX	-----	ENSGALG00000014688	zyxin	0.32	7.10455	27.27895	1.76E-07	1.11E-05
TBCB	-----	-----	tubulin folding cofactor B	0.32	6.11512	17.01605	3.71E-05	9.35E-04
PRR7	-----	ENSGALG00000041981	proline rich 7, synaptic	0.32	5.27858	20.09519	7.37E-06	2.54E-04
JPT2	-----	-----	-----	0.32	8.60599	26.89714	2.15E-07	1.30E-05
BROX	-----	ENSGALG00000009413	BRO1 domain and CAAX motif containing	0.32	5.20128	14.80665	1.19E-04	2.35E-03
FADS1	-----	ENSGALG00000007127	fatty acid desaturase 1	0.32	6.41988	36.76941	1.33E-09	1.48E-07
CDC20	-----	ENSGALG00000009971	cell division cycle 20	0.31	7.69815	27.13538	1.90E-07	1.17E-05
USP43	-----	ENSGALG00000037812	ubiquitin specific peptidase 43	0.31	5.37032	7.69824	5.53E-03	4.09E-02
TMEM199	-----	ENSGALG00000023757	transmembrane protein 199	0.31	4.97420	15.85585	6.84E-05	1.55E-03
NMRK2	-----	ENSGALG00000025751	nicotinamide riboside kinase 2	0.31	4.82557	15.36900	8.84E-05	1.88E-03
LOC107053944	-----	-----	uncharacterized LOC107053944	0.31	5.38288	8.13818	4.33E-03	3.44E-02
SATB1	-----	ENSGALG00000011254	SATB homeobox 1	0.31	4.21084	8.45566	3.64E-03	3.05E-02
DTNB	-----	-----	dystrobrevin beta	0.31	5.47033	21.29962	3.93E-06	1.51E-04
IER5L	-----	ENSGALG00000053552	immediate early response 5 like	0.31	6.94178	11.68349	6.31E-04	8.58E-03
SS18L2	-----	ENSGALG00000004943	SS18 like 2	0.31	4.48349	15.50999	8.21E-05	1.78E-03
LOC107056278	-----	-----	probable N-acetyltransferase camello	0.31	5.04002	8.61021	3.34E-03	2.86E-02
NSDHL	-----	ENSGALG00000007493	NAD(P) dependent steroid dehydrogenase-like	0.31	4.37155	7.88355	4.99E-03	3.82E-02
ZRANB2	ZNF265	ENSGALG00000011340	zinc finger RANBP2-type containing 2	0.31	7.07814	22.06781	2.63E-06	1.07E-04
IFI35	-----	ENSGALG00000002832	interferon-induced protein 35	0.31	3.99079	8.74597	3.10E-03	2.70E-02
CTSH	-----	ENSGALG00000033557	cathepsin H	0.31	5.52223	16.90103	3.94E-05	9.82E-04
ANXA5	ANX5	ENSGALG00000011885	annexin A5	0.31	6.82847	23.82507	1.05E-06	4.97E-05
CRELD2	-----	ENSGALG00000008551	cysteine rich with EGF like domains 2	0.31	5.76529	14.65524	1.29E-04	2.52E-03
LOC107051531	PPP1R14CL	-----	protein phosphatase 1 regulatory subunit 14C like	0.31	5.89869	18.50432	1.70E-05	4.92E-04
CREB5	-----	ENSGALG00000038265	cAMP responsive element binding protein 5	0.31	4.29376	9.85734	1.69E-03	1.77E-02

TGFB1	-----	ENSGALG00000031325	transforming growth factor beta 1	0.31	4.83647	15.26530	9.34E-05	1.96E-03
HMGA1	-----	ENSGALG00000030396	high mobility group AT-hook 1	0.31	6.81632	25.63604	4.12E-07	2.28E-05
DUSP8	-----	ENSGALG00000006647	dual specificity phosphatase 8	0.31	4.98313	11.49978	6.96E-04	9.23E-03
LOC112531536	-----		uncharacterized LOC112531536	0.31	5.13370	12.50949	4.05E-04	6.19E-03
AAAS	-----	ENSGALG00000032843	aladin WD repeat nucleoporin	0.31	7.27204	25.09461	5.46E-07	2.89E-05
RFXANK	-----	ENSGALG00000037261	regulatory factor X associated ankyrin containing protein	0.31	4.64332	16.62770	4.55E-05	1.11E-03
GAS2L3	-----	ENSGALG00000028373	growth arrest specific 2 like 3	0.31	4.72986	9.61278	1.93E-03	1.96E-02
TGFB2	TGF-beta-2	ENSGALG00000009612	transforming growth factor beta 2	0.31	5.54526	8.61529	3.33E-03	2.85E-02
HSD17B4	-----	ENSGALG00000002187	hydroxysteroid 17-beta dehydrogenase 4	0.31	6.25256	11.86001	5.74E-04	8.04E-03
LMNB1	lamin-B1	ENSGALG00000014692	lamin B1	0.31	7.32189	12.50829	4.05E-04	6.19E-03
CCDC189	-----	ENSGALG00000041514	coiled-coil domain containing 189	0.31	4.21516	11.13782	8.46E-04	1.06E-02
EXOSC1	-----	ENSGALG00000039917	exosome component 1	0.30	4.92820	16.44001	5.02E-05	1.20E-03
ORC5	ORC5L	ENSGALG00000008175	origin recognition complex subunit 5	0.30	5.18173	10.84889	9.89E-04	1.19E-02
RAB11FIP3	-----	ENSGALG00000002666	RAB11 family interacting protein 3	0.30	6.63889	21.89653	2.88E-06	1.15E-04
CBS	-----	-----	-----	0.30	7.53064	15.02034	1.06E-04	2.16E-03
NKIRAS2	-----	ENSGALG00000028971	NFKB inhibitor interacting Ras like 2	0.30	5.79833	20.58811	5.69E-06	2.07E-04
GTF3C3	-----	ENSGALG00000007958	general transcription factor IIIC subunit 3	0.30	4.96835	17.27875	3.23E-05	8.27E-04
APOOL	-----	ENSGALG00000006978	apolipoprotein O like	0.30	6.46995	20.97974	4.64E-06	1.73E-04
LOC421106	-----	-----	KIAA0146	0.30	5.02463	13.44480	2.46E-04	4.24E-03
RARA	RAR-ALPHA1	ENSGALG00000037935	retinoic acid receptor alpha	0.30	6.30790	9.74703	1.80E-03	1.86E-02
GALNT6	-----	ENSGALG00000041101	polypeptide N-acetylgalactosaminyltransferase 6	0.30	4.09825	9.19900	2.42E-03	2.28E-02
NDUFB2	-----	ENSGALG00000032595	NADH:ubiquinone oxidoreductase subunit B2	0.30	5.57953	8.55946	3.44E-03	2.91E-02
CCDC34	-----	-----	coiled-coil domain containing 34	0.30	3.72225	7.86986	5.03E-03	3.83E-02
OSGEPL1	-----	ENSGALG00000037727	O-sialoglycoprotein endopeptidase like 1	0.30	4.83170	14.97034	1.09E-04	2.19E-03
ALPL	-----	ENSGALG00000023542	alkaline phosphatase, liver/bone/kidney	0.30	5.30991	14.06151	1.77E-04	3.24E-03
PMPCB	-----	ENSGALG00000008280	peptidase, mitochondrial processing beta subunit	0.30	6.25293	17.32627	3.15E-05	8.16E-04
RASGEF1B	-----	ENSGALG00000010903	RasGEF domain family member 1B	0.30	4.42683	8.58402	3.39E-03	2.88E-02
SDCCAG8	-----	ENSGALG00000010713	serologically defined colon cancer antigen 8	0.30	4.79484	14.34328	1.52E-04	2.86E-03
MKNK2	-----	ENSGALG00000003845	MAP kinase interacting serine/threonine kinase 2	0.30	5.71458	13.89969	1.93E-04	3.47E-03
UBE4B	-----	ENSGALG00000002649	ubiquitination factor E4B	0.30	7.32902	34.47324	4.32E-09	4.13E-07
IL12RB2	-----	ENSGALG00000011222	interleukin 12 receptor subunit beta 2	0.30	5.14765	14.74355	1.23E-04	2.43E-03
TYMS	-----	-----	thymidylate synthetase	0.30	6.60425	25.20965	5.14E-07	2.76E-05
PQLC2L	-----	ENSGALG00000020626	PQ loop repeat containing 2 like	0.30	5.36030	10.06913	1.51E-03	1.63E-02
GREB1	-----	ENSGALG00000016455	growth regulating estrogen receptor binding 1	0.30	6.65964	13.80394	2.03E-04	3.62E-03
POLE3	-----	ENSGALG00000008873	DNA polymerase epsilon 3, accessory subunit	0.30	7.36074	32.64132	1.11E-08	9.55E-07
DAPK3	-----	ENSGALG00000037733	death-associated protein kinase 3	0.30	6.92271	17.97167	2.24E-05	6.19E-04
IFT74	-----	ENSGALG00000001801	intraflagellar transport 74	0.30	5.18672	9.28949	2.30E-03	2.21E-02
JPH1	-----	ENSGALG00000035845	junctophilin 1	0.30	4.19089	9.89173	1.66E-03	1.74E-02
PDZD2	-----	ENSGALG00000002854	PDZ domain containing 2	0.30	5.38628	8.20712	4.17E-03	3.35E-02
SALL1	SAL1	ENSGALG00000039238	spalt like transcription factor 1	0.30	6.84150	9.46180	2.10E-03	2.08E-02
TULP4	-----	ENSGALG00000037377	tubby like protein 4	0.30	6.68813	16.49446	4.88E-05	1.17E-03
SEC23A	-----	ENSGALG00000010150	Sec23 homolog A, coat complex II component	0.30	6.75334	27.45438	1.61E-07	1.03E-05
GALNT11	-----	ENSGALG00000006233	polypeptide N-acetylgalactosaminyltransferase 11	0.30	5.66554	25.81165	3.76E-07	2.13E-05
PPM1M	-----	ENSGALG00000033277	protein phosphatase, Mg2+/Mn2+ dependent 1M	0.30	4.59023	12.36938	4.36E-04	6.54E-03

URB1	-----	ENSGALG00000015887	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	0.30	6.20122	14.39245	1.48E-04	2.81E-03
CTDP1	-----	ENSGALG00000031461	CTD phosphatase subunit 1	0.29	5.74594	16.91436	3.91E-05	9.77E-04
IBA57	C1orf69	ENSGALG00000005328	IBA57 homolog, iron-sulfur cluster assembly	0.29	5.45724	16.91874	3.90E-05	9.77E-04
MCPH1	-----	ENSGALG00000016332	microcephalin 1	0.29	5.06891	10.39962	1.26E-03	1.41E-02
PCCB	-----	ENSGALG00000037238	propionyl-CoA carboxylase beta subunit	0.29	5.71387	16.01882	6.27E-05	1.44E-03
RBKS	-----	ENSGALG00000010043	ribokinase	0.29	4.63306	11.83503	5.81E-04	8.11E-03
TUSC5	-----	ENSGALG00000047441	tumor suppressor candidate 5	0.29	5.87151	8.82322	2.97E-03	2.63E-02
IFT140	-----	ENSGALG00000009318	intraflagellar transport 140	0.29	5.58583	18.07422	2.12E-05	5.90E-04
EED	-----	ENSGALG00000014060	embryonic ectoderm development	0.29	5.18224	16.24889	5.55E-05	1.31E-03
PNPLA6	NTE	ENSGALG00000039408	patatin like phospholipase domain containing 6	0.29	4.89315	7.57541	5.92E-03	4.29E-02
BID	-----	ENSGALG00000013039	BH3 interacting domain death agonist	0.29	7.19257	25.97113	3.47E-07	1.99E-05
HIP1	-----	ENSGALG00000040908	huntingtin interacting protein 1	0.29	7.64223	16.52613	4.80E-05	1.15E-03
SRSF4	-----	ENSGALG00000050314	serine and arginine rich splicing factor 4	0.29	5.51476	10.05646	1.52E-03	1.63E-02
LOC112532285	-----		uncharacterized LOC112532285	0.29	4.54346	11.28328	7.82E-04	1.00E-02
MRTO4	-----	ENSGALG00000003991	MRT4 homolog, ribosome maturation factor	0.29	6.50379	19.66267	9.24E-06	3.04E-04
EPS8	-----	ENSGALG00000013091	epidermal growth factor receptor pathway substrate 8	0.29	5.00849	9.07900	2.59E-03	2.38E-02
DDX31	-----	ENSGALG00000041473	DEAD-box helicase 31	0.29	5.63881	23.06701	1.56E-06	6.90E-05
FKBP11	-----	ENSGALG00000035060	FK506 binding protein 11	0.29	3.80476	9.00258	2.70E-03	2.45E-02
ACAD11	-----	ENSGALG00000035949	acyl-CoA dehydrogenase family member 11	0.29	5.08534	9.44017	2.12E-03	2.09E-02
ATXN10	-----	ENSGALG00000014234	ataxin 10	0.29	4.20060	12.62485	3.81E-04	5.90E-03
TMEM135	-----	ENSGALG00000047269	transmembrane protein 135	0.29	4.86787	10.81794	1.01E-03	1.21E-02
RTEL1	-----	ENSGALG00000006123	regulator of telomere elongation helicase 1	0.29	5.97506	15.19490	9.70E-05	2.02E-03
SLC25A22	-----	ENSGALG00000039335	solute carrier family 25 member 22	0.29	4.44918	11.54281	6.80E-04	9.09E-03
CARNMT1	-----	ENSGALG00000015155	carnosine N-methyltransferase 1	0.29	5.53329	7.48175	6.23E-03	4.47E-02
XBP1	-----	ENSGALG00000005796	X-box binding protein 1	0.29	6.47420	21.02511	4.53E-06	1.70E-04
EIF2B4	-----	ENSGALG00000033575	eukaryotic translation initiation factor 2B subunit delta	0.29	5.86254	12.80309	3.46E-04	5.48E-03
MYCBPAP	-----	ENSGALG00000007661	radical S-adenosyl methionine domain containing 1	0.28	4.81373	7.85339	5.07E-03	3.86E-02
GALK2	-----	ENSGALG00000036201	galactokinase 2	0.28	4.45339	7.54837	6.01E-03	4.34E-02
SLC25A11	-----	ENSGALG00000029383	solute carrier family 25 member 11	0.28	6.49162	15.22738	9.53E-05	2.00E-03
EVC	DWF-1	ENSGALG00000015037	EvC ciliary complex subunit 1	0.28	4.93513	12.08868	5.07E-04	7.34E-03
INTU	-----	-----	inturned planar cell polarity protein	0.28	4.80982	10.56476	1.15E-03	1.33E-02
TMSB15B	-----	ENSGALG00000031593	thymosin beta 15B	0.28	7.29783	8.93136	2.80E-03	2.52E-02
EPHA7	CEPHA7	ENSGALG00000015593	EPH receptor A7	0.28	4.60149	8.33877	3.88E-03	3.18E-02
EIF4G3	-----	ENSGALG00000010084	eukaryotic translation initiation factor 4 gamma 3	0.28	7.84866	15.63462	7.68E-05	1.70E-03
FASTKD1	-----	ENSGALG00000009841	FAST kinase domains 1	0.28	4.44420	11.35756	7.51E-04	9.75E-03
NRG4	-----	ENSGALG00000002952	neuregulin 4	0.28	3.72710	8.92899	2.81E-03	2.52E-02
NNF1	PMF1	ENSGALG00000046965	Nnf1 protein	0.28	6.11553	9.05440	2.62E-03	2.40E-02
QDPR	-----	ENSGALG00000030070	quinoid dihydropteridine reductase	0.28	6.03060	13.73742	2.10E-04	3.72E-03
KATNAL1	-----	ENSGALG00000017083	katanin catalytic subunit A1 like 1	0.28	4.84051	15.03453	1.06E-04	2.15E-03
JAKMIP2	-----	ENSGALG00000007593	janus kinase and microtubule interacting protein 2	0.28	5.66008	14.40240	1.48E-04	2.80E-03
COMMD6	-----	ENSGALG00000016922	COMM domain containing 6	0.28	6.39939	15.87072	6.78E-05	1.54E-03
FAM114A1	-----	ENSGALG00000013583	family with sequence similarity 114 member A1	0.28	3.79904	7.64557	5.69E-03	4.18E-02
C1H12orf29	-----	-----	-----	0.28	4.85159	13.45244	2.45E-04	4.22E-03
GRSF1	-----	ENSGALG00000031160	G-rich RNA sequence binding factor 1	0.28	6.99229	17.82826	2.42E-05	6.58E-04

APBA3	-----	ENSGALG00000000740	amyloid beta (A4) precursor protein-binding, family A, member 3	0.28	5.11250	14.24789	1.60E-04	2.99E-03
TMEFF2	-----	ENSGALG000000007759	transmembrane protein with EGF like and two follistatin like domains 2	0.28	3.94017	8.38434	3.78E-03	3.13E-02
USP21	-----	ENSGALG000000051012	ubiquitin specific peptidase 21	0.28	4.86595	11.29001	7.79E-04	9.99E-03
FIGNL1	-----	ENSGALG000000026363	fidgetin like 1	0.28	4.65917	10.08524	1.49E-03	1.61E-02
RFX3	-----	ENSGALG000000010179	regulatory factor X3	0.28	5.79581	7.97792	4.74E-03	3.68E-02
SEL1L3	-----	ENSGALG000000039549	SEL1L family member 3	0.27	5.26640	15.97727	6.41E-05	1.47E-03
ARL3	-----	ENSGALG000000008049	ADP ribosylation factor like GTPase 3	0.27	7.03367	19.12333	1.23E-05	3.80E-04
MRPS22	-----	ENSGALG000000005367	mitochondrial ribosomal protein S22	0.27	5.71289	13.56196	2.31E-04	4.02E-03
MDC1	-----	-----	-----	0.27	6.82473	16.61085	4.59E-05	1.12E-03
NUAK1	-----	ENSGALG000000012662	NUAK family kinase 1	0.27	6.08246	11.83839	5.80E-04	8.10E-03
GUF1	-----	ENSGALG000000014217	GUF1 homolog, GTPase	0.27	4.50261	7.61061	5.80E-03	4.23E-02
CALML4	-----	ENSGALG000000007979	calmodulin like 4	0.27	3.79979	7.29519	6.91E-03	4.79E-02
DYM	-----	ENSGALG000000037426	dymeclin	0.27	5.32546	11.18446	8.25E-04	1.05E-02
CAMKK2	-----	ENSGALG000000040131	calcium/calmodulin dependent protein kinase kinase 2	0.27	6.33650	11.12132	8.53E-04	1.07E-02
CISD1	ZCD1	ENSGALG000000002705	CDGSH iron sulfur domain 1	0.27	6.78014	24.16472	8.84E-07	4.34E-05
B4GALT6	-----	ENSGALG000000015151	beta-1,4-galactosyltransferase 6	0.27	5.18628	10.08057	1.50E-03	1.62E-02
TARS	-----	ENSGALG000000003288	threonyl-tRNA synthetase	0.27	7.33680	8.98594	2.72E-03	2.46E-02
PARP9	-----	ENSGALG000000045511	poly(ADP-ribose) polymerase family member 9	0.27	3.94174	8.84422	2.94E-03	2.61E-02
ENO1	-----	ENSGALG000000002377	enolase 1, (alpha)	0.27	11.20888	8.74295	3.11E-03	2.71E-02
ABCC6	-----	ENSGALG000000038152	ATP binding cassette subfamily C member 6	0.27	4.21813	7.74100	5.40E-03	4.03E-02
PLEKHB1	-----	ENSGALG000000017321	pleckstrin homology domain containing B1	0.27	4.64795	8.40456	3.74E-03	3.10E-02
CHST13	-----	ENSGALG000000029632	carbohydrate sulfotransferase 13	0.27	5.52157	10.74483	1.05E-03	1.24E-02
BCAS3	-----	ENSGALG000000005295	BCAS3, microtubule associated cell migration factor	0.27	4.97406	8.92893	2.81E-03	2.52E-02
DACH1	DACH	ENSGALG000000037015	dachshund family transcription factor 1	0.27	5.22275	10.34386	1.30E-03	1.45E-02
PSRC1	-----	-----	proline and serine rich coiled-coil 1	0.27	5.22166	15.16369	9.86E-05	2.04E-03
LZTR1	-----	ENSGALG000000031175	leucine zipper like transcription regulator 1	0.27	5.68614	20.52297	5.89E-06	2.12E-04
FAM53B	-----	ENSGALG000000009718	family with sequence similarity 53 member B	0.27	5.37546	7.97274	4.75E-03	3.69E-02
ELP2	-----	ENSGALG000000039034	elongator acetyltransferase complex subunit 2	0.27	5.18873	15.54207	8.07E-05	1.76E-03
SLC25A4	-----	ENSGALG000000010614	solute carrier family 25 member 4	0.27	5.91756	10.58525	1.14E-03	1.32E-02
LOC107052085	-----	-----	uncharacterized LOC107052085	0.27	5.28063	8.21981	4.14E-03	3.33E-02
TRMT10A	-----	ENSGALG000000012264	tRNA methyltransferase 10A	0.27	4.17803	8.41254	3.73E-03	3.10E-02
CTSZ	-----	ENSGALG000000007462	cathepsin Z	0.27	5.29071	13.07762	2.99E-04	4.91E-03
MRPS14	-----	ENSGALG000000030028	mitochondrial ribosomal protein S14	0.27	5.20393	10.43333	1.24E-03	1.40E-02
CCDC58	-----	ENSGALG000000014413	coiled-coil domain containing 58	0.26	4.80765	7.63590	5.72E-03	4.19E-02
YY2	NF-E1	ENSGALG000000017388	YY2 transcription factor	0.26	6.54108	19.79913	8.60E-06	2.91E-04
PC	PCX (retired)	ENSGALG000000053095	pyruvate carboxylase	0.26	5.11775	8.20806	4.17E-03	3.35E-02
PSMA4	-----	ENSGALG000000003046	proteasome subunit alpha 4	0.26	7.64828	19.30544	1.11E-05	3.57E-04
LMO2	-----	ENSGALG000000029892	LIM domain only 2	0.26	6.03394	10.68087	1.08E-03	1.27E-02
FKBP5	FKBP51	ENSGALG000000042148	FK506 binding protein 5	0.26	5.39740	12.66841	3.72E-04	5.79E-03
MRS2	-----	ENSGALG000000040084	MRS2, magnesium transporter	0.26	4.24320	8.68971	3.20E-03	2.76E-02
EHBP1L1	-----	-----	EH domain binding protein 1 like 1	0.26	3.96693	7.36309	6.66E-03	4.67E-02
NKAIN4	-----	ENSGALG000000005774	Na+/K+ transporting ATPase interacting 4	0.26	5.44718	7.57230	5.93E-03	4.30E-02
KEAP1	-----	-----	-----	0.26	5.53265	7.95492	4.80E-03	3.72E-02
TMEM18	-----	ENSGALG000000028744	transmembrane protein 18	0.26	4.89895	9.33993	2.24E-03	2.17E-02

FANCI	-----	ENSGALG00000006658	Fanconi anemia complementation group I	0.26	5.77614	15.72413	7.33E-05	1.63E-03
MYL9	DTNB	ENSGALG00000028567	myosin, light chain 9, regulatory	0.26	6.79380	13.80296	2.03E-04	3.62E-03
PASK	-----	ENSGALG00000006016	PAS domain containing serine/threonine kinase	0.26	5.02959	10.50039	1.19E-03	1.36E-02
TSPAN13	tetraspanin-13	ENSGALG00000027240	tetraspanin 13	0.26	5.54985	13.78103	2.05E-04	3.65E-03
SPDL1	-----	ENSGALG00000001942	spindle apparatus coiled-coil protein 1	0.26	6.01354	22.74504	1.85E-06	7.89E-05
CENPH	CENP-H	ENSGALG00000014788	centromere protein H	0.26	6.42928	7.87024	5.03E-03	3.83E-02
TTL4	-----	ENSGALG00000027991	tubulin tyrosine ligase like 4	0.26	4.93779	10.01213	1.56E-03	1.66E-02
PRMT7	-----	ENSGALG00000038865	protein arginine methyltransferase 7	0.26	5.24857	9.49463	2.06E-03	2.06E-02
ORC6	ORC6L	ENSGALG00000004342	origin recognition complex subunit 6	0.26	5.78619	10.90512	9.59E-04	1.17E-02
CBY1	-----	ENSGALG00000012218	chibby family member 1, beta catenin antagonist	0.26	4.92294	7.32573	6.80E-03	4.73E-02
LOC424740	-----	-----	uncharacterized LOC424740	0.26	7.51417	12.07009	5.12E-04	7.39E-03
SEM1	-----	-----	-----	0.26	6.98687	10.11063	1.47E-03	1.60E-02
AUH	-----	ENSGALG00000021843	AU RNA binding methylglutaconyl-CoA hydratase	0.26	5.02778	8.84502	2.94E-03	2.61E-02
PCDH1	-----	ENSGALG00000002553	protocadherin 1	0.26	6.08777	8.97526	2.74E-03	2.47E-02
HSPA4L	-----	ENSGALG00000010185	heat shock protein family A (Hsp70) member 4 like	0.26	7.28681	14.40789	1.47E-04	2.80E-03
HOXB7	-----	ENSGALG00000032740	homeobox B7	0.26	6.71775	13.12439	2.91E-04	4.83E-03
MAPKAPK2	-----	ENSGALG00000000883	mitogen-activated protein kinase-activated protein kinase 2	0.26	6.94108	23.87964	1.03E-06	4.87E-05
USP16	-----	ENSGALG00000015813	ubiquitin specific peptidase 16	0.26	6.56619	17.82951	2.42E-05	6.58E-04
PPID	-----	ENSGALG00000009451	peptidylprolyl isomerase D	0.26	6.41249	17.33254	3.14E-05	8.14E-04
BBS9	-----	ENSGALG00000031650	Bardet-Biedl syndrome 9	0.25	4.99322	10.59282	1.14E-03	1.32E-02
PPOX	-----	ENSGALG00000054130	protoporphyrinogen oxidase	0.25	5.17291	9.32970	2.25E-03	2.18E-02
RGMA	-----	ENSGALG00000039173	repulsive guidance molecule family member a	0.25	6.57980	8.27425	4.02E-03	3.26E-02
ZNF704	-----	ENSGALG00000030011	zinc finger protein 704	0.25	5.05163	7.55260	5.99E-03	4.33E-02
DYNLT1	-----	ENSGALG00000019979	dynein light chain Tctex-type 1	0.25	5.47765	15.42414	8.59E-05	1.84E-03
DCK	-----	ENSGALG00000028501	deoxycytidine kinase	0.25	5.79197	16.84257	4.06E-05	1.01E-03
PHB	-----	ENSGALG00000038604	prohibitin	0.25	6.39268	17.63993	2.67E-05	7.15E-04
MTERF3	MTERFD1	ENSGALG00000040511	mitochondrial transcription termination factor 3	0.25	5.49501	8.08314	4.47E-03	3.52E-02
DLL1	-----	ENSGALG00000011182	delta like canonical Notch ligand 1	0.25	5.62670	7.29027	6.93E-03	4.80E-02
CDC34	-----	ENSGALG00000024332	cell division cycle 34	0.25	5.04676	9.08932	2.57E-03	2.37E-02
CHCHD6	-----	ENSGALG00000006056	coiled-coil-helix-coiled-coil-helix domain containing 6	0.25	5.65915	11.24535	7.98E-04	1.02E-02
TRMT5	-----	ENSGALG00000011904	tRNA methyltransferase 5	0.25	4.90593	10.74592	1.05E-03	1.24E-02
MOB3A	-----	ENSGALG00000031729	MOB kinase activator 3A	0.25	5.48461	9.66688	1.88E-03	1.92E-02
CNN3	calponin-3	ENSGALG00000005597	calponin 3	0.25	8.54193	23.12355	1.52E-06	6.74E-05
LOC107049885	-----	-----	M-phase inducer phosphatase 2-like	0.25	7.43478	13.83340	2.00E-04	3.57E-03
LOC101748569	-----	-----	caseinolytic peptidase B protein homolog	0.25	4.15230	9.15219	2.48E-03	2.31E-02
SMC6	SMC6L1	ENSGALG00000016467	structural maintenance of chromosomes 6	0.25	5.95176	14.54530	1.37E-04	2.63E-03
STK38L	-----	ENSGALG00000014094	serine/threonine kinase 38 like	0.25	5.06041	9.18272	2.44E-03	2.29E-02
ALG12	6-mannosyltransferase)	ENSGALG00000008539	ALG12, alpha-1,6-mannosyltransferase	0.25	7.07042	17.79264	2.46E-05	6.68E-04
NSMAF	-----	ENSGALG00000038838	neutral sphingomyelinase activation associated factor	0.25	5.60782	13.26079	2.71E-04	4.58E-03
TMEM62	-----	ENSGALG00000009260	transmembrane protein 62	0.25	4.50505	7.26516	7.03E-03	4.84E-02
CCT4	-----	ENSGALG00000008812	chaperonin containing TCP1 subunit 4	0.25	8.99825	15.70785	7.39E-05	1.64E-03
H2A2BL	-----	-----	-----	0.25	6.51745	10.06324	1.51E-03	1.63E-02
NUP188	-----	ENSGALG00000043394	nucleoporin 188	0.25	7.51489	15.46722	8.39E-05	1.81E-03
PAWR	-----	ENSGALG00000010320	pro-apoptotic WT1 regulator	0.25	6.39826	8.71200	3.16E-03	2.74E-02

SEPSECS	-----	ENSGALG00000014386	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	0.25	5.42836	11.08038	8.72E-04	1.09E-02
TAB2	-----	ENSGALG00000012356	TGF-beta activated kinase 1/MAP3K7 binding protein 2	0.25	6.91616	15.18081	9.77E-05	2.03E-03
PIGH	-----	ENSGALG00000009510	phosphatidylinositol glycan anchor biosynthesis class H	0.25	4.98004	9.63057	1.91E-03	1.95E-02
ACTN4	-----	ENSGALG00000036496	actinin, alpha 4	0.25	8.20983	13.57042	2.30E-04	4.01E-03
PXN	-----	-----	-----	0.25	6.26703	11.42452	7.25E-04	9.52E-03
MIS12	-----	-----	MIS12, kinetochore complex component	0.25	4.24411	7.60044	5.84E-03	4.25E-02
ATP5G1	-----	ENSGALG00000001330	ATP synthase, H+ transporting, mitochondrial Fo complex subunit C1 (subunit 9)	0.25	7.32672	14.29752	1.56E-04	2.92E-03
WDR55	-----	ENSGALG00000029199	WD repeat domain 55	0.25	6.17020	10.47577	1.21E-03	1.38E-02
FAM126A	-----	ENSGALG00000010925	family with sequence similarity 126 member A	0.25	6.85737	19.64713	9.31E-06	3.06E-04
LOXL3	-----	ENSGALG00000036142	lysyl oxidase like 3	0.25	5.36065	7.40966	6.49E-03	4.60E-02
RTFDC1	C20H20ORF43	ENSGALG00000007709	replication termination factor 2 domain containing 1	0.24	6.42555	17.37972	3.06E-05	7.97E-04
TLE1	-----	ENSGALG00000012575	transducin like enhancer of split 1	0.24	5.92589	8.54319	3.47E-03	2.93E-02
GLRX3	TXNL2	ENSGALG00000010464	glutaredoxin 3	0.24	7.12783	15.57941	7.91E-05	1.74E-03
LRRC28	-----	ENSGALG00000007057	leucine rich repeat containing 28	0.24	5.20778	13.39970	2.52E-04	4.32E-03
LARS	-----	ENSGALG00000007494	leucyl-tRNA synthetase	0.24	7.51089	22.93560	1.68E-06	7.27E-05
PLAA	-----	ENSGALG00000001782	phospholipase A2 activating protein	0.24	6.31391	9.22432	2.39E-03	2.26E-02
MRPS10	-----	ENSGALG00000009890	mitochondrial ribosomal protein S10	0.24	4.95445	8.41252	3.73E-03	3.10E-02
NTMT1	AD-003	ENSGALG00000017611	N-terminal Xaa-Pro-Lys N-methyltransferase 1	0.24	5.96174	9.90844	1.65E-03	1.73E-02
RPA3	-----	ENSGALG00000010700	replication protein A3	0.24	5.88040	12.04083	5.20E-04	7.47E-03
PHF14	-----	ENSGALG00000038041	PHD finger protein 14	0.24	6.84283	13.25160	2.72E-04	4.59E-03
GREB1L	-----	ENSGALG00000014935	GREB1 like retinoic acid receptor coactivator	0.24	7.00002	8.01831	4.63E-03	3.62E-02
MRPS17	-----	ENSGALG00000002379	mitochondrial ribosomal protein S17	0.24	6.23440	11.94654	5.47E-04	7.77E-03
DRAM2	-----	ENSGALG00000036491	DNA damage regulated autophagy modulator 2	0.24	4.34734	9.14914	2.49E-03	2.32E-02
RECQL5	-----	ENSGALG00000002424	RecQ like helicase 5	0.24	5.19822	7.49279	6.19E-03	4.45E-02
GPATCH11	CCDC75	ENSGALG00000010561	G-patch domain containing 11	0.24	5.23341	10.15944	1.44E-03	1.57E-02
EOGT	AER61	ENSGALG00000013406	EGF domain specific O-linked N-acetylglucosamine transferase	0.24	5.03937	8.82784	2.97E-03	2.62E-02
ACO2	-----	ENSGALG00000011950	aconitase 2	0.24	7.98686	15.40480	8.68E-05	1.85E-03
KNTC1	-----	-----	kinetochore associated 1	0.24	6.71099	11.41802	7.27E-04	9.52E-03
NFYB	-----	ENSGALG00000041193	Nuclear transcription factor Y subunit beta D346	0.24	5.32316	7.24613	7.11E-03	4.87E-02
FAM120B	-----	ENSGALG00000011180	family with sequence similarity 120B	0.24	4.69085	7.55859	5.97E-03	4.33E-02
NAT10	-----	ENSGALG00000014573	N-acetyltransferase 10	0.24	7.13831	12.75044	3.56E-04	5.59E-03
CSRNP3	-----	ENSGALG00000010971	cysteine and serine rich nuclear protein 3	0.24	4.10734	7.92963	4.86E-03	3.75E-02
UBB	polyubiquitin-C	ENSGALG00000041277	ubiquitin B	0.24	9.35011	7.30022	6.89E-03	4.78E-02
CAPN10	-----	ENSGALG00000034562	calpain 10	0.24	5.86666	11.73247	6.14E-04	8.44E-03
EHD4	-----	ENSGALG00000008950	EH domain containing 4	0.24	4.76549	9.24150	2.37E-03	2.25E-02
LARP1B	-----	ENSGALG00000010207	La ribonucleoprotein domain family member 1B	0.24	4.92840	7.36102	6.67E-03	4.67E-02
FAAH	-----	ENSGALG00000010433	fatty acid amide hydrolase	0.24	4.70069	8.18925	4.21E-03	3.38E-02
LOC107050659	-----	-----	valine--tRNA ligase-like	0.24	5.38592	8.51512	3.52E-03	2.97E-02
ANKRD46	-----	ENSGALG00000041445	ankyrin repeat domain 46	0.24	6.31290	17.56495	2.78E-05	7.34E-04
DIRC2	-----	-----	disrupted in renal carcinoma 2	0.24	4.64376	8.85346	2.93E-03	2.60E-02
SDF2L1	-----	ENSGALG00000031982	stromal cell derived factor 2 like 1	0.24	5.79707	10.11129	1.47E-03	1.60E-02
FAM63A	-----	ENSGALG00000028499	family with sequence similarity 63 member A	0.24	6.50941	13.60696	2.25E-04	3.94E-03
TMEM14C	-----	ENSGALG00000034591	transmembrane protein 14C	0.24	5.47265	7.35203	6.70E-03	4.69E-02
ACTR10	-----	ENSGALG00000012041	actin-related protein 10 homolog	0.24	6.07869	18.53481	1.67E-05	4.88E-04

NDE1	-----	ENSGALG00000032590	nudE neurodevelopment protein 1	0.24	6.06873	11.89479	5.63E-04	7.90E-03
PRKG1	-----	-----	protein kinase, cGMP-dependent, type I	0.24	6.42627	8.40007	3.75E-03	3.11E-02
C2CD2	-----	ENSGALG00000016148	C2 calcium dependent domain containing 2	0.24	6.08293	16.19396	5.72E-05	1.33E-03
SPICE1	-----	ENSGALG00000045606	spindle and centriole associated protein 1	0.24	5.90207	15.46307	8.41E-05	1.81E-03
PACSIN2	FAP52	ENSGALG00000014159	protein kinase C and casein kinase substrate in neurons 2	0.24	5.72071	15.68334	7.49E-05	1.66E-03
SMUG1	-----	ENSGALG00000053068	single-strand-selective monofunctional uracil-DNA glycosylase 1	0.24	6.06992	9.18621	2.44E-03	2.29E-02
TRMT6	-----	ENSGALG00000009169	tRNA methyltransferase 6	0.24	5.53981	11.46227	7.10E-04	9.37E-03
ALDH18A1	-----	ENSGALG00000034655	aldehyde dehydrogenase 18 family member A1	0.23	6.44183	10.80583	1.01E-03	1.21E-02
PPWD1	-----	ENSGALG00000014756	peptidylprolyl isomerase domain and WD repeat containing 1	0.23	6.19289	7.41180	6.48E-03	4.60E-02
NEPRO	-----	ENSGALG00000015182	nucleolus and neural progenitor protein	0.23	4.74453	8.44806	3.65E-03	3.06E-02
LAMTOR1	-----	ENSGALG00000050119	late endosomal/lysosomal adaptor, MAPK and MTOR activator 1	0.23	5.60330	9.31964	2.27E-03	2.19E-02
ADAR	-----	ENSGALG00000021475	adenosine deaminase, RNA specific	0.23	6.68016	21.26386	4.00E-06	1.53E-04
CENPE	-----	ENSGALG00000013208	centromere protein E	0.23	7.40760	17.81938	2.43E-05	6.60E-04
DTD1	-----	ENSGALG00000008808	D-tyrosyl-tRNA deacylase 1	0.23	5.64118	12.40037	4.29E-04	6.46E-03
HEXIM1	-----	ENSGALG00000041926	HEXIM P-TEFb complex subunit 1	0.23	6.85336	11.14049	8.45E-04	1.06E-02
TIPIN	-----	ENSGALG00000007649	TIMELESS interacting protein	0.23	5.85431	10.20105	1.40E-03	1.54E-02
C18H17orf62	CYBC1	ENSGALG00000001607	chromosome 18 C17orf62 homolog	0.23	6.15960	11.51891	6.89E-04	9.17E-03
CDKL5	-----	ENSGALG00000016529	cyclin dependent kinase like 5	0.23	4.61079	7.96454	4.77E-03	3.70E-02
POT1	-----	ENSGALG00000008740	protection of telomeres 1	0.23	5.16395	9.28783	2.31E-03	2.21E-02
FBXO39	-----	ENSGALG00000029322	F-box protein 39	0.23	5.00193	9.93794	1.62E-03	1.71E-02
CLCC1	-----	ENSGALG00000002106	chloride channel CLIC like 1	0.23	5.74986	9.61659	1.93E-03	1.96E-02
CDK1	CDC2	ENSGALG00000003085	cyclin dependent kinase 1	0.23	7.94959	10.85260	9.87E-04	1.19E-02
ECHDC3	-----	ENSGALG00000006690	enoyl-CoA hydratase domain containing 3	0.23	5.03755	9.85825	1.69E-03	1.77E-02
BIN3	-----	ENSGALG00000052825	bridging integrator 3	0.23	6.36570	11.69517	6.27E-04	8.54E-03
RAD18	-----	ENSGALG00000008368	RAD18, E3 ubiquitin protein ligase	0.23	5.73937	10.82532	1.00E-03	1.20E-02
CCND1	-----	ENSGALG00000007555	cyclin D1	0.23	6.05195	7.55117	6.00E-03	4.33E-02
NAPA	-----	ENSGALG00000034747	NSF attachment protein alpha	0.23	6.75884	12.01171	5.29E-04	7.56E-03
RTN4IP1	-----	ENSGALG00000015343	reticulon 4 interacting protein 1	0.23	4.70930	7.90832	4.92E-03	3.79E-02
TYRO3	-----	-----	-----	0.23	6.28525	8.61790	3.33E-03	2.85E-02
C14H16orf91	-----	-----	chromosome 14 C16orf91 homolog	0.23	4.40611	8.11083	4.40E-03	3.48E-02
FAM149B1	-----	ENSGALG00000002693	family with sequence similarity 149 member B1	0.23	6.32258	13.66306	2.19E-04	3.85E-03
STRA6	-----	ENSGALG00000001449	stimulated by retinoic acid 6	0.23	7.35311	7.85197	5.08E-03	3.86E-02
COPB2	-----	ENSGALG00000005357	coatomer protein complex subunit beta 2	0.23	7.98743	20.01227	7.69E-06	2.64E-04
ATM	-----	ENSGALG00000017159	ATM serine/threonine kinase	0.23	6.05522	11.37772	7.43E-04	9.68E-03
HYPK	-----	ENSGALG00000013916	huntingtin interacting protein K	0.23	5.76116	11.80249	5.92E-04	8.19E-03
CTNND2	-----	-----	catenin delta 2	0.23	6.08532	11.06677	8.79E-04	1.09E-02
CEP83	-----	ENSGALG00000019336	centrosomal protein 83	0.23	4.82223	8.40399	3.74E-03	3.10E-02
C2H18ORF8	-----	-----	-----	0.23	4.82235	8.18510	4.22E-03	3.38E-02
IPO13	importin-13	ENSGALG00000010087	importin 13	0.23	6.29662	9.73664	1.81E-03	1.86E-02
BUB1B	BUBR1	ENSGALG00000036892	BUB1 mitotic checkpoint serine/threonine kinase B	0.23	7.79571	9.99985	1.57E-03	1.67E-02
FUNDC2	-----	ENSGALG00000029585	FUN14 domain containing 2	0.23	6.48786	21.21341	4.11E-06	1.56E-04
FKBP4	-----	ENSGALG00000014331	FK506 binding protein 4	0.23	8.64115	13.92515	1.90E-04	3.44E-03
BAG3	-----	ENSGALG00000009433	BCL2 associated athanogene 3	0.23	6.13865	11.17045	8.31E-04	1.05E-02
TSFM	-----	-----	-----	0.23	4.53471	8.77979	3.05E-03	2.67E-02

WWC1	-----	ENSGALG00000001826	WW and C2 domain containing 1	0.23	6.27476	14.34219	1.52E-04	2.86E-03
VAPA	-----	ENSGALG00000039455	VAMP associated protein A	0.22	7.27048	18.00004	2.21E-05	6.12E-04
ESD	-----	ENSGALG00000016991	esterase D	0.22	6.36058	12.13661	4.94E-04	7.21E-03
CPSF3	-----	ENSGALG00000016424	cleavage and polyadenylation specific factor 3	0.22	6.56983	14.39730	1.48E-04	2.81E-03
ALG8	-----	ENSGALG00000019042	ALG8, alpha-1,3-glucosyltransferase	0.22	5.55924	10.06046	1.51E-03	1.63E-02
PAPSS1	-----	ENSGALG00000010542	3'-phosphoadenosine 5'-phosphosulfate synthase 1	0.22	6.98528	11.03428	8.94E-04	1.10E-02
INTS11	CPSF3L	ENSGALG00000001691	integrator complex subunit 11	0.22	6.11686	12.77871	3.51E-04	5.53E-03
MBD4	-----	ENSGALG00000020747	methyl-CpG binding domain 4, DNA glycosylase	0.22	4.65172	7.87089	5.02E-03	3.83E-02
NRP2	neuropilin-2	ENSGALG00000008621	neuropilin 2	0.22	8.71159	8.38615	3.78E-03	3.12E-02
TMEM43	-----	ENSGALG00000006345	transmembrane protein 43	0.22	5.70904	10.41066	1.25E-03	1.41E-02
GUCY1B3	-----	ENSGALG00000009361	guanylate cyclase 1 soluble subunit beta	0.22	5.06100	9.03299	2.65E-03	2.42E-02
DIAPH3	-----	ENSGALG00000016937	diaphanous related formin 3	0.22	4.92897	7.73639	5.41E-03	4.03E-02
TRIP13	-----	ENSGALG00000033834	thyroid hormone receptor interactor 13	0.22	5.70814	8.69989	3.18E-03	2.75E-02
CRCP	RCP9	ENSGALG00000002587	CGRP receptor component	0.22	5.69892	9.65500	1.89E-03	1.93E-02
MPV17L2	-----	ENSGALG00000041429	MPV17 mitochondrial inner membrane protein like 2	0.22	4.89425	7.70618	5.50E-03	4.08E-02
CDYL	-----	-----	chromodomain Y-like	0.22	5.31184	7.64459	5.69E-03	4.18E-02
UACA	-----	ENSGALG00000034100	uveal autoantigen with coiled-coil domains and ankyrin repeats	0.22	6.85444	13.84665	1.98E-04	3.55E-03
DACH2	-----	ENSGALG00000006886	dachshund family transcription factor 2	0.22	6.11926	7.38523	6.58E-03	4.64E-02
SNN	-----	ENSGALG00000028876	stannin	0.22	4.77734	9.23022	2.38E-03	2.26E-02
SIVA1	-----	ENSGALG00000011619	SIVA1 apoptosis inducing factor	0.22	4.79301	8.55840	3.44E-03	2.91E-02
TTC37	-----	ENSGALG00000014670	tetratricopeptide repeat domain 37	0.22	6.65755	7.33943	6.75E-03	4.71E-02
KNSTRN	C15ORF23	ENSGALG00000039576	kinetochore-localized astrin/SPAG5 binding protein	0.22	6.34051	12.05803	5.16E-04	7.41E-03
WDHD1	-----	ENSGALG00000012199	WD repeat and HMG-box DNA binding protein 1	0.22	6.42327	12.15840	4.89E-04	7.15E-03
POLR1E	-----	ENSGALG00000005395	RNA polymerase I subunit E	0.22	6.23700	9.32158	2.26E-03	2.18E-02
C3H6ORF203	C6orf203	ENSGALG00000015316	chromosome 3 open reading frame, human C6orf203	0.22	4.83158	7.40192	6.52E-03	4.61E-02
COMMD10	-----	ENSGALG00000002308	COMM domain containing 10	0.22	5.80969	7.61772	5.78E-03	4.22E-02
RNGTT	-----	ENSGALG00000015787	RNA guanylyltransferase and 5'-phosphatase	0.21	5.99327	8.74673	3.10E-03	2.70E-02
HMCES	C12H3ORF37	ENSGALG00000005897	5-hydroxymethylcytosine (hmC) binding, ES cell-specific	0.21	5.65425	8.14280	4.32E-03	3.43E-02
ECE1	ECE-1	ENSGALG00000031343	endothelin converting enzyme 1	0.21	6.79756	11.90609	5.60E-04	7.88E-03
STT3A	-----	ENSGALG00000042730	STT3A, catalytic subunit of the oligosaccharyltransferase complex	0.21	7.61485	19.15268	1.21E-05	3.76E-04
FIP1L1	-----	ENSGALG00000013943	factor interacting with PAPOLA and CPSF1	0.21	6.20385	11.32778	7.64E-04	9.85E-03
GPHN	-----	ENSGALG00000009587	gephyrin	0.21	5.89127	10.43515	1.24E-03	1.40E-02
RBM12B	-----	ENSGALG00000035129	RNA binding motif protein 12B	0.21	6.57951	15.60808	7.79E-05	1.72E-03
CCT3	-----	ENSGALG00000048034	chaperonin containing TCP1 subunit 3	0.21	7.46963	8.26706	4.04E-03	3.27E-02
STK16	-----	ENSGALG00000011326	serine/threonine kinase 16	0.21	4.99177	7.33773	6.75E-03	4.71E-02
GNL3	-----	ENSGALG00000001613	G protein nucleolar 3	0.21	7.79089	11.24519	7.98E-04	1.02E-02
PSIP1	PSIP2	ENSGALG00000015105	PC4 and SFRS1 interacting protein 1	0.21	7.46882	8.79522	3.02E-03	2.65E-02
MAP9	-----	ENSGALG00000020253	microtubule associated protein 9	0.21	5.37132	8.82685	2.97E-03	2.62E-02
SLITRK2	-----	ENSGALG00000009192	SLIT and NTRK like family member 2	0.21	5.53252	12.57824	3.90E-04	6.01E-03
STIP1	-----	ENSGALG00000046811	stress induced phosphoprotein 1	0.21	7.99707	9.24821	2.36E-03	2.25E-02
MYEF2	-----	ENSGALG00000032546	myelin expression factor 2	0.21	7.46448	17.50186	2.87E-05	7.53E-04
KIRREL	-----	ENSGALG00000029528	kin of IRRE like (Drosophila)	0.21	8.45365	13.00736	3.10E-04	5.06E-03
RRN3	-----	ENSGALG00000041989	RRN3 homolog, RNA polymerase I transcription factor	0.21	5.82923	10.63808	1.11E-03	1.29E-02
GARS	-----	ENSGALG00000005694	glycyl-tRNA synthetase	0.21	7.86267	15.21601	9.59E-05	2.00E-03

PPP4R2	-----	ENSGALG00000007810	protein phosphatase 4 regulatory subunit 2	0.21	7.49860	17.85314	2.39E-05	6.52E-04
WDCP	-----	ENSGALG00000019867	WD repeat and coiled coil containing	0.21	5.36850	10.38836	1.27E-03	1.42E-02
ZNF706	-----	ENSGALG000000041200	zinc finger protein 706	0.21	7.41346	11.10054	8.63E-04	1.08E-02
COG6	-----	ENSGALG000000017035	component of oligomeric golgi complex 6	0.21	5.84731	10.82088	1.00E-03	1.21E-02
HPF1	-----	ENSGALG000000009668	histone PARylation factor 1	0.21	6.44703	14.37191	1.50E-04	2.83E-03
HNRNPLL	HNRPLL	ENSGALG000000008504	heterogeneous nuclear ribonucleoprotein L like	0.21	7.12424	15.59177	7.86E-05	1.73E-03
AHSA1	-----	ENSGALG000000010463	activator of Hsp90 ATPase activity 1	0.21	6.93121	8.59232	3.38E-03	2.88E-02
KPNA2	-----	ENSGALG000000003584	karyopherin subunit alpha 2	0.21	8.96834	11.52233	6.88E-04	9.16E-03
REV1	REV1L	ENSGALG000000016766	REV1, DNA directed polymerase	0.21	5.54681	7.29082	6.93E-03	4.80E-02
SRM	-----	ENSGALG000000003039	spermidine synthase	0.21	6.49134	14.51409	1.39E-04	2.67E-03
RCN1L	-----	-----	----	0.21	7.09829	18.19934	1.99E-05	5.62E-04
ATP2C1	-----	ENSGALG000000034340	ATPase secretory pathway Ca2+ transporting 1	0.21	6.85174	16.53784	4.77E-05	1.15E-03
TWSG1	-----	ENSGALG000000052629	twisted gastrulation BMP signaling modulator 1	0.21	6.60112	10.92534	9.49E-04	1.16E-02
MKL1	-----	ENSGALG000000012024	megakaryoblastic leukemia (translocation) 1	0.21	6.70139	10.72175	1.06E-03	1.25E-02
FCHSD2	-----	ENSGALG000000017329	FCH and double SH3 domains 2	0.21	5.35022	8.23257	4.11E-03	3.31E-02
EVI5	-----	ENSGALG000000029582	ecotropic viral integration site 5	0.21	6.23157	14.61247	1.32E-04	2.56E-03
DDX17	-----	ENSGALG000000037360	DEAD-box helicase 17	0.21	8.99892	8.60174	3.36E-03	2.87E-02
G6PD	-----	-----	----	0.21	4.77391	8.16433	4.27E-03	3.40E-02
CKAP2	-----	ENSGALG000000017025	cytoskeleton associated protein 2	0.21	8.48512	10.27348	1.35E-03	1.49E-02
IGSF9	-----	ENSGALG000000031193	immunoglobulin superfamily member 9	0.21	7.38102	12.24810	4.66E-04	6.87E-03
KIF1BP	kbp	ENSGALG000000004156	KIF1 binding protein	0.21	5.69318	12.03104	5.23E-04	7.50E-03
GEMIN5	-----	ENSGALG000000003937	gem nuclear organelle associated protein 5	0.20	7.16899	11.89963	5.61E-04	7.89E-03
PSMB1	-----	ENSGALG000000011174	proteasome subunit beta 1	0.20	7.49922	12.27478	4.59E-04	6.79E-03
CD2AP	-----	ENSGALG000000016720	CD2 associated protein	0.20	6.03195	7.74440	5.39E-03	4.02E-02
SNU13	-----	ENSGALG000000011931	small nuclear ribonucleoprotein 13	0.20	6.76330	11.54212	6.80E-04	9.09E-03
CIR1	CIR	ENSGALG000000014276	corepressor interacting with RBPJ, 1	0.20	6.17022	10.96727	9.27E-04	1.14E-02
POLR2E	-----	ENSGALG000000002591	RNA polymerase II subunit E	0.20	6.71610	12.38725	4.32E-04	6.50E-03
VASH2	-----	ENSGALG000000020067	vasohibin 2	0.20	6.77793	8.64241	3.28E-03	2.82E-02
PRR11	-----	ENSGALG000000054015	proline rich 11	0.20	5.09606	7.69986	5.52E-03	4.09E-02
PKM	-----	-----	----	0.20	10.80797	8.17438	4.25E-03	3.39E-02
NUP205	-----	ENSGALG000000011662	nucleoporin 205	0.20	7.98813	12.22984	4.70E-04	6.92E-03
GNG5	-----	ENSGALG000000027561	G protein subunit gamma 5	0.20	6.02537	9.28527	2.31E-03	2.21E-02
KIF18B	-----	ENSGALG000000031553	kinesin family member 18B	0.20	5.91159	11.84270	5.79E-04	8.09E-03
NUP160	-----	ENSGALG000000043074	nucleoporin 160	0.20	8.08976	12.12431	4.98E-04	7.23E-03
DCPS	-----	ENSGALG000000031143	decapping enzyme, scavenger	0.20	5.99075	10.32512	1.31E-03	1.46E-02
GTF3C2	-----	-----	general transcription factor IIIC subunit 2	0.20	5.89233	10.72955	1.05E-03	1.25E-02
TARSL2	-----	ENSGALG000000003985	threonyl-tRNA synthetase like 2	0.20	6.02396	12.42364	4.24E-04	6.39E-03
TMTC2	-----	ENSGALG000000010975	transmembrane and tetratricopeptide repeat containing 2	0.20	5.86305	9.23215	2.38E-03	2.26E-02
MTMR14	-----	ENSGALG000000006601	myotubularin related protein 14	0.20	5.60525	8.65914	3.25E-03	2.80E-02
IARS	-----	ENSGALG000000004813	isoleucyl-tRNA synthetase	0.20	7.66079	10.50864	1.19E-03	1.36E-02
CBFB	-----	ENSGALG000000003169	core-binding factor beta subunit	0.20	7.05393	11.53065	6.85E-04	9.14E-03
SRGAP2	-----	ENSGALG000000000816	SLIT-ROBO Rho GTPase activating protein 2	0.20	7.20917	9.64269	1.90E-03	1.94E-02
CDC16	-----	ENSGALG000000016816	cell division cycle 16	0.20	5.76570	10.29548	1.33E-03	1.48E-02
DTNBP1	-----	ENSGALG000000012703	dystrobrevin binding protein 1	0.20	5.39249	12.14618	4.92E-04	7.19E-03

PWP1	-----	ENSGALG00000012631	PWP1 homolog, endonuclein	0.20	6.65138	11.06322	8.81E-04	1.09E-02
SCHIP1	-----	ENSGALG00000039468	schwannomin interacting protein 1	0.20	5.95743	8.75046	3.10E-03	2.70E-02
LOC107057078	-----	-----	acyl-CoA dehydrogenase family member 10-like	0.20	7.07544	9.56873	1.98E-03	2.00E-02
FAM110B	-----	ENSGALG00000035065	family with sequence similarity 110 member B	0.20	6.16831	7.41275	6.48E-03	4.60E-02
CHM	CHML	ENSGALG00000006906	CHM, Rab escort protein 1	0.20	6.22184	9.19862	2.42E-03	2.28E-02
CEP295	-----	ENSGALG00000040433	centrosomal protein 295	0.20	6.50438	9.36703	2.21E-03	2.15E-02
MUM1	-----	ENSGALG00010028034	-----	0.20	5.79930	9.25057	2.35E-03	2.25E-02
UQCC1	UQCC	ENSGALG00000040254	ubiquinol-cytochrome c reductase complex assembly factor 1	0.20	5.77838	9.76263	1.78E-03	1.84E-02
TPM1	alpha-fTM	ENSGALG00000003521	tropomyosin 1 (alpha)	0.20	9.01033	12.66974	3.72E-04	5.79E-03
MXI1	-----	ENSGALG00000008555	MAX interactor 1, dimerization protein	0.20	5.29509	8.43498	3.68E-03	3.07E-02
OAZ2	-----	ENSGALG00000036288	ornithine decarboxylase antizyme 2	0.20	6.45986	13.09922	2.95E-04	4.87E-03
SELENOT	-----	ENSGALG00000010399	selenoprotein T	0.20	6.18247	9.93755	1.62E-03	1.71E-02
LOC426821	-----	-----	zinc finger protein 624-like	0.20	5.36857	7.31065	6.85E-03	4.76E-02
POLR1A	-----	ENSGALG00000038160	RNA polymerase I subunit A	0.20	6.59943	9.84366	1.70E-03	1.78E-02
XPNPEP1	-----	ENSGALG00000008523	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	0.20	6.96913	13.55910	2.31E-04	4.02E-03
RCOR3	-----	ENSGALG00000009871	REST corepressor 3	0.20	6.98026	17.70703	2.58E-05	6.95E-04
PCBP4	-----	ENSGALG00000027695	poly(rC)-binding protein 4-like	0.20	6.81729	11.48998	7.00E-04	9.26E-03
SMC4	SMC4L1	ENSGALG00000009553	structural maintenance of chromosomes 4	0.20	7.76906	18.71707	1.52E-05	4.54E-04
UBE2S	-----	ENSGALG00000052573	ubiquitin conjugating enzyme E2 S	0.19	7.06969	10.15179	1.44E-03	1.57E-02
LOC422214	-----	-----	nuclear cap binding protein subunit 2, 20kDa	0.19	6.16354	8.03811	4.58E-03	3.59E-02
TTLL12	-----	ENSGALG00000014167	tubulin tyrosine ligase like 12	0.19	7.15043	11.57741	6.68E-04	9.00E-03
ECT2	-----	ENSGALG00000009157	epithelial cell transforming 2	0.19	6.75610	11.03109	8.96E-04	1.11E-02
HMBS	-----	ENSGALG00000042939	hydroxymethylbilane synthase	0.19	6.10410	9.10010	2.56E-03	2.36E-02
HOXA6	HOX1	ENSGALG00000028908	homeobox A6	0.19	5.68488	7.72668	5.44E-03	4.05E-02
ACTN1	-----	ENSGALG00000042458	actinin, alpha 1	0.19	7.48797	14.05935	1.77E-04	3.24E-03
FUS	FUS/TLS	ENSGALG00000032219	FUS RNA binding protein	0.19	9.39909	9.70129	1.84E-03	1.89E-02
KCTD3	-----	ENSGALG00000009678	SH3KBP1 binding protein 1	0.19	6.89329	10.42640	1.24E-03	1.40E-02
RPF1	-----	ENSGALG00000008796	ribosome production factor 1 homolog	0.19	5.90904	7.44631	6.36E-03	4.54E-02
ACTR6	GARPX	ENSGALG00000040976	ARP6 actin-related protein 6 homolog	0.19	7.02980	7.88233	4.99E-03	3.82E-02
RAD54L	GdRAD54	ENSGALG00000010356	RAD54-like (<i>S. cerevisiae</i>)	0.19	5.68809	8.12667	4.36E-03	3.45E-02
SLC39A14	-----	ENSGALG00000033989	solute carrier family 39 member 14	0.19	6.17039	8.05392	4.54E-03	3.56E-02
DPP7	-----	ENSGALG00000038145	dipeptidyl peptidase 7	0.19	5.58289	7.74626	5.38E-03	4.02E-02
KAT2A	-----	ENSGALG00000003369	lysine acetyltransferase 2A	0.19	6.87670	11.84411	5.78E-04	8.09E-03
SLC25A15	-----	ENSGALG00000017032	solute carrier family 25 member 15	0.19	5.65290	8.13786	4.34E-03	3.44E-02
NSF	-----	ENSGALG00000001055	N-ethylmaleimide sensitive factor, vesicle fusing ATPase	0.19	6.39086	7.84850	5.09E-03	3.86E-02
LOC107057310	-----	-----	uncharacterized LOC107057310	0.19	5.28197	8.56078	3.43E-03	2.91E-02
SELENON	-----	-----	selenoprotein N	0.19	6.92180	11.84913	5.77E-04	8.07E-03
HJURP	-----	ENSGALG00000015363	Holliday junction recognition protein	0.19	5.67883	7.63136	5.74E-03	4.20E-02
AKR1A1	-----	ENSGALG00000010244	aldo-keto reductase family 1 member A1	0.19	6.53082	10.51714	1.18E-03	1.35E-02
PTP4A2	-----	ENSGALG00000003265	protein tyrosine phosphatase type IVA, member 2	0.19	6.78516	9.69398	1.85E-03	1.90E-02
MSH6	-----	ENSGALG00000008957	mutS homolog 6	0.19	7.59165	10.53939	1.17E-03	1.34E-02
NVL	-----	ENSGALG00000009322	nuclear VCP-like	0.19	6.01991	11.11297	8.57E-04	1.07E-02
EIF3D	-----	ENSGALG00000012529	eukaryotic translation initiation factor 3 subunit D	0.19	8.67997	9.62119	1.92E-03	1.96E-02
EPB41L2	-----	-----	erythrocyte membrane protein band 4.1 like 2	0.19	6.53254	8.45534	3.64E-03	3.05E-02

TUBB4B	TUBB2C	ENSGALG00000008586	tubulin beta 4B class IVb	0.19	7.53232	12.90643	3.27E-04	5.25E-03
RASAL3	-----	ENSGALG00000039156	RAS protein activator like 3	0.19	7.66323	9.44451	2.12E-03	2.09E-02
RARS	-----	ENSGALG00000001850	arginyl-tRNA synthetase	0.19	7.33114	8.36214	3.83E-03	3.15E-02
TIMMDC1	-----	ENSGALG00000024480	translocase of inner mitochondrial membrane domain containing 1	0.19	6.15640	9.19503	2.43E-03	2.28E-02
SCOC	BERT	ENSGALG00000009813	short coiled-coil protein	0.19	6.42050	8.48365	3.58E-03	3.01E-02
PKNOX1	-----	ENSGALG00000016191	PBX/knotted 1 homeobox 1	0.19	6.30135	7.72906	5.43E-03	4.05E-02
TBC1D13	-----	ENSGALG00000004645	TBC1 domain family member 13	0.19	6.86690	10.27746	1.35E-03	1.49E-02
TSPAN4	-----	ENSGALG00000006837	tetraspanin 4	0.18	6.37562	10.69402	1.07E-03	1.26E-02
RIMKLB	-----	ENSGALG00000040184	ribosomal modification protein rimK like family member B	0.18	6.27990	8.24394	4.09E-03	3.30E-02
CASP3	caspase-3	ENSGALG00000010638	caspase 3	0.18	6.97980	12.41387	4.26E-04	6.42E-03
FARSA	FARSLA	ENSGALG00000040258	phenylalanyl-tRNA synthetase alpha subunit	0.18	6.57360	8.35168	3.85E-03	3.16E-02
RNF14	-----	ENSGALG00000043085	ring finger protein 14	0.18	6.45820	8.09331	4.44E-03	3.51E-02
HSPA4	-----	ENSGALG00000040882	heat shock protein family A (Hsp70) member 4	0.18	7.41320	8.07521	4.49E-03	3.53E-02
LRWD1	-----	ENSGALG00000001852	leucine rich repeats and WD repeat domain containing 1	0.18	6.71920	8.70804	3.17E-03	2.74E-02
CAD	-----	ENSGALG00000016524	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	0.18	8.80548	8.15286	4.30E-03	3.42E-02
MRE11	MRE11A	ENSGALG00000017211	MRE11 homolog, double strand break repair nuclease	0.18	6.66016	9.89294	1.66E-03	1.74E-02
LUC7L2	-----	ENSGALG00000036238	LUC7 like 2, pre-mRNA splicing factor	0.18	7.78479	11.19821	8.19E-04	1.04E-02
RAB8B	-----	ENSGALG00000003487	RAB8B, member RAS oncogene family	0.18	6.95609	14.89990	1.13E-04	2.26E-03
LTBP1	-----	ENSGALG00000010448	latent transforming growth factor beta binding protein 1	0.18	8.50873	7.88666	4.98E-03	3.82E-02
KLHL2	-----	ENSGALG00000009554	kelch like family member 2	0.18	6.29348	9.04413	2.64E-03	2.41E-02
PI4KB	-----	ENSGALG00000024034	phosphatidylinositol 4-kinase beta	0.18	6.57973	8.96595	2.75E-03	2.48E-02
KANSL1L	-----	ENSGALG00000002866	KAT8 regulatory NSL complex subunit 1-like	0.18	5.51502	8.07294	4.49E-03	3.54E-02
CCT6A	CCT6	ENSGALG00000002448	chaperonin containing TCP1 subunit 6A	0.18	8.88016	8.07870	4.48E-03	3.53E-02
CCT8	-----	ENSGALG00000015821	chaperonin containing TCP1 subunit 8	0.18	8.80978	7.64928	5.68E-03	4.18E-02
GTF2E2	-----	ENSGALG00000010283	general transcription factor IIE subunit 2	0.18	5.63125	8.82348	2.97E-03	2.63E-02
NDC1	-----	ENSGALG00000031606	NDC1 transmembrane nucleoporin	0.18	6.99153	8.01652	4.64E-03	3.62E-02
C1QBP	-----	ENSGALG00000001654	complement C1q binding protein	0.18	8.46853	7.96579	4.77E-03	3.70E-02
LAS1L	-----	ENSGALG00000043447	LAS1 like, ribosome biogenesis factor	0.18	6.80656	13.69747	2.15E-04	3.79E-03
SUGT1	-----	ENSGALG00000016946	SGT1 homolog, MIS12 kinetochore complex assembly cochaperone	0.18	6.59409	11.15275	8.39E-04	1.06E-02
AIFM1	PDCD8	ENSGALG00000004003	apoptosis inducing factor, mitochondria associated 1	0.18	7.11476	11.31443	7.69E-04	9.90E-03
SEC31A	SEC31L1	ENSGALG00000040484	SEC31 homolog A, COPII coat complex component	0.18	8.94655	7.53139	6.06E-03	4.37E-02
USPL1	-----	ENSGALG00000017079	ubiquitin specific peptidase like 1	0.18	7.18107	8.08569	4.46E-03	3.52E-02
EXOSC9	-----	ENSGALG00000011884	exosome component 9	0.18	6.16976	8.36805	3.82E-03	3.14E-02
RHOT1	-----	ENSGALG00000003397	ras homolog family member T1	0.18	5.93000	10.34641	1.30E-03	1.45E-02
ZCCHC24	-----	ENSGALG00000026864	zinc finger CCHC-type containing 24	0.18	6.79975	8.63039	3.31E-03	2.84E-02
CBR1	-----	-----	-----	0.18	5.87704	7.41616	6.46E-03	4.60E-02
ALDH9A1	-----	ENSGALG00000003495	aldehyde dehydrogenase 9 family member A1	0.18	7.73656	12.89524	3.29E-04	5.27E-03
NID2	-----	ENSGALG00000012394	nidogen 2	0.18	7.77914	8.71029	3.16E-03	2.74E-02
ANGEL2	-----	ENSGALG00000009802	angel homolog 2	0.18	5.17148	7.18505	7.35E-03	5.00E-02
USP51	-----	-----	-----	0.17	6.97992	10.76146	1.04E-03	1.23E-02
WDR76	-----	ENSGALG00000035465	WD repeat domain 76	0.17	6.25639	7.79504	5.24E-03	3.95E-02
THOC5	-----	ENSGALG00000029223	THO complex 5	0.17	7.59716	10.11834	1.47E-03	1.59E-02
NCBP2	-----	ENSGALG00000006843	nuclear cap binding protein subunit 2, 20kDa	0.17	7.75306	12.93923	3.22E-04	5.19E-03
ITSN1	-----	ENSGALG00000036677	intersectin 1	0.17	7.30274	10.49524	1.20E-03	1.36E-02

DDR1	-----	ENSGALG00000008616	discoidin domain receptor tyrosine kinase 1	0.17	7.36127	8.15690	4.29E-03	3.41E-02
SUFU	-----	ENSGALG00000008096	SUFU negative regulator of hedgehog signaling	0.17	5.92754	7.37487	6.61E-03	4.65E-02
FAR1	MLSTD2	ENSGALG00000005353	fatty acyl-CoA reductase 1	0.17	6.65960	10.92832	9.47E-04	1.16E-02
SKA2	-----	ENSGALG00000005090	spindle and kinetochore associated complex subunit 2 pseudogene 1	0.17	6.61783	8.00305	4.67E-03	3.64E-02
CCDC30	-----	-----	coiled-coil domain containing 30	0.17	5.71402	7.84732	5.09E-03	3.86E-02
NT5C2	-----	ENSGALG00000008179	5'-nucleotidase, cytosolic II	0.17	6.59796	9.96518	1.60E-03	1.70E-02
LOC112530429	-----	-----	uncharacterized LOC112530429	0.17	7.87196	7.31137	6.85E-03	4.76E-02
NDUFB4	-----	ENSGALG00000027688	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	0.17	6.47359	7.40063	6.52E-03	4.61E-02
PITPNB	-----	ENSGALG00000005654	phosphatidylinositol transfer protein beta	0.17	7.09819	13.01104	3.10E-04	5.06E-03
TIAL1	-----	ENSGALG00000009427	TIA1 cytotoxic granule associated RNA binding protein like 1	0.17	5.74865	8.26084	4.05E-03	3.27E-02
PTK2	FAK	ENSGALG00000031741	protein tyrosine kinase 2	0.16	7.56296	8.71820	3.15E-03	2.74E-02
CSE1L	-----	ENSGALG00000004707	chromosome segregation 1 like	0.16	8.31603	8.83647	2.95E-03	2.62E-02
ZBTB33	-----	ENSGALG00000008611	zinc finger and BTB domain containing 33	0.16	6.10804	10.13543	1.45E-03	1.58E-02
ELMO2	-----	ENSGALG00000007246	engulfment and cell motility 2	0.16	7.12961	9.18384	2.44E-03	2.29E-02
NAP1L1	-----	ENSGALG00000010238	nucleosome assembly protein 1 like 1	0.16	9.37804	7.25787	7.06E-03	4.85E-02
IGSF3	-----	ENSGALG00000036738	immunoglobulin superfamily member 3	0.16	7.33400	7.62534	5.76E-03	4.21E-02
NF2	-----	ENSGALG00000008073	neurofibromin 2	0.16	7.64640	9.38993	2.18E-03	2.14E-02
UBA3	-----	ENSGALG00000013410	ubiquitin like modifier activating enzyme 3	0.16	6.40388	7.53157	6.06E-03	4.37E-02
MCMBP	C10orf119	ENSGALG00000009455	minichromosome maintenance complex binding protein	0.16	6.84461	9.41677	2.15E-03	2.11E-02
UBL3	-----	ENSGALG00000017084	ubiquitin like 3	0.16	5.71265	8.30922	3.94E-03	3.22E-02
GALNT1	-----	ENSGALG00000013135	polypeptide N-acetylgalactosaminyltransferase 1	0.16	7.23504	9.64190	1.90E-03	1.94E-02
RBM4B	-----	-----	-----	0.16	6.43610	7.93616	4.85E-03	3.74E-02
GLT8D1	-----	ENSGALG00000001642	glycosyltransferase 8 domain containing 1	0.16	5.87780	8.06235	4.52E-03	3.55E-02
ESPL1	-----	ENSGALG00000041923	extra spindle pole bodies like 1, separase	0.16	7.48066	7.29187	6.93E-03	4.80E-02
SAE1	-----	ENSGALG00000048152	SUMO1 activating enzyme subunit 1	0.16	7.12681	8.40559	3.74E-03	3.10E-02
TOP1	-----	ENSGALG00000003681	DNA topoisomerase I	0.16	8.39688	8.88458	2.88E-03	2.57E-02
RALGAPB	-----	ENSGALG00000001420	Ral GTPase activating protein non-catalytic beta subunit	0.16	7.00473	8.40260	3.75E-03	3.10E-02
UBE2N	-----	ENSGALG00000030515	ubiquitin conjugating enzyme E2 N	0.16	7.45731	9.13228	2.51E-03	2.33E-02
ACTR1A	-----	ENSGALG00000008086	ARP1 actin-related protein 1 homolog A, centractin alpha	0.16	7.43269	9.99464	1.57E-03	1.67E-02
FAM171A1	-----	ENSGALG00000008764	family with sequence similarity 171, member A1	0.16	6.73748	9.15734	2.48E-03	2.31E-02
USP48	-----	ENSGALG00000030857	ubiquitin specific peptidase 48	0.16	6.34104	7.81376	5.18E-03	3.92E-02
BCL7A	-----	ENSGALG00000004379	BAF chromatin remodeling complex subunit BCL7A	0.16	6.56648	8.70153	3.18E-03	2.75E-02
PSMC3	-----	ENSGALG00000008108	proteasome 26S subunit, ATPase 3	0.16	7.90511	9.45255	2.11E-03	2.09E-02
PSME4	-----	ENSGALG00000008163	proteasome activator subunit 4	0.16	6.94939	8.03178	4.60E-03	3.60E-02
PTGES3	CPGES	ENSGALG00000036837	prostaglandin E synthase 3	0.15	8.54975	7.38560	6.57E-03	4.64E-02
COPS4	-----	ENSGALG00000011130	COP9 signalosome subunit 4	0.15	6.85243	9.09810	2.56E-03	2.37E-02
MAP2K1	-----	ENSGALG00000007687	mitogen-activated protein kinase kinase 1	0.15	6.50021	7.44726	6.35E-03	4.54E-02
DCTN1	Chip150	ENSGALG00000035156	dynactin subunit 1	0.15	8.06230	7.58112	5.90E-03	4.29E-02
FAM98A	-----	ENSGALG00000010428	family with sequence similarity 98 member A	0.15	6.50419	8.56445	3.43E-03	2.91E-02
TMEM184C	TMEM34	ENSGALG00000010019	transmembrane protein 184C	0.15	6.35126	8.37205	3.81E-03	3.14E-02
FAM168A	-----	ENSGALG00000017323	family with sequence similarity 168 member A	0.15	6.12791	8.13110	4.35E-03	3.45E-02
PLK1	-----	ENSGALG00000006110	polo like kinase 1	0.15	8.60063	7.37373	6.62E-03	4.65E-02
TXNRD3	-----	ENSGALG00000039363	thioredoxin reductase 3	0.15	7.19262	8.16335	4.27E-03	3.40E-02
CTNNBL1	-----	ENSGALG00000006817	catenin beta like 1	0.15	6.48073	7.62565	5.75E-03	4.21E-02

TRAF7	-----	ENSGALG00000005767	TNF receptor associated factor 7	0.15	6.12917	7.98610	4.71E-03	3.67E-02
BUB1	-----	ENSGALG00000008233	BUB1 mitotic checkpoint serine/threonine kinase	0.15	7.50334	8.19880	4.19E-03	3.36E-02
NOMO3	-----	-----	-----	0.15	7.31348	7.44394	6.37E-03	4.54E-02
SMAD5	-----	ENSGALG00000006309	SMAD family member 5	0.15	7.43835	7.47020	6.27E-03	4.49E-02
DERL1	derlin-1	ENSGALG00000033950	derlin 1	0.15	6.87055	10.15857	1.44E-03	1.57E-02
MRPL20	-----	ENSGALG00000001542	mitochondrial ribosomal protein L20	0.15	6.41045	8.27522	4.02E-03	3.26E-02
AKIRIN2	akirin-2	ENSGALG00000015791	akirin 2	0.14	7.35705	8.30505	3.95E-03	3.22E-02
CYFIP1	-----	ENSGALG00000016736	cytoplasmic FMR1 interacting protein 1	0.14	7.49180	10.56257	1.15E-03	1.33E-02
DNAJC10	-----	ENSGALG00000008862	DnaJ heat shock protein family (Hsp40) member C10	0.14	6.95216	8.12550	4.36E-03	3.45E-02
TARDBP	-----	ENSGALG00000002906	TAR DNA binding protein	0.14	6.95887	7.26923	7.01E-03	4.83E-02
EZH2	-----	ENSGALG00000043399	enhancer of zeste 2 polycomb repressive complex 2 subunit	0.14	7.23331	7.40500	6.50E-03	4.60E-02
RYK	-----	ENSGALG00000006488	receptor-like tyrosine kinase	0.14	6.41822	9.00065	2.70E-03	2.45E-02
FAM109B	-----	-----	family with sequence similarity 109, member B	0.14	6.98127	8.28774	3.99E-03	3.24E-02
GNB4	-----	ENSGALG00000008983	G protein subunit beta 4	0.14	8.41167	7.64491	5.69E-03	4.18E-02
MEMO1	-----	ENSGALG00000010624	mediator of cell motility 1	0.14	6.62089	7.41002	6.49E-03	4.60E-02
DARS	-----	ENSGALG00000012355	aspartyl-tRNA synthetase	0.14	7.51766	7.83355	5.13E-03	3.89E-02
COPG2	-----	ENSGALG00000008144	coatomer protein complex subunit gamma 2	0.14	7.02805	7.23220	7.16E-03	4.90E-02
UBE2G1	-----	ENSGALG00000001441	ubiquitin conjugating enzyme E2 G1	0.13	7.35639	7.21169	7.24E-03	4.94E-02
TAX1BP3	-----	ENSGALG00000004618	Tax1 binding protein 3	0.13	7.70103	7.73536	5.41E-03	4.03E-02
SEC13	SEC13L1	ENSGALG00000008419	SEC13 homolog, nuclear pore and COPII coat complex component	0.13	7.52425	7.24027	7.13E-03	4.89E-02
MSI2	-----	ENSGALG00000005567	musashi RNA binding protein 2	0.12	7.30733	7.69426	5.54E-03	4.10E-02

Gene name	Gene stable ID	Gene description	log2FC	logCPM	LR	PValue	FDR
LOC770705	-----	envelope glycoprotein gp95-like	-3.83	3.5830	39.9227	2.64E-10	3.51E-08
LOC107049175	-----	withdrawn	-3.57	-0.2832	51.8086	6.12E-13	1.55E-10
LOC107057413	-----	collagen alpha-1(I) chain-like	-3.43	1.4229	58.4631	2.07E-14	7.41E-12
ERNI	ENSGALG00010002022	early response to neural induction ERNI	-3.38	0.5707	40.1275	2.38E-10	3.21E-08
LOC107049890	-----	pre-mRNA-splicing factor CWC22-like	-3.36	0.2618	109.2566	1.43E-25	1.68E-22
LOC107049106	-----	withdrawn	-3.36	1.2159	83.2042	7.40E-20	6.09E-17
LOC776874	-----	uncharacterized LOC776874	-3.09	0.1795	63.5687	1.55E-15	7.28E-13
LOC107049408	-----	uncharacterized LOC107049408	-2.96	0.5184	34.4442	4.39E-09	4.17E-07
LOC112531874	-----	uncharacterized LOC112531874	-2.96	1.3292	32.2181	1.38E-08	1.17E-06
LOC107051278	-----	withdrawn	-2.79	1.4534	113.1360	2.01E-26	2.55E-23
HOXD11	ENSGALG00000039629	homeobox D11	-2.78	2.0347	7.3249	6.80E-03	4.73E-02
NPHS2	ENSGALG00000004163	NPHS2, podocin	-2.71	5.9236	19.7944	8.62E-06	2.91E-04
HOXA11	ENSGALG00000040021	homeobox A11	-2.60	0.8886	13.1208	2.92E-04	4.83E-03
LOC112531841	-----	uncharacterized LOC112531841	-2.47	-0.1148	24.9291	5.95E-07	3.12E-05
LOC112530433	-----	withdrawn	-2.45	1.4217	38.4635	5.58E-10	6.60E-08
LOC107051196	-----	withdrawn	-2.34	0.8007	19.1453	1.21E-05	3.77E-04
LOC112531766	-----	uncharacterized LOC112531766	-2.33	1.9104	61.4955	4.44E-15	1.74E-12
LOC112533579	-----	withdrawn	-2.33	1.0453	38.5655	5.29E-10	6.31E-08
LOC112531027	-----	withdrawn	-2.30	1.1980	38.8920	4.48E-10	5.42E-08
LOC112532782	-----	uncharacterized LOC112532782	-2.25	1.5293	84.1345	4.62E-20	4.00E-17
LOC107053233	-----	uncharacterized LOC107053233	-2.23	0.1156	47.2946	6.11E-12	1.29E-09
GSC	ENSGALG00000010974	goosecoid homeobox	-2.21	2.0263	15.0176	1.07E-04	2.16E-03
LOC101747821	-----	uncharacterized LOC101747821	-2.14	4.9115	39.7066	2.95E-10	3.82E-08
LOC112532134	-----	uncharacterized LOC112532134	-2.05	0.1194	29.1734	6.62E-08	4.76E-06
LOC112531014	-----	withdrawn	-2.04	0.2655	22.4415	2.17E-06	9.02E-05
LOC107052944	-----	withdrawn	-2.03	-0.2492	52.7948	3.70E-13	1.03E-10
LOC112531457	-----	withdrawn	-2.03	-0.3387	27.6143	1.48E-07	9.63E-06
MYH1F	ENSGALG00000042257	myosin, heavy chain 1F, skeletal muscle	-2.02	1.3999	20.2047	6.96E-06	2.42E-04
LOC107054528	-----	uncharacterized LOC107054528	-2.00	0.8390	51.8370	6.03E-13	1.55E-10
LOC107054238	-----	uncharacterized LOC107054238	-2.00	1.1706	14.8267	1.18E-04	2.34E-03
CD69L	-----	CD69 molecule like	-1.99	6.3941	36.3386	1.66E-09	1.77E-07
OPN4-1	ENSGALG00000041662	photopigment melanopsin-like	-1.98	1.2905	45.6812	1.39E-11	2.63E-09
CLC2BL1	-----	c-type lectin like 13, MHCY region	-1.97	2.3077	62.8385	2.24E-15	9.72E-13
POMC	ENSGALG00000016600	proopiomelanocortin	-1.95	-0.1350	18.6478	1.57E-05	4.67E-04
LOC107054230	-----	uncharacterized LOC107054230	-1.94	0.1815	47.1049	6.73E-12	1.37E-09
GIMAP1	-----	GIMAP1-GIMAP5 readthrough	-1.93	2.5829	149.4346	2.30E-34	7.58E-31
HOXA10	ENSGALG00000026631	homeobox A10	-1.93	0.9354	9.5798	1.97E-03	1.99E-02
LOC107049467	-----	uncharacterized LOC107049467	-1.87	3.1810	28.8176	7.95E-08	5.54E-06
LOC107049564	-----	uncharacterized LOC107049564	-1.86	1.9839	58.8550	1.70E-14	6.21E-12
LOC107053000	-----	uncharacterized LOC107053000	-1.84	0.9609	71.7903	2.39E-17	1.27E-14
SLC9A2	ENSGALG00000016791	solute carrier family 9 member A2	-1.82	0.0793	42.3935	7.46E-11	1.17E-08
LOC107057189	-----	withdrawn	-1.82	2.7086	42.3222	7.74E-11	1.19E-08

SST		somatostatin	-1.81	3.1571	25.7276	3.93E-07	2.20E-05
LOC107052779	-----	withdrawn	-1.80	0.7403	76.9193	1.78E-18	1.13E-15
LOC107052419	-----	withdrawn	-1.79	-0.1847	24.4238	7.73E-07	3.84E-05
LOC107055075	-----	withdrawn	-1.79	-0.1392	30.5064	3.33E-08	2.56E-06
TRBV19	ENSGALG00000014750	T cell receptor beta variable 19	-1.79	-0.4286	19.5641	9.73E-06	3.18E-04
LOC107056991	-----	withdrawn	-1.78	0.7548	20.8835	4.88E-06	1.81E-04
CCR4	ENSGALG00000039146	C-C motif chemokine receptor 4	-1.77	-0.1060	26.8226	2.23E-07	1.33E-05
MYH1D	ENSGALG00000027323	myosin, heavy chain 1D, skeletal muscle	-1.76	4.8111	19.5131	9.99E-06	3.24E-04
LOC112530773	-----	withdrawn	-1.76	2.7706	117.8886	1.83E-27	2.74E-24
YF5	ENSGALG00000047314	MHC class I antigen YF5	-1.74	0.7700	55.9557	7.41E-14	2.54E-11
LOC112531946	-----	withdrawn	-1.74	-0.9087	17.5967	2.73E-05	7.27E-04
LOC107052216	-----	uncharacterized LOC107052216	-1.72	0.8875	33.0242	9.10E-09	7.97E-07
LOC107049103	-----	proline-rich protein 36-like	-1.71	-0.4585	23.4500	1.28E-06	5.84E-05
LOC101748467	-----	G2/M phase-specific E3 ubiquitin-protein ligase-like	-1.69	-0.7904	15.1993	9.67E-05	2.02E-03
LOC107055072	-----	uncharacterized LOC107055072	-1.68	-0.6072	22.5898	2.01E-06	8.48E-05
LOC112531094	-----	withdrawn	-1.67	0.0306	39.2369	3.75E-10	4.68E-08
LOC112533488	-----	uncharacterized LOC112533488	-1.66	0.1181	36.1457	1.83E-09	1.91E-07
LOC107051988	-----	withdrawn	-1.66	-0.5014	18.1208	2.07E-05	5.78E-04
LOC107053477	-----	withdrawn	-1.64	4.1892	22.4785	2.13E-06	8.90E-05
LOC107052164	-----	uncharacterized LOC107052164	-1.64	-0.6131	22.0547	2.65E-06	1.07E-04
LOC107053870	-----	translation initiation factor IF-2-like	-1.63	2.4895	10.5706	1.15E-03	1.33E-02
LOC101748511	-----	uncharacterized LOC101748511	-1.62	0.5462	28.3316	1.02E-07	6.89E-06
HIST1H2A4L3	ENSGALG00000032645	histone cluster 1, H2A-IV-like 3	-1.61	-0.4712	28.8464	7.84E-08	5.49E-06
LOC101750546	-----	circumsporozoite protein-like	-1.61	0.3854	33.1317	8.61E-09	7.58E-07
LOC112531945	-----	uncharacterized LOC112531945	-1.61	0.2160	13.5177	2.36E-04	4.10E-03
CDKN1A	ENSGALG00000028318	cyclin dependent kinase inhibitor 1A	-1.60	0.9699	12.4588	4.16E-04	6.30E-03
C1QC	ENSGALG00000029669	complement C1q C chain	-1.60	0.5115	16.6195	4.57E-05	1.11E-03
LOC101750035	-----	G2/M phase-specific E3 ubiquitin-protein ligase-like	-1.59	1.2593	63.2869	1.79E-15	8.17E-13
MYH13	-----	myosin, heavy chain 13, skeletal muscle	-1.59	0.2335	11.6420	6.45E-04	8.74E-03
LOC107053886	-----	withdrawn	-1.57	2.3576	49.7580	1.74E-12	4.09E-10
LOC107053584	-----	uncharacterized LOC107053584	-1.56	-0.4039	21.1381	4.27E-06	1.62E-04
LOC101749515	-----	withdrawn	-1.56	0.3308	41.6956	1.07E-10	1.60E-08
LOC101749127	-----	uncharacterized LOC101749127	-1.55	-0.4074	20.7914	5.12E-06	1.89E-04
LOC107055074	-----	withdrawn	-1.54	0.2841	20.6338	5.56E-06	2.03E-04
LOC101752000	-----	uncharacterized LOC101752000	-1.52	0.1583	34.8831	3.50E-09	3.47E-07
FADS1L1	-----	fatty acid desaturase 1-like	-1.52	0.7620	19.1620	1.20E-05	3.75E-04
LOC112531034	-----	withdrawn	-1.50	1.7884	21.4520	3.63E-06	1.40E-04
C1QA	ENSGALG00000021569	complement C1q A chain	-1.50	0.8949	20.4098	6.25E-06	2.22E-04
UROC1	ENSGALG00000006306	urocanate hydratase 1	-1.49	2.3029	39.7228	2.93E-10	3.82E-08
LOC107055024	-----	uncharacterized LOC107055024	-1.49	0.8652	46.2974	1.02E-11	1.94E-09
CD44	ENSGALG00000039080	CD44 molecule (Indian blood group)	-1.49	1.7337	14.0232	1.81E-04	3.29E-03
ACKR4	ENSGALG00000041491	atypical chemokine receptor 4	-1.49	-0.1858	27.9939	1.22E-07	8.07E-06
LOC112533411	-----	protocadherin beta-15-like	-1.48	-0.6070	15.2921	9.21E-05	1.94E-03
LOC107054516	-----	uncharacterized LOC107054516	-1.47	0.1094	19.7021	9.05E-06	2.99E-04

LOC107053122	-----	endogenous retrovirus group K member 18 Pol protein-like	-1.46	1.3590	15.4499	8.47E-05	1.82E-03
VCAM1	ENSGALG00000005257	vascular cell adhesion molecule 1	-1.46	-0.1018	15.6032	7.81E-05	1.72E-03
LOC112532661	-----	uncharacterized LOC112532661	-1.45	0.4106	37.6133	8.63E-10	9.79E-08
C14orf180	ENSGALG00000053336	chromosome 14 open reading frame 180	-1.45	-0.4925	9.2377	2.37E-03	2.25E-02
C1QB	ENSGALG00000004771	complement C1q B chain	-1.44	0.6999	14.5875	1.34E-04	2.58E-03
LOC112532651	-----	uncharacterized LOC112532651	-1.43	-0.9547	14.4186	1.46E-04	2.78E-03
LOC100859625	-----	uncharacterized LOC100859625	-1.43	1.3269	26.1392	3.18E-07	1.83E-05
LOC112532141	-----	withdrawn	-1.43	2.1305	10.7123	1.06E-03	1.26E-02
LOC112530090	-----	small nucleolar RNA SNORD49	-1.42	0.0995	17.2964	3.20E-05	8.22E-04
LOC107050560	-----	protocadherin beta-15-like	-1.41	-0.1443	8.7364	3.12E-03	2.71E-02
LOC112531208	-----	withdrawn	-1.41	3.4992	22.1792	2.48E-06	1.02E-04
CERS4L	-----	ceramide synthase 4-like	-1.40	-0.9479	15.1877	9.73E-05	2.02E-03
LOC107051926	-----	uncharacterized LOC107051926	-1.39	2.3194	43.5600	4.11E-11	6.82E-09
LOC107051856	-----	withdrawn	-1.38	-0.8604	11.1092	8.59E-04	1.07E-02
GUCA1C	ENSGALG00000015364	guanylate cyclase activator 1C	-1.37	1.9929	11.9129	5.57E-04	7.88E-03
LOC107050024	-----	withdrawn	-1.37	2.1710	31.1484	2.39E-08	1.90E-06
LOC107054094	-----	withdrawn	-1.35	-0.6452	10.8485	9.89E-04	1.19E-02
LOC112531155	-----	withdrawn	-1.35	5.4080	124.2262	7.52E-29	1.37E-25
LOC107049730	-----	protocadherin beta-15-like	-1.34	1.3557	20.3810	6.35E-06	2.25E-04
LOC107051715	-----	uncharacterized LOC107051715	-1.34	-0.5309	16.2199	5.64E-05	1.32E-03
LOC112532459	-----	small nucleolar RNA SNORA26	-1.34	0.2309	14.6360	1.30E-04	2.55E-03
NAT8	ENSGALG00000050294	N-acetyltransferase 8 (GCN5-related, putative)	-1.33	1.8156	40.2256	2.26E-10	3.10E-08
LOC112530111	-----	uncharacterized LOC112530111	-1.33	0.7827	23.8761	1.03E-06	4.87E-05
LOC101751866	-----	uncharacterized LOC101751866	-1.33	-0.0816	23.5966	1.19E-06	5.48E-05
ACHE	ENSGALG00000047182	acetylcholinesterase (Cartwright blood group)	-1.33	4.7552	82.3940	1.11E-19	8.74E-17
LOC107054189	-----	uncharacterized LOC107054189	-1.33	-0.5886	12.9260	3.24E-04	5.21E-03
LOC107054055	-----	withdrawn	-1.32	1.2740	28.6882	8.50E-08	5.83E-06
LOC112533200	-----	withdrawn	-1.32	0.8788	22.0806	2.61E-06	1.06E-04
LOC107057188	-----	borealin-like	-1.32	5.8994	48.9107	2.68E-12	6.12E-10
TIMD4	ENSGALG00000003876	T-cell immunoglobulin and mucin domain containing 4	-1.32	0.6782	21.0526	4.47E-06	1.68E-04
LOC107054707	-----	withdrawn	-1.32	1.4918	31.7419	1.76E-08	1.47E-06
PFKFB4	ENSGALG00000032385	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	-1.31	1.7097	36.5918	1.46E-09	1.59E-07
LOC107049676	-----	uncharacterized LOC107049676	-1.31	-0.3008	7.3558	6.68E-03	4.68E-02
LOC101748554	-----	uncharacterized LOC101748554	-1.31	-0.6596	15.0139	1.07E-04	2.16E-03
TOR1BL	ENSGALG00000023709	torsin family 1, member B-like	-1.31	-0.7463	14.1319	1.70E-04	3.15E-03
LOC107052166	-----	uncharacterized LOC107052166	-1.31	-0.6254	15.5180	8.17E-05	1.78E-03
LOC101748762	-----	uncharacterized LOC101748762	-1.30	-0.1021	20.4451	6.14E-06	2.20E-04
CCL26	ENSGALG00000014585	C-C motif chemokine ligand 26	-1.30	0.0391	17.7663	2.50E-05	6.75E-04
LOC112532055	-----	uncharacterized LOC112532055	-1.29	0.3688	22.3064	2.32E-06	9.66E-05
LOC112532631	-----	uncharacterized LOC112532631	-1.29	-0.0652	9.3475	2.23E-03	2.17E-02
KRT9L	-----	keratin, type I cytoskeletal 9-like	-1.29	0.1826	29.6588	5.15E-08	3.80E-06
TLX1	ENSGALG00000007831	T-cell leukemia homeobox 1	-1.28	-0.1156	10.0592	1.52E-03	1.63E-02
LOC101747910	-----	uncharacterized LOC101747910	-1.26	1.0686	51.8017	6.14E-13	1.55E-10
LOC112531200	-----	withdrawn	-1.26	0.0957	18.8667	1.40E-05	4.26E-04

OGN	ENSGALG000000026736	osteoglycin	-1.26	3.3039	18.0957	2.10E-05	5.84E-04
IP6K3	ENSGALG000000026536	inositol hexakisphosphate kinase 3	-1.26	0.2558	21.8882	2.89E-06	1.15E-04
GLRA4	ENSGALG000000004936	glycine receptor alpha 4	-1.26	1.8450	30.5518	3.25E-08	2.51E-06
ZP3L1	-----	zona pellucida sperm-binding protein 3-like	-1.26	-0.1198	20.1940	7.00E-06	2.43E-04
LOC107053858	-----	uncharacterized LOC107053858	-1.26	-0.8405	11.0724	8.76E-04	1.09E-02
PHF24	ENSGALG000000001900	PHD finger protein 24	-1.25	0.8339	17.4179	3.00E-05	7.85E-04
ECM2	ENSGALG000000004695	extracellular matrix protein 2	-1.25	3.0014	44.0048	3.28E-11	5.61E-09
NRXN3	ENSGALG000000027255	neurexin 3	-1.25	2.7336	35.5530	2.48E-09	2.52E-07
HAL	ENSGALG000000011421	histidine ammonia-lyase	-1.25	2.0860	27.2704	1.77E-07	1.11E-05
DRD2	ENSGALG000000007794	dopamine receptor D2	-1.25	-0.0675	17.0046	3.73E-05	9.40E-04
LOC112533486	-----	withdrawn	-1.25	1.2086	30.7156	2.99E-08	2.32E-06
SHOX	ENSGALG000000016698	short stature homeobox	-1.24	1.0476	7.1853	7.35E-03	5.00E-02
LOC107049937	-----	solute carrier family 2, facilitated glucose transporter member 4-like	-1.24	0.5272	23.2300	1.44E-06	6.42E-05
MROH2BL2	-----	maestro heat-like repeat-containing protein family member 2B	-1.23	-0.8546	9.9854	1.58E-03	1.68E-02
LOC112530427	-----	withdrawn	-1.23	3.1434	10.5478	1.16E-03	1.34E-02
LOC112532894	-----	uncharacterized LOC112532894	-1.23	2.0193	36.6773	1.39E-09	1.54E-07
TMEM61	ENSGALG000000010801	transmembrane protein 61	-1.23	2.2488	14.6135	1.32E-04	2.56E-03
LOC112533473	-----	withdrawn	-1.23	-0.5365	14.6277	1.31E-04	2.55E-03
LOC107049565	-----	uncharacterized LOC107049565	-1.21	1.1272	22.8171	1.78E-06	7.72E-05
TDRD5	ENSGALG000000033634	tudor domain containing 5	-1.21	0.3269	16.3951	5.14E-05	1.22E-03
LOC112531252	-----	withdrawn	-1.21	1.3395	11.8205	5.86E-04	8.12E-03
FFAR4	ENSGALG000000026733	free fatty acid receptor 4	-1.21	-0.7963	12.6217	3.81E-04	5.90E-03
LOC112533409	-----	withdrawn	-1.21	1.0258	19.4386	1.04E-05	3.35E-04
LOC107054197	-----	withdrawn	-1.20	0.0800	18.6578	1.56E-05	4.65E-04
LOC101748439	-----	uncharacterized LOC101748439	-1.20	2.4470	13.4069	2.51E-04	4.31E-03
LOC107057093	-----	c-type lectin like 17, MHCY region	-1.20	-0.3664	17.3489	3.11E-05	8.09E-04
LOC101748259	-----	uncharacterized LOC101748259	-1.20	2.2407	14.4520	1.44E-04	2.75E-03
SLC6A19	ENSGALG000000019527	solute carrier family 6 member 19	-1.20	0.0204	19.1867	1.19E-05	3.74E-04
LOC101751481	-----	withdrawn	-1.20	-0.6135	11.3453	7.56E-04	9.80E-03
LOC112531018	-----	withdrawn	-1.20	1.0949	20.3118	6.58E-06	2.31E-04
CAPN13	ENSGALG000000020084	calpain 13	-1.19	-0.6607	10.5451	1.16E-03	1.34E-02
LOC425214	-----	withdrawn	-1.19	2.1665	29.4373	5.78E-08	4.21E-06
LRIT2	ENSGALG000000002307	leucine rich repeat, Ig-like and transmembrane domains 2	-1.19	-0.0662	7.8774	5.01E-03	3.83E-02
LOC100859202	-----	c-type lectin like 17, MHCY region	-1.19	0.0656	15.4128	8.64E-05	1.85E-03
LOC100857473	-----	alpha-1,2-mannosyltransferase ALG9-like	-1.18	2.0710	49.1459	2.38E-12	5.51E-10
TLR7	ENSGALG000000016590	toll like receptor 7	-1.18	0.1917	9.6154	1.93E-03	1.96E-02
LOC769128	-----	withdrawn	-1.18	-0.3311	16.2212	5.64E-05	1.32E-03
LOC107054803	-----	withdrawn	-1.17	-0.5491	8.9354	2.80E-03	2.51E-02
WISP1	ENSGALG000000030115	WNT1 inducible signaling pathway protein 1	-1.17	0.6096	15.1615	9.87E-05	2.04E-03
CNGA3	ENSGALG000000039826	cyclic nucleotide gated channel alpha 3	-1.17	3.7080	24.6941	6.72E-07	3.47E-05
LOC107051325	-----	uncharacterized LOC107051325	-1.17	-0.1867	12.9022	3.28E-04	5.26E-03
LOC107054433	-----	uncharacterized LOC107054433	-1.17	1.2119	18.5614	1.65E-05	4.84E-04
YF6	-----	major histocompatibility complex Y, class I heavy chain 4	-1.16	2.1438	36.4422	1.57E-09	1.70E-07
LOC101748035	-----	uncharacterized LOC101748035	-1.16	0.1557	20.5678	5.76E-06	2.08E-04

LOC107052408	-----	uncharacterized LOC107052408	-1.16	1.4291	15.8253	6.95E-05	1.57E-03
FAM135B	ENSGALG00000039831	family with sequence similarity 135 member B	-1.15	-0.5442	8.4234	3.70E-03	3.09E-02
LOC107055022	-----	uncharacterized LOC107055022	-1.15	-0.5479	9.4654	2.09E-03	2.08E-02
LOC101750579	-----	uncharacterized LOC101750579	-1.14	1.3095	18.5637	1.64E-05	4.84E-04
LOC100859665	-----	uncharacterized LOC100859665	-1.14	-0.4256	11.1401	8.45E-04	1.06E-02
ANXA13	ENSGALG00000036418	annexin A13	-1.14	-0.4609	10.5486	1.16E-03	1.34E-02
LOC112531893	-----	withdrawn	-1.13	4.8767	67.9387	1.69E-16	8.41E-14
TSHR	ENSGALG00000010572	thyroid stimulating hormone receptor	-1.13	-0.3684	11.4443	7.17E-04	9.44E-03
BG8	ENSGALG00000049461	MHC B-G antigen	-1.13	3.8175	66.9738	2.75E-16	1.33E-13
DIRAS2	ENSGALG00000005323	DIRAS family GTPase 2	-1.13	0.6415	10.1380	1.45E-03	1.58E-02
FRMPD3	ENSGALG00000028975	FERM and PDZ domain containing 3	-1.12	2.5916	12.0915	5.07E-04	7.33E-03
LOC101751606	-----	withdrawn	-1.12	-0.6816	9.8348	1.71E-03	1.78E-02
LOC107054464	-----	withdrawn	-1.12	0.4291	9.1950	2.43E-03	2.28E-02
COR8	-----	olfactory receptor family 5 subfamily J member 2	-1.12	0.4188	11.5562	6.75E-04	9.05E-03
LOC112530987	-----	trichohyalin-like	-1.12	1.4065	33.4620	7.27E-09	6.53E-07
LOC100857439	-----	histone H3.2-like	-1.11	-0.7538	11.3204	7.67E-04	9.88E-03
SH3RF2	ENSGALG00000043904	SH3 domain containing ring finger 2	-1.11	-0.2390	17.0165	3.71E-05	9.35E-04
LOC101747844	-----	carbohydrate sulfotransferase 9-like	-1.11	1.8658	16.9590	3.82E-05	9.60E-04
THRB	ENSGALG00000011294	thyroid hormone receptor beta	-1.10	1.8904	8.4576	3.64E-03	3.05E-02
TDRD15	ENSGALG00000016492	tudor domain containing 15	-1.09	0.7286	11.1719	8.30E-04	1.05E-02
LOC101750063	-----	uncharacterized LOC101750063	-1.09	0.8986	14.2687	1.58E-04	2.96E-03
MOG	ENSGALG00000022875	myelin oligodendrocyte glycoprotein	-1.09	0.9298	15.0505	1.05E-04	2.14E-03
LDHD	ENSGALG00000048399	lactate dehydrogenase D	-1.09	2.1942	16.1696	5.79E-05	1.35E-03
PTER	ENSGALG00000008728	phosphotriesterase related	-1.09	4.7433	77.1523	1.58E-18	1.04E-15
LOC101747727	-----	uncharacterized LOC101747727	-1.08	2.1762	27.4037	1.65E-07	1.05E-05
LOC112533302	-----	withdrawn	-1.08	-0.1280	12.1028	5.03E-04	7.30E-03
LOC416951	-----	uncharacterized LOC416951	-1.08	-0.6478	8.4652	3.62E-03	3.03E-02
LOC107051082	-----	withdrawn	-1.08	6.6021	54.2742	1.74E-13	5.74E-11
LOC101751655	-----	uncharacterized LOC101751655	-1.07	-0.0644	13.4674	2.43E-04	4.20E-03
TRPM2	ENSGALG00000005631	transient receptor potential cation channel subfamily M member 2	-1.07	2.5581	25.8265	3.74E-07	2.12E-05
LOC112532477	-----	fibrinogen-like protein 1-like protein	-1.07	1.0951	27.0347	2.00E-07	1.22E-05
LOC107053147	-----	uncharacterized LOC107053147	-1.07	0.2723	8.3908	3.77E-03	3.12E-02
LOC112533187	-----	withdrawn	-1.07	1.5061	16.1902	5.73E-05	1.34E-03
LRIT1	ENSGALG00000002303	leucine rich repeat, Ig-like and transmembrane domains 1	-1.07	2.3944	7.4108	6.48E-03	4.60E-02
LOC107054716	-----	uncharacterized LOC107054716	-1.07	-0.9416	9.2358	2.37E-03	2.25E-02
TMC3	ENSGALG00000006376	transmembrane channel like 3	-1.06	2.2190	17.3176	3.16E-05	8.17E-04
LOC101748916	-----	extensin-like	-1.06	6.2215	88.3271	5.55E-21	5.07E-18
HIST1H2A3	ENSGALG00000049268	histone cluster 1, H2A, III	-1.06	0.0473	11.3444	7.57E-04	9.80E-03
PROX2	-----	prospero homeobox 2	-1.06	0.5407	18.9468	1.34E-05	4.11E-04
TBX15	ENSGALG00000014776	T-box 15	-1.05	4.9235	9.9786	1.58E-03	1.69E-02
LOC107053136	-----	uncharacterized LOC107053136	-1.05	-0.7293	7.8612	5.05E-03	3.84E-02
CMYA5	ENSGALG00000026553	cardiomyopathy associated 5	-1.05	1.1028	11.3136	7.69E-04	9.90E-03
MSX2	ENSGALG00000038848	msh homeobox 2	-1.05	4.2172	9.6171	1.93E-03	1.96E-02
MR1	-----	major histocompatibility complex Y, class I heavy chain like	-1.05	2.0465	24.6020	7.05E-07	3.61E-05

CD300LG	ENSGALG00000007713	CD300 molecule like family member g	-1.04	1.7064	41.2373	1.35E-10	1.98E-08
LOC107052834	-----	withdrawn	-1.04	2.3910	14.5560	1.36E-04	2.62E-03
LOC112531637	-----	small nucleolar RNA SNORA40	-1.03	0.7744	13.3099	2.64E-04	4.49E-03
TMEM8C	ENSGALG000000021520	transmembrane protein 8C	-1.03	-0.0793	9.8864	1.67E-03	1.75E-02
LOC107052588	-----	withdrawn	-1.03	0.5329	11.7805	5.99E-04	8.27E-03
TNFRSF10B	ENSGALG00000000452	tumor necrosis factor receptor superfamily, member 10b	-1.03	3.0715	21.7413	3.12E-06	1.24E-04
LOC112530989	-----	periodic tryptophan protein 2 homolog	-1.03	-0.1656	7.4942	6.19E-03	4.45E-02
UBXN11	ENSGALG000000054685	UBX domain protein 11	-1.03	0.4344	18.5650	1.64E-05	4.84E-04
FMO3	ENSGALG000000040573	flavin containing monooxygenase 3	-1.02	0.3124	14.0714	1.76E-04	3.24E-03
LOC112530944	-----	withdrawn	-1.02	1.1667	15.3056	9.14E-05	1.93E-03
CX3CR1	ENSGALG000000038000	C-X3-C motif chemokine receptor 1	-1.02	-0.3079	9.0877	2.57E-03	2.37E-02
SYTL2L	ENSGALG000000008326	synaptotagmin-like protein 2-like	-1.01	0.8700	18.8265	1.43E-05	4.34E-04
TMEM163	ENSGALG000000012190	transmembrane protein 163	-1.01	2.5935	24.3814	7.90E-07	3.92E-05
LOC112533550	-----	withdrawn	-1.01	-0.5442	8.3024	3.96E-03	3.22E-02
LOC112531154	-----	withdrawn	-1.01	3.6098	31.3933	2.11E-08	1.72E-06
TGM3	ENSGALG000000004804	transglutaminase 3	-1.01	0.0482	11.1602	8.36E-04	1.06E-02
CDH10	ENSGALG000000032022	cadherin 10	-1.01	1.3337	9.8263	1.72E-03	1.79E-02
LOC101748470	-----	uncharacterized LOC101748470	-1.01	0.2654	15.5571	8.01E-05	1.75E-03
NDST4	ENSGALG000000012015	N-deacetylase and N-sulfotransferase 4	-1.01	0.9871	23.3553	1.35E-06	6.09E-05
CHRNA10	ENSGALG000000007906	cholinergic receptor nicotinic gamma subunit	-1.00	1.9579	19.2824	1.13E-05	3.60E-04
ANKK1	ENSGALG000000007815	ankyrin repeat and kinase domain containing 1	-1.00	0.9434	10.7645	1.03E-03	1.23E-02
LOC107051247	-----	uncharacterized LOC107051247	-0.99	0.5967	14.2528	1.60E-04	2.98E-03
CHRNA10	ENSGALG000000022702	cholinergic receptor, nicotinic, alpha 10 (neuronal)	-0.99	0.9824	10.9502	9.36E-04	1.15E-02
IGSF5	ENSGALG000000016132	immunoglobulin superfamily member 5	-0.99	-0.4849	10.4920	1.20E-03	1.37E-02
MYL2	ENSGALG000000004582	myosin, light chain 2, regulatory, cardiac, slow	-0.99	2.3645	10.5889	1.14E-03	1.32E-02
LOC771200	-----	uncharacterized LOC771200	-0.99	2.4641	23.9572	9.85E-07	4.76E-05
LOC107054020	-----	uncharacterized LOC107054020	-0.99	-0.1544	7.3347	6.76E-03	4.72E-02
C5H14orf159	ENSGALG000000010703	chromosome 5 C14orf159 homolog	-0.99	3.1955	62.7268	2.37E-15	1.00E-12
USH1G	ENSGALG000000038769	USH1 protein network component sans	-0.99	-0.8892	7.7667	5.32E-03	3.99E-02
NCAM2	ENSGALG000000015737	neural cell adhesion molecule 2	-0.98	2.0462	11.5257	6.86E-04	9.15E-03
FSHR	ENSGALG000000009100	follicle stimulating hormone receptor	-0.98	0.5245	8.8798	2.88E-03	2.58E-02
LOC107049782	-----	uncharacterized LOC107049782	-0.98	0.5337	10.4243	1.24E-03	1.40E-02
ADMP	ENSGALG000000037408	anti-dorsalizing morphogenetic protein	-0.97	-0.8098	7.8708	5.02E-03	3.83E-02
LOC112531854	-----	uncharacterized LOC112531854	-0.97	1.4673	19.6333	9.38E-06	3.08E-04
PLSCR5	ENSGALG000000006807	phospholipid scramblase family member 5	-0.97	1.7322	24.2189	8.60E-07	4.25E-05
LOC416695	-----	tubulin alpha-3 chain-like	-0.97	2.4335	35.2768	2.86E-09	2.87E-07
SIRPA	ENSGALG000000025778	signal-regulatory protein alpha	-0.97	2.0011	20.1774	7.06E-06	2.45E-04
LOC101747373	-----	uncharacterized LOC101747373	-0.96	4.7909	72.9961	1.30E-17	7.13E-15
NRSN2	-----	neurensin 2	-0.96	-0.6441	8.0680	4.51E-03	3.54E-02
C31H17orf49	-----	chromosome unknown C17orf49 homolog	-0.96	5.4093	127.5499	1.41E-29	2.90E-26
DLX3	ENSGALG000000040529	distal-less homeobox 3	-0.96	1.4655	7.9152	4.90E-03	3.77E-02
ABCA13	-----	ATP-binding cassette, sub-family A (ABC1), member 13	-0.95	-0.6732	8.9546	2.77E-03	2.49E-02
LOC107055338	-----	uncharacterized LOC107055338	-0.95	-0.3273	9.0576	2.62E-03	2.40E-02
AOAH	ENSGALG000000035505	acyloxyacyl hydrolase	-0.95	1.9665	13.3487	2.59E-04	4.42E-03

ADAM5P	ENSGALG00000009606	ADAM metallopeptidase domain 5, pseudogene	-0.95	1.6585	33.5602	6.91E-09	6.25E-07
LOC101749363	-----	uncharacterized LOC101749363	-0.95	4.3702	34.1263	5.16E-09	4.86E-07
LOC101750312	-----	uncharacterized LOC101750312	-0.95	1.2905	12.7718	3.52E-04	5.54E-03
LOC112532770	-----	putative methyltransferase DDB_G0268948	-0.95	4.8362	44.4035	2.67E-11	4.68E-09
MB	ENSGALG000000012541	myoglobin	-0.95	0.8093	7.4822	6.23E-03	4.47E-02
AKR1D1	ENSGALG000000012834	aldo-keto reductase family 1 member D1	-0.95	5.8071	47.1968	6.42E-12	1.34E-09
LOC112531894	-----	VPS28 subunit of ESCRT-I	-0.95	6.0543	167.4991	2.60E-38	1.07E-34
LOC107051491	-----	withdrawn	-0.94	4.3215	25.8916	3.61E-07	2.06E-05
LOC112530177	-----	uncharacterized LOC112530177	-0.94	-0.5097	8.7506	3.09E-03	2.70E-02
PXDNL	ENSGALG000000036838	peroxidasin like	-0.94	2.7196	10.5981	1.13E-03	1.32E-02
NPBWR2	ENSGALG000000029170	neuropeptides B and W receptor 2	-0.94	-0.2248	9.2074	2.41E-03	2.27E-02
LOC112529916	-----	small nucleolar SNORD12/SNORD106	-0.94	1.1979	19.4765	1.02E-05	3.29E-04
LOC112532269	-----	uncharacterized LOC112532269	-0.94	0.2725	16.0060	6.31E-05	1.45E-03
CRB1	ENSGALG000000002287	crumbs cell polarity complex component 1	-0.93	2.1877	14.3448	1.52E-04	2.86E-03
LOC112532647	-----	uncharacterized LOC112532647	-0.93	0.7096	14.3633	1.51E-04	2.84E-03
LDLRAD1	ENSGALG000000020647	low density lipoprotein receptor class A domain containing 1	-0.93	3.0225	32.6531	1.10E-08	9.54E-07
LOC100859819	-----	cocaine- and amphetamine-regulated transcript protein-like	-0.93	0.6455	15.5078	8.22E-05	1.78E-03
LOC101748820	-----	uncharacterized LOC101748820	-0.93	1.9421	8.8674	2.90E-03	2.58E-02
DLGAP1L	-----	-----	-0.93	-0.3793	9.9291	1.63E-03	1.72E-02
LOC101747354	-----	alanine and glycine-rich protein-like	-0.93	-0.6566	8.3417	3.87E-03	3.17E-02
LOC107054704	-----	major histocompatibility complex Y, class I heavy chain 36	-0.93	1.6416	16.1938	5.72E-05	1.33E-03
CPXM2	-----	carboxypeptidase X, M14 family member 2	-0.93	0.6144	8.6400	3.29E-03	2.82E-02
PTPRQ	ENSGALG000000010935	protein tyrosine phosphatase, receptor type Q	-0.92	4.6318	25.5327	4.35E-07	2.40E-05
LOC101747644	-----	uncharacterized LOC101747644	-0.92	-0.7038	8.8103	3.00E-03	2.64E-02
TACR1	ENSGALG000000036638	tachykinin receptor 1	-0.92	-0.4400	10.0426	1.53E-03	1.64E-02
LOC112533261	-----	uncharacterized LOC112533261	-0.92	-0.5360	7.9129	4.91E-03	3.78E-02
LOC421892	-----	transcription elongation factor B polypeptide 3-like	-0.92	0.3373	10.2842	1.34E-03	1.48E-02
LOC112530519	-----	translation initiation factor IF-2	-0.92	-0.6255	8.3797	3.79E-03	3.13E-02
TLR2A	ENSGALG000000034722	toll-like receptor 2 family member A	-0.92	1.7878	12.0189	5.27E-04	7.54E-03
HIST1H4I	ENSGALG000000048097	histone cluster 1, H4i	-0.92	2.6999	21.4858	3.56E-06	1.38E-04
AQP3	ENSGALG000000002452	aquaporin 3 (Gill blood group)	-0.91	1.9235	9.5944	1.95E-03	1.98E-02
TUBA4B	-----	-----	-0.91	1.1991	18.3617	1.83E-05	5.23E-04
CYSLTR1	ENSGALG000000004128	cysteinyl leukotriene receptor 1	-0.91	3.1795	47.6275	5.15E-12	1.13E-09
AWAT1	ENSGALG000000004367	acyl-CoA wax alcohol acyltransferase 1	-0.91	1.4629	21.6427	3.28E-06	1.29E-04
NPR1	ENSGALG000000015753	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	-0.91	0.3596	11.3495	7.55E-04	9.79E-03
TMEM68L	-----	-----	-0.91	0.6544	12.9185	3.25E-04	5.22E-03
LOC112532643	-----	uncharacterized LOC112532643	-0.90	-0.6656	7.3664	6.65E-03	4.67E-02
DYNLRB2	ENSGALG000000005402	dynein light chain roadblock-type 2	-0.89	1.7377	10.0742	1.50E-03	1.62E-02
F7	ENSGALG000000016833	coagulation factor VII	-0.89	-0.4675	8.9886	2.72E-03	2.46E-02
LOC112531865	-----	uncharacterized LOC112531865	-0.89	-0.4476	7.9000	4.94E-03	3.80E-02
RASGRF2	ENSGALG000000015598	Ras protein specific guanine nucleotide releasing factor 2	-0.89	2.3171	17.5854	2.75E-05	7.30E-04
LOC112533090	-----	small Cajal body-specific RNA 6	-0.89	-0.1418	7.6745	5.60E-03	4.13E-02
SPTSSBL	ENSGALG000000048373	serine palmitoyltransferase small subunit B-like	-0.89	1.6928	20.2231	6.89E-06	2.41E-04
LOC112530210	-----	uncharacterized LOC112530210	-0.88	0.5528	9.0453	2.63E-03	2.41E-02

LOC112531846	-----	uncharacterized LOC112531846	-0.88	1.7800	11.3695	7.47E-04	9.70E-03
SP9	ENSGALG00000043079	Sp9 transcription factor	-0.88	-0.5359	7.3397	6.74E-03	4.71E-02
LOC107049660	-----	glycogen phosphorylase, muscle form-like	-0.88	1.1245	14.4569	1.43E-04	2.75E-03
LOC107054255	-----	uncharacterized LOC107054255	-0.88	0.1284	10.2935	1.34E-03	1.48E-02
KCNK18	ENSGALG00000009265	potassium two pore domain channel subfamily K member 18	-0.88	0.7770	10.3650	1.28E-03	1.44E-02
THEMIS2	ENSGALG00000000731	thymocyte selection associated family member 2	-0.88	1.1781	10.2958	1.33E-03	1.48E-02
TNFSF13B	ENSGALG00000016852	tumor necrosis factor superfamily member 13b	-0.88	0.2918	8.2654	4.04E-03	3.27E-02
ITGBL1	ENSGALG00000016867	integrin subunit beta like 1	-0.87	1.1139	15.8228	6.96E-05	1.57E-03
RNASEK	ENSGALG00000050001	ribonuclease K	-0.87	7.1111	139.7589	3.01E-32	8.24E-29
CLDN9	-----	-----	-0.87	-0.0349	12.4765	4.12E-04	6.26E-03
ACTR10L	-----	actin related protein 10-like	-0.87	3.6453	24.5135	7.38E-07	3.73E-05
MYH1G	ENSGALG00000028612	myosin, heavy chain 1G, skeletal muscle	-0.87	0.8824	7.5569	5.98E-03	4.33E-02
SCML4	-----	Scm polycomb group protein like 4	-0.87	3.9183	17.5725	2.77E-05	7.33E-04
BEST4	ENSGALG00000043605	bestrophin 4	-0.87	1.3020	9.5522	2.00E-03	2.01E-02
PCSK9	ENSGALG00000047448	proprotein convertase subtilisin/kexin type 9	-0.87	0.1239	8.0626	4.52E-03	3.55E-02
LOC107050768	-----	histone-lysine N-methyltransferase SETD1A-like	-0.86	5.9723	17.0174	3.70E-05	9.35E-04
TRPA1	ENSGALG00000034751	transient receptor potential cation channel subfamily A member 1	-0.86	1.1498	9.0953	2.56E-03	2.37E-02
SLC5A7	ENSGALG00000016804	solute carrier family 5 member 7	-0.86	3.8045	8.3261	3.91E-03	3.20E-02
ST8SIA3Z	ENSGALG00000039151	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3-Z	-0.86	0.9577	9.3143	2.27E-03	2.19E-02
LOC107052234	-----	uncharacterized LOC107052234	-0.86	1.7663	18.9072	1.37E-05	4.18E-04
PAK6	-----	p21 (RAC1) activated kinase 6	-0.86	1.2269	14.0701	1.76E-04	3.24E-03
TNR	ENSGALG00000004526	tenascin R	-0.86	0.7556	8.2194	4.14E-03	3.33E-02
LOC112531887	-----	uncharacterized LOC112531887	-0.86	1.8382	9.3653	2.21E-03	2.16E-02
ASIP	ENSGALG00000039101	agouti signaling protein	-0.85	1.3824	7.3685	6.64E-03	4.66E-02
CRYBA2	ENSGALG00000011354	crystallin beta A2	-0.85	0.5738	9.4605	2.10E-03	2.08E-02
TRPM8	ENSGALG00000004116	transient receptor potential cation channel subfamily M member 8	-0.85	0.1614	10.9820	9.20E-04	1.13E-02
LOC107054371	-----	uncharacterized LOC107054371	-0.85	-0.3310	9.5429	2.01E-03	2.02E-02
TRIM39.2	ENSGALG00000037170	tripartite motif containing 39.2	-0.85	-0.2506	8.9352	2.80E-03	2.51E-02
LOC112531323	-----	nephrin-like	-0.85	0.3236	8.7506	3.10E-03	2.70E-02
TRIM65	-----	tripartite motif containing 65	-0.84	1.9285	15.0642	1.04E-04	2.13E-03
LOC101749220	-----	uncharacterized LOC101749220	-0.84	1.3203	12.9234	3.25E-04	5.21E-03
LEFTY2	ENSGALG00010017549	left-right determination factor 1	-0.84	1.6610	13.0996	2.95E-04	4.87E-03
ITGB4	ENSGALG00000002389	integrin subunit beta 4	-0.84	2.5900	29.7481	4.92E-08	3.66E-06
LOC112532409	-----	uncharacterized LOC112532409	-0.84	1.7056	13.9499	1.88E-04	3.40E-03
IL16	ENSGALG00000006388	interleukin 16	-0.84	1.8450	13.1206	2.92E-04	4.83E-03
LOC107049615	-----	withdrawn	-0.84	3.4636	19.7546	8.80E-06	2.96E-04
NTN4	ENSGALG00000011406	netrin 4	-0.83	2.2899	18.5214	1.68E-05	4.89E-04
LOC112532757	-----	uncharacterized LOC112532757	-0.83	0.1231	7.9419	4.83E-03	3.74E-02
LOC112531521	-----	uncharacterized LOC112531521	-0.83	-0.2687	11.5134	6.91E-04	9.19E-03
ITIH6	-----	inter-alpha-trypsin inhibitor heavy chain family member 6	-0.83	1.5468	12.6418	3.77E-04	5.86E-03
HOXA9	ENSGALG00000028983	homeobox A9	-0.83	4.4537	10.3578	1.29E-03	1.44E-02
TNNI3K	ENSGALG00000011353	TNNI3 interacting kinase	-0.83	0.0924	7.4181	6.46E-03	4.60E-02
LOC112532925	-----	uncharacterized LOC112532925	-0.83	-0.4197	7.2729	7.00E-03	4.83E-02
CXCR1	ENSGALG00000036627	C-X-C motif chemokine receptor 1	-0.82	0.0681	10.5414	1.17E-03	1.34E-02

F13A1	ENSGALG00000012802	coagulation factor XIII A chain	-0.82	0.5466	8.9228	2.82E-03	2.53E-02
EDA2R	ENSGALG00000031094	ectodysplasin A2 receptor	-0.82	2.9892	9.4860	2.07E-03	2.07E-02
NEK10	ENSGALG00000011322	NIMA related kinase 10	-0.82	0.3430	10.9420	9.40E-04	1.15E-02
SLC5A1	ENSGALG00000006728	solute carrier family 5 member 1	-0.82	1.6325	20.5742	5.74E-06	2.08E-04
LOC107053028	-----	uncharacterized LOC107053028	-0.82	1.1374	9.4789	2.08E-03	2.07E-02
ABLIM3	ENSGALG00000002790	actin binding LIM protein family member 3	-0.82	2.6373	33.3213	7.81E-09	6.95E-07
GAL	ENSGALG00000007047	galanin and GMAP prepropeptide	-0.82	0.9198	9.0468	2.63E-03	2.41E-02
LOC112532982	-----	uncharacterized LOC112532982	-0.81	3.0178	11.5669	6.71E-04	9.03E-03
LOC107053889	-----	uncharacterized LOC107053889	-0.81	1.1145	10.9805	9.21E-04	1.13E-02
LOC107052229	-----	uncharacterized LOC107052229	-0.81	2.5227	19.5318	9.89E-06	3.22E-04
LOC101751319	-----	uncharacterized LOC101751319	-0.81	1.2655	8.7658	3.07E-03	2.69E-02
LOC107053148	-----	uncharacterized LOC107053148	-0.81	-0.2788	9.2333	2.38E-03	2.26E-02
KCNQ4	ENSGALG00000005502	potassium voltage-gated channel modifier subfamily G member 4	-0.81	0.0922	7.3257	6.80E-03	4.73E-02
LOC112530028	-----	uncharacterized LOC112530028	-0.81	0.1278	7.4684	6.28E-03	4.50E-02
GRM3	ENSGALG00000006576	glutamate metabotropic receptor 3	-0.81	4.5135	25.4180	4.62E-07	2.51E-05
SLC26A6	ENSGALG00000026089	solute carrier family 26 member 6	-0.81	0.9376	7.8413	5.11E-03	3.87E-02
LOC112532504	-----	uncharacterized LOC112532504	-0.80	2.8152	38.2433	6.25E-10	7.29E-08
LOC112533555	-----	olfactory receptor 14C36-like	-0.80	2.1750	11.7142	6.20E-04	8.50E-03
LOC112532781	-----	uncharacterized LOC112532781	-0.80	0.6585	12.5769	3.91E-04	6.01E-03
CD109	ENSGALG00000015910	CD109 molecule	-0.80	3.0583	15.9946	6.35E-05	1.46E-03
LOC100858131	-----	trichohyalin-like	-0.80	2.0516	23.2280	1.44E-06	6.42E-05
LOC101749506	-----	uncharacterized LOC101749506	-0.80	1.2322	17.6977	2.59E-05	6.97E-04
VNN1	ENSGALG00000013993	vanin 1	-0.80	-0.0144	10.7674	1.03E-03	1.23E-02
TCEA3	ENSGALG00000050173	transcription elongation factor A3	-0.80	1.8113	18.1158	2.08E-05	5.79E-04
LOC422150	-----	c-X-C chemokine receptor type 3-like	-0.79	-0.2648	9.0512	2.63E-03	2.41E-02
LOC112532109	-----	uncharacterized LOC112532109	-0.79	0.8221	9.3371	2.25E-03	2.17E-02
LOC107053787	-----	uncharacterized LOC107053787	-0.79	0.1913	8.2128	4.16E-03	3.34E-02
CCR7	ENSGALG00000035733	C-C motif chemokine receptor 7	-0.79	1.4940	9.2958	2.30E-03	2.21E-02
SNX20	ENSGALG00000038374	sorting nexin 20	-0.79	2.4642	23.4923	1.25E-06	5.75E-05
LOC107053086	-----	uncharacterized LOC107053086	-0.79	1.8956	16.5378	4.77E-05	1.15E-03
LOC107051875	-----	uncharacterized LOC107051875	-0.79	3.3660	17.4025	3.02E-05	7.89E-04
CACNG3	ENSGALG00000038087	calcium voltage-gated channel auxiliary subunit gamma 3	-0.79	3.2388	25.1016	5.44E-07	2.89E-05
LRRC55	-----	leucine rich repeat containing 55	-0.79	0.4716	9.2168	2.40E-03	2.27E-02
LOC112533354	-----	maestro heat-like repeat-containing protein family member 7	-0.79	3.5521	36.1750	1.80E-09	1.89E-07
SEMA5A	ENSGALG00000028685	semaphorin 5A	-0.78	5.8966	17.7692	2.49E-05	6.75E-04
HIST1H46L2	ENSGALG00000053680	histone cluster 1, H4-IV, germinal H4-like 2	-0.78	0.1069	9.6075	1.94E-03	1.97E-02
C3	ENSGALG00000030038	complement component 3	-0.78	1.9876	11.0908	8.68E-04	1.08E-02
MYOCD	ENSGALG00000001021	myocardin	-0.78	2.2193	7.7694	5.31E-03	3.99E-02
LOC107052021	-----	uncharacterized LOC107052021	-0.78	1.1790	7.3718	6.63E-03	4.66E-02
AIPL1	-----	aryl hydrocarbon receptor interacting protein like 1	-0.78	0.7967	11.4503	7.15E-04	9.42E-03
UPK1B	ENSGALG00000015079	uroplakin 1B	-0.78	3.3279	11.8997	5.61E-04	7.89E-03
AGTR2	ENSGALG00000005936	angiotensin II receptor type 2	-0.78	0.7899	8.0834	4.47E-03	3.52E-02
LOC107048987	-----	putative methyltransferase DDB_G0268948	-0.78	5.1298	32.1065	1.46E-08	1.23E-06
LOC107053414	-----	mucin 5 like	-0.77	1.2801	8.1672	4.27E-03	3.40E-02

LOC107053617	-----	uncharacterized LOC107053617	-0.77	-0.1445	7.6584	5.65E-03	4.16E-02
TRMU	ENSGALG00000031922	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	-0.77	4.8616	79.3074	5.32E-19	3.80E-16
ARL2	-----	ADP-ribosylation factor-like 2	-0.77	-0.1459	11.0303	8.96E-04	1.11E-02
COL17A1	ENSGALG00000029617	collagen type XVII alpha 1 chain	-0.77	3.2570	12.9637	3.18E-04	5.14E-03
PDGFD	ENSGALG00000017179	platelet derived growth factor D	-0.77	5.0233	53.5912	2.47E-13	7.81E-11
C16orf96	-----	chromosome 16 open reading frame 96	-0.77	1.6082	12.4714	4.13E-04	6.27E-03
LOC112532562	-----	translation initiation factor IF-2-like	-0.76	1.3958	12.9662	3.17E-04	5.14E-03
MYLK2	ENSGALG00000006273	myosin light chain kinase 2	-0.76	0.0385	11.5677	6.71E-04	9.03E-03
LOC107055181	-----	uncharacterized LOC107055181	-0.76	-0.1918	9.1107	2.54E-03	2.35E-02
FBP1	ENSGALG00000012613	fructose-bisphosphatase 1	-0.76	1.7639	15.0109	1.07E-04	2.16E-03
LOC112531456	-----	uncharacterized LOC112531456	-0.76	3.7788	26.6167	2.48E-07	1.46E-05
BAMBI	ENSGALG00000040993	BMP and activin membrane bound inhibitor	-0.76	5.4853	9.5464	2.00E-03	2.02E-02
LOC101747954	-----	uncharacterized LOC101747954	-0.76	1.3608	10.2534	1.36E-03	1.50E-02
WDYHV1	ENSGALG00000030059	WDYHV motif containing 1	-0.76	5.5439	41.4030	1.24E-10	1.84E-08
LOC112530195	-----	uncharacterized LOC112530195	-0.76	0.4629	9.0948	2.56E-03	2.37E-02
DSCAM	ENSGALG00000016138	DS cell adhesion molecule	-0.75	1.5117	8.4660	3.62E-03	3.03E-02
JAKMIP1	ENSGALG00000015528	janus kinase and microtubule interacting protein 1	-0.75	-0.0988	7.2389	7.13E-03	4.89E-02
LOC112532500	-----	uncharacterized LOC112532500	-0.75	0.4271	7.9277	4.87E-03	3.75E-02
LOC768418	-----	zinc finger FYVE domain-containing protein 16-like	-0.75	1.4173	10.1718	1.43E-03	1.56E-02
NPAS2	ENSGALG00000016774	neuronal PAS domain protein 2	-0.75	1.9196	16.6953	4.39E-05	1.07E-03
ABI3	ENSGALG00000044071	ABI family member 3	-0.75	1.9854	21.4543	3.62E-06	1.40E-04
GALNTL6	ENSGALG00000030588	polypeptide N-acetylgalactosaminyltransferase-like 6	-0.75	1.0325	13.3254	2.62E-04	4.46E-03
STOX1	-----	storkhead box 1	-0.75	4.4966	23.7998	1.07E-06	5.01E-05
LOC112532293	-----	translation initiation factor IF-2-like	-0.74	1.4276	15.8989	6.68E-05	1.51E-03
SEZ6	ENSGALG00000026431	seizure related 6 homolog	-0.74	3.3221	8.5883	3.38E-03	2.88E-02
MLPH	ENSGALG00000003904	melanophilin	-0.74	0.9784	14.6313	1.31E-04	2.55E-03
SLC22A7	ENSGALG00000001661	solute carrier family 22 member 7	-0.74	0.0138	7.3613	6.66E-03	4.67E-02
HHLA2	ENSGALG000000022871	HERV-H LTR-associating 2	-0.74	2.4883	17.6465	2.66E-05	7.15E-04
LOC101750376	-----	kallikrein-15-like	-0.74	1.0311	14.9426	1.11E-04	2.22E-03
CSMD1	ENSGALG00000035230	CUB and Sushi multiple domains 1	-0.74	2.2912	8.7970	3.02E-03	2.65E-02
DLGAP2	ENSGALG00000032937	DLG associated protein 2	-0.74	1.4084	12.5772	3.90E-04	6.01E-03
CALCR	ENSGALG00000009509	calcitonin receptor	-0.73	1.3389	14.5301	1.38E-04	2.65E-03
C5H11orf16	-----	-----	-0.73	0.8950	8.5988	3.36E-03	2.87E-02
LOC107056111	-----	uncharacterized LOC107056111	-0.73	0.6635	9.9350	1.62E-03	1.71E-02
LOC112530469	-----	cytochrome P450 2G1-like	-0.73	2.5844	8.9001	2.85E-03	2.55E-02
A2ML4	ENSGALG00000000293	alpha-2-macroglobulin-like 4	-0.73	4.3589	13.6936	2.15E-04	3.80E-03
NLRC3	ENSGALG00000033278	NLR family CARD domain containing 3	-0.73	1.0725	12.9447	3.21E-04	5.19E-03
ATP2C2	-----	ATPase secretory pathway Ca2+ transporting 2	-0.73	2.7038	11.8243	5.85E-04	8.12E-03
LOC112531849	-----	paired mesoderm homeobox protein 2A-like	-0.73	1.9789	7.9011	4.94E-03	3.80E-02
LRRC34	ENSGALG00000009402	leucine rich repeat containing 34	-0.73	1.9383	14.0928	1.74E-04	3.21E-03
RGS4	ENSGALG00000002564	regulator of G-protein signaling 4	-0.73	2.4443	8.2858	4.00E-03	3.24E-02
SYT15	ENSGALG00000002046	synaptotagmin 15	-0.73	1.8851	11.9119	5.58E-04	7.88E-03
MSLN	ENSGALG00000005349	mesothelin	-0.73	1.8040	11.7130	6.21E-04	8.50E-03
BTN3A3L1	-----	butyrophilin subfamily 3 member A3-like 1	-0.73	1.7781	8.5328	3.49E-03	2.94E-02

SNAP91	ENSGALG00000015846	synaptosome associated protein 91	-0.72	3.6163	19.0341	1.28E-05	3.95E-04
DUSP18	-----	-----	-0.72	1.5410	11.1533	8.39E-04	1.06E-02
STK32B	ENSGALG00000029510	serine/threonine kinase 32B	-0.72	1.3437	8.3146	3.93E-03	3.21E-02
KCNJ15	ENSGALG00000016055	potassium inwardly rectifying channel subfamily J member 15	-0.72	1.6621	18.6585	1.56E-05	4.65E-04
ALKBH8	ENSGALG00000017170	alkB homolog 8, tRNA methyltransferase	-0.72	4.2026	19.9052	8.14E-06	2.79E-04
LOC107057099	-----	MHCY region zinc finger protein 2	-0.72	2.4613	16.6385	4.52E-05	1.10E-03
STMN2	ENSGALG00000039690	stathmin 2	-0.72	5.1126	9.5454	2.00E-03	2.02E-02
SNCA	ENSGALG00000010379	synuclein alpha	-0.71	0.7653	12.9829	3.14E-04	5.11E-03
LOC112532090	-----	uncharacterized LOC112532090	-0.71	0.7088	8.0034	4.67E-03	3.64E-02
LOC112532494	-----	uncharacterized LOC112532494	-0.71	0.3321	7.9243	4.88E-03	3.76E-02
ACACB	-----	acetyl-CoA carboxylase beta	-0.71	1.0666	9.4787	2.08E-03	2.07E-02
DGKK	ENSGALG00000003841	diacylglycerol kinase eta	-0.71	1.6248	15.9042	6.66E-05	1.51E-03
CAPG	ENSGALG00000036175	capping actin protein, gelsolin like	-0.70	2.9246	11.6439	6.44E-04	8.74E-03
C3H1orf95	ENSGALG00000009219	chromosome 3 C1orf95 homolog	-0.70	1.7966	7.5088	6.14E-03	4.42E-02
LOC107051601	-----	uncharacterized LOC107051601	-0.70	0.3026	8.9693	2.75E-03	2.48E-02
LOC101751026	-----	uncharacterized LOC101751026	-0.70	1.9480	17.1901	3.38E-05	8.63E-04
CLRN1	ENSGALG00000010384	clarin 1	-0.69	0.1588	7.6916	5.55E-03	4.10E-02
RAMP1	ENSGALG00000003821	receptor activity modifying protein 1	-0.69	2.4873	13.3670	2.56E-04	4.39E-03
BATF	ENSGALG00000010323	basic leucine zipper ATF-like transcription factor	-0.69	0.3015	9.0188	2.67E-03	2.43E-02
RBFOX1	ENSGALG00000034325	RNA binding protein, fox-1 homolog 1	-0.69	4.6657	30.7869	2.88E-08	2.26E-06
LOC771422	-----	transmembrane protein 151B-like	-0.68	1.6909	8.7163	3.15E-03	2.74E-02
KLF2	ENSGALG00000003939	Kruppel like factor 2	-0.68	2.2220	9.2247	2.39E-03	2.26E-02
ADRA1D	ENSGALG00000038787	adrenoceptor alpha 1D	-0.68	0.2885	7.7091	5.49E-03	4.07E-02
TUBA4A	-----	-----	-0.68	2.5652	17.5444	2.81E-05	7.40E-04
GCNT4	ENSGALG00000014944	glucosaminyl (N-acetyl) transferase 4, core 2	-0.68	0.9834	7.3806	6.59E-03	4.65E-02
LOC101748220	-----	uncharacterized LOC101748220	-0.68	0.8233	7.7172	5.47E-03	4.06E-02
LOC112531072	-----	zinc finger protein 135-like	-0.68	1.9019	7.2849	6.95E-03	4.80E-02
LOC112532340	-----	uncharacterized LOC112532340	-0.68	0.7885	9.4087	2.16E-03	2.12E-02
LOC112532555	-----	uncharacterized LOC112532555	-0.67	1.2094	12.6497	3.76E-04	5.84E-03
MEI1	-----	meiotic double-stranded break formation protein 1	-0.67	2.3256	15.0111	1.07E-04	2.16E-03
LOC107053805	-----	uncharacterized LOC107053805	-0.67	2.8661	23.9827	9.72E-07	4.72E-05
SFRP4	ENSGALG00000031997	secreted frizzled related protein 4	-0.67	0.9313	9.1743	2.45E-03	2.30E-02
LOC101748673	-----	uncharacterized LOC101748673	-0.67	2.5692	18.3257	1.86E-05	5.32E-04
LOC770617	-----	transmembrane protein 100-like	-0.67	4.6940	40.5001	1.97E-10	2.77E-08
FBLN5	ENSGALG00000010747	fibulin 5	-0.67	2.6138	13.2465	2.73E-04	4.59E-03
CA3A	ENSGALG00000033700	carbonic anhydrase 3A	-0.66	1.2402	9.8495	1.70E-03	1.78E-02
LOC107053811	-----	uncharacterized LOC107053811	-0.66	2.0932	8.9050	2.84E-03	2.55E-02
LOC112530132	-----	uncharacterized LOC112530132	-0.66	0.4762	9.1434	2.50E-03	2.32E-02
CD3E	ENSGALG00000007416	CD3e molecule	-0.66	2.5889	20.4130	6.24E-06	2.22E-04
MREG	ENSGALG00000003758	melanoregulin	-0.66	2.1988	11.6271	6.50E-04	8.80E-03
CYP26C1	ENSGALG00000043213	cytochrome P450 family 26 subfamily C member 1	-0.66	2.5367	11.3762	7.44E-04	9.68E-03
LOC100859492	-----	uncharacterized LOC100859492	-0.66	0.4901	7.3751	6.61E-03	4.65E-02
MTFP1	ENSGALG00000038952	mitochondrial fission process 1	-0.65	3.8482	26.5864	2.52E-07	1.48E-05
RXRA	ENSGALG00000042055	retinoid X receptor alpha	-0.65	4.6947	23.1304	1.51E-06	6.73E-05

LOC101747725	-----	uncharacterized LOC101747725	-0.65	0.8168	12.1261	4.97E-04	7.23E-03
LOC107052937	-----	uncharacterized LOC107052937	-0.65	-0.0025	8.5973	3.37E-03	2.87E-02
LCP1	ENSGALG00000016986	lymphocyte cytosolic protein 1	-0.65	4.1589	18.8988	1.38E-05	4.19E-04
CLCN4	ENSGALG00000016607	chloride voltage-gated channel 4	-0.65	4.2664	21.7876	3.05E-06	1.21E-04
LOC107053523	-----	uncharacterized LOC107053523	-0.65	1.8325	13.9731	1.85E-04	3.36E-03
SOUL	ENSGALG00000012464	SOUL protein	-0.65	0.6092	7.8810	5.00E-03	3.83E-02
FAM46C	ENSGALG00000014453	family with sequence similarity 46 member C	-0.65	0.9583	8.8533	2.93E-03	2.60E-02
SAT1	ENSGALG00000016348	spermidine/spermine N1-acetyltransferase 1	-0.64	5.7613	76.7383	1.95E-18	1.19E-15
LOC101747455	-----	uncharacterized LOC101747455	-0.64	2.4163	8.5819	3.40E-03	2.88E-02
TYW3	ENSGALG00000032549	tRNA-yW synthesizing protein 3 homolog	-0.64	4.1539	23.6861	1.13E-06	5.27E-05
PPFIA2	ENSGALG00000010958	PTPRF interacting protein alpha 2	-0.64	2.9270	12.9502	3.20E-04	5.18E-03
GJB5	ENSGALG00000054289	gap junction protein beta 5	-0.64	1.0311	7.7958	5.24E-03	3.95E-02
LOC107054593	-----	uncharacterized LOC107054593	-0.63	1.2465	14.5217	1.39E-04	2.66E-03
FAM43B	ENSGALG00000026367	family with sequence similarity 43 member B	-0.63	2.3047	11.7913	5.95E-04	8.23E-03
GHDC	ENSGALG00000003333	GH3 domain containing	-0.63	3.5499	19.0313	1.29E-05	3.95E-04
LOC107053391	-----	uncharacterized LOC107053391	-0.63	2.0366	15.7536	7.22E-05	1.62E-03
LOC112533362	-----	uncharacterized LOC112533362	-0.63	1.5042	8.8284	2.97E-03	2.62E-02
LOC112530592	-----	uncharacterized LOC112530592	-0.63	1.3093	11.2445	7.99E-04	1.02E-02
ABCA12	ENSGALG00000003553	ATP binding cassette subfamily A member 12	-0.63	2.3211	11.4941	6.98E-04	9.24E-03
LOC107051864	-----	uncharacterized LOC107051864	-0.63	1.2503	8.8953	2.86E-03	2.56E-02
LOC101749170	-----	uncharacterized LOC101749170	-0.63	2.5927	9.5499	2.00E-03	2.02E-02
SCEL	ENSGALG00000027514	sciellin	-0.63	2.1434	14.0312	1.80E-04	3.28E-03
RANBP17	-----	RAN binding protein 17	-0.63	4.0731	10.0388	1.53E-03	1.64E-02
MIR1683	ENSGALG00000025224	microRNA 1683	-0.63	1.0486	9.9201	1.63E-03	1.72E-02
GABRA1	ENSGALG00000001698	gamma-aminobutyric acid type A receptor alpha1 subunit	-0.62	0.7749	7.7692	5.31E-03	3.99E-02
APCDD1	ENSGALG00000050840	APC down-regulated 1	-0.62	7.5974	8.2240	4.13E-03	3.33E-02
LOC101749495	-----	uncharacterized LOC101749495	-0.62	3.8348	26.9476	2.09E-07	1.27E-05
MYO3A	ENSGALG00000007647	myosin IIIA	-0.62	2.3665	11.5516	6.77E-04	9.06E-03
C1H11ORF87	-----	-----	-0.62	4.4501	22.7893	1.81E-06	7.75E-05
LOC107051956	-----	uncharacterized LOC107051956	-0.62	0.2756	7.6153	5.79E-03	4.23E-02
C10orf10	-----	withdrawn	-0.62	1.0263	10.4182	1.25E-03	1.40E-02
LOC107052369	-----	uncharacterized LOC107052369	-0.62	2.8834	13.9957	1.83E-04	3.33E-03
ANKRD34B	ENSGALG00000044727	ankyrin repeat domain 34B	-0.62	2.4974	15.4610	8.42E-05	1.81E-03
AVD	ENSGALG00000025945	avidin	-0.62	0.8939	7.3441	6.73E-03	4.71E-02
ZNF408	-----	-----	-0.62	3.8465	34.5453	4.16E-09	4.01E-07
SERPINB6L	-----	-----	-0.62	3.7655	36.5862	1.46E-09	1.59E-07
LOC101749148	-----	uncharacterized LOC101749148	-0.62	1.3384	10.0186	1.55E-03	1.66E-02
KIAA1257	ENSGALG00000044299	KIAA1257	-0.62	2.3959	8.2706	4.03E-03	3.26E-02
TMEM240	ENSGALG00000035387	transmembrane protein 240	-0.61	2.8689	15.3099	9.12E-05	1.93E-03
LOC107052653	-----	uncharacterized LOC107052653	-0.61	2.2899	12.0689	5.13E-04	7.39E-03
LOC100858386	ENSGALG00000050166	uncharacterized LOC100858386	-0.61	4.6717	52.1753	5.08E-13	1.35E-10
LOC101750048	-----	uncharacterized LOC101750048	-0.61	1.0595	9.2951	2.30E-03	2.21E-02
IQUB	ENSGALG00000008823	IQ motif and ubiquitin domain containing	-0.61	2.0614	13.5577	2.31E-04	4.02E-03
LOC107055206	-----	uncharacterized LOC107055206	-0.61	2.3012	13.0304	3.06E-04	5.02E-03

CES1L1	-----	-----	-0.61	2.0585	9.2384	2.37E-03	2.25E-02
RPE65	ENSGALG00000011259	RPE65, retinoid isomerohydrolase	-0.61	1.9700	7.9619	4.78E-03	3.71E-02
SLC9A5	ENSGALG00000007867	solute carrier family 9 member A5	-0.61	1.1952	10.9982	9.12E-04	1.12E-02
PNOC	ENSGALG00000016620	prepronociceptin	-0.61	1.4567	9.3255	2.26E-03	2.18E-02
LOC101751097	-----	uncharacterized LOC101751097	-0.61	4.0127	9.3322	2.25E-03	2.18E-02
NINJ2	ENSGALG00000012989	ninjurin 2	-0.61	3.4420	16.7892	4.18E-05	1.03E-03
LOC101748935	-----	uncharacterized LOC101748935	-0.61	1.2335	9.5425	2.01E-03	2.02E-02
EVA1B	ENSGALG00000022440	eva-1 homolog B	-0.61	4.5409	19.5898	9.60E-06	3.14E-04
CFAP57	ENSGALG00000009902	cilia and flagella associated protein 57	-0.61	0.8498	10.4506	1.23E-03	1.39E-02
PDK4	ENSGALG00000009700	pyruvate dehydrogenase kinase 4	-0.61	1.5851	10.2414	1.37E-03	1.51E-02
RGS9	ENSGALG00000029610	regulator of G-protein signaling 9	-0.60	4.4991	13.7774	2.06E-04	3.65E-03
PLEKHD1	ENSGALG00000009431	pleckstrin homology and coiled-coil domain containing D1	-0.60	3.2272	20.8565	4.95E-06	1.83E-04
GRID1	ENSGALG00000037366	glutamate ionotropic receptor delta type subunit 1	-0.60	1.8335	10.8658	9.80E-04	1.19E-02
LOC112531640	-----	small nucleolar RNA SNORD89	-0.60	0.8284	8.5160	3.52E-03	2.97E-02
LXN	ENSGALG00000009651	latexin	-0.60	0.8134	9.5271	2.02E-03	2.03E-02
ENTPD8L	-----	-----	-0.59	2.6038	14.2452	1.60E-04	2.99E-03
TTC9	ENSGALG00000017652	tetratricopeptide repeat domain 9	-0.59	2.5747	13.9138	1.91E-04	3.45E-03
FCN2	ENSGALG00000040771	ficolin 2	-0.59	2.1294	14.9104	1.13E-04	2.25E-03
LOC107054619	-----	uncharacterized LOC107054619	-0.59	0.6093	9.6675	1.88E-03	1.92E-02
FAM129A	ENSGALG00000004812	family with sequence similarity 129 member A	-0.59	4.0733	25.7122	3.96E-07	2.21E-05
RAB39A	ENSGALG00000017166	RAB39A, member RAS oncogene family	-0.59	2.0707	16.4637	4.96E-05	1.19E-03
NOX3	ENSGALG00000013659	NADPH oxidase 3	-0.59	1.8679	7.9441	4.82E-03	3.74E-02
LOC107051605	-----	uncharacterized LOC107051605	-0.59	0.4401	8.5813	3.40E-03	2.88E-02
ALKBH1	ENSGALG00000010485	alkB homolog 1, histone H2A dioxygenase	-0.59	4.8547	73.7406	8.91E-18	5.05E-15
IGFN1	ENSGALG00000000295	immunoglobulin-like and fibronectin type III domain containing 1	-0.59	2.4379	10.4591	1.22E-03	1.38E-02
LOC107054771	-----	N-alpha-acetyltransferase 38, NatC auxiliary subunit-like	-0.59	2.5409	13.3528	2.58E-04	4.41E-03
CDH23	ENSGALG00000036824	cadherin related 23	-0.59	3.1835	11.4216	7.26E-04	9.52E-03
ZNF764L	-----	-----	-0.59	3.7304	12.4949	4.08E-04	6.22E-03
LOC101748755	-----	copine-5-like	-0.58	0.9298	8.4062	3.74E-03	3.10E-02
PTPRO	ENSGALG00000013085	protein tyrosine phosphatase, receptor type O	-0.58	5.1930	16.7045	4.37E-05	1.07E-03
DTX3L	ENSGALG00000012075	deltex E3 ubiquitin ligase 3L	-0.58	2.8566	16.7682	4.22E-05	1.04E-03
LOC107049475	-----	uncharacterized LOC107049475	-0.58	4.9430	11.0678	8.78E-04	1.09E-02
CLMN	ENSGALG000000030719	calmin	-0.58	5.7188	12.5238	4.02E-04	6.16E-03
TUBAL3	ENSGALG00000008444	tubulin alpha like 3	-0.58	4.9124	20.3189	6.55E-06	2.31E-04
SULT1B1	ENSGALG00000023120	sulfotransferase family cytosolic 1B member 1	-0.58	3.1448	16.0277	6.24E-05	1.44E-03
XKR8	ENSGALG00000030305	XK related 8	-0.58	3.1437	17.6120	2.71E-05	7.24E-04
LOC414835	-----	cHz-cadherin	-0.58	1.9729	8.7731	3.06E-03	2.68E-02
OCA2	ENSGALG00000016740	OCA2 melanosomal transmembrane protein	-0.57	2.3083	9.3240	2.26E-03	2.18E-02
TESC	ENSGALG00000008206	tescalcin	-0.57	3.7337	17.5115	2.86E-05	7.51E-04
LOC112531294	-----	withdrawn	-0.57	5.4016	13.2972	2.66E-04	4.51E-03
GLRB	ENSGALG00000009395	glycine receptor beta	-0.57	2.4441	7.8516	5.08E-03	3.86E-02
TMCC3	ENSGALG00000011320	transmembrane and coiled-coil domain family 3	-0.57	3.2348	7.7967	5.23E-03	3.95E-02
LOC107054482	-----	protocadherin gamma-B1 pseudogene	-0.57	0.6980	7.9322	4.86E-03	3.75E-02
SCIN	ENSGALG00000010770	scinderin	-0.57	3.1764	11.4200	7.27E-04	9.52E-03

LOC107055055	-----	uncharacterized LOC107055055	-0.57	2.6447	7.8587	5.06E-03	3.85E-02
MKRN3	-----	makorin ring finger protein 3	-0.57	1.8523	8.7334	3.12E-03	2.72E-02
PROKR2	-----	-----	-0.57	1.7994	7.6012	5.83E-03	4.25E-02
TPD52L1	ENSGALG00000014843	tumor protein D52-like 1	-0.57	2.2362	11.5760	6.68E-04	9.00E-03
LOC107052050	-----	uncharacterized LOC107052050	-0.57	1.7602	9.5070	2.05E-03	2.05E-02
LOC112531576	-----	translation initiation factor IF-2-like	-0.57	1.8913	10.3649	1.28E-03	1.44E-02
ACTN2	ENSGALG00000014463	actinin alpha 2	-0.57	4.1916	8.0277	4.61E-03	3.60E-02
BAALC	ENSGALG00000051919	brain and acute leukemia, cytoplasmic	-0.57	2.2481	8.0826	4.47E-03	3.52E-02
FAM184B	ENSGALG00000041854	family with sequence similarity 184 member B	-0.56	2.3435	10.1434	1.45E-03	1.57E-02
MCF2	ENSGALG00000006562	MCF.2 cell line derived transforming sequence	-0.56	5.1185	31.2599	2.26E-08	1.83E-06
LOC107050638	-----	vinexin-like	-0.56	1.5712	7.8827	4.99E-03	3.82E-02
GPR17	-----	G protein-coupled receptor 17	-0.56	3.3991	9.6987	1.84E-03	1.90E-02
KCNQ5	ENSGALG00000037249	potassium voltage-gated channel subfamily Q member 5	-0.56	3.0778	13.6604	2.19E-04	3.85E-03
TEX14	-----	testis expressed 14, intercellular bridge forming factor	-0.56	3.1851	13.2464	2.73E-04	4.59E-03
ACBD7	ENSGALG00000019663	acyl-CoA binding domain containing 7	-0.56	3.1633	19.0320	1.29E-05	3.95E-04
PIGP	-----	phosphatidylinositol glycan anchor biosynthesis class P	-0.55	4.0440	14.9808	1.09E-04	2.18E-03
SELENOM	ENSGALG00000047792	selenoprotein M	-0.55	6.0708	46.8719	7.58E-12	1.50E-09
TAPBP	ENSGALG00000008022	TAP binding protein	-0.55	3.1231	9.8378	1.71E-03	1.78E-02
SUSD5	ENSGALG00000042289	sushi domain containing 5	-0.55	4.6856	15.8503	6.86E-05	1.55E-03
VEGFD	ENSGALG00000016558	vascular endothelial growth factor D	-0.55	6.8709	12.2425	4.67E-04	6.88E-03
EFHC1	ENSGALG00000016674	EF-hand domain containing 1	-0.55	1.9693	8.2215	4.14E-03	3.33E-02
PHACTR1	ENSGALG00000012732	phosphatase and actin regulator 1	-0.55	2.3840	9.0308	2.65E-03	2.42E-02
CYP26A1	ENSGALG00000033695	cytochrome P450 family 26 subfamily A member 1	-0.55	4.8935	9.3085	2.28E-03	2.19E-02
EML5	ENSGALG00000010639	echinoderm microtubule associated protein like 5	-0.55	2.4259	8.2025	4.18E-03	3.35E-02
CNNM1	ENSGALG00000007489	cyclin and CBS domain divalent metal cation transport mediator 1	-0.55	3.1578	9.0929	2.57E-03	2.37E-02
EHHADH	ENSGALG00000053254	enoyl-CoA hydratase and 3-hydroxyacyl CoA dehydrogenase	-0.55	3.9621	20.7643	5.19E-06	1.91E-04
LOC107054545	-----	uncharacterized LOC107054545	-0.54	1.6631	8.3006	3.96E-03	3.22E-02
LOC101749129	-----	uncharacterized LOC101749129	-0.54	2.7393	15.5227	8.15E-05	1.78E-03
LOC112530163	-----	SH2B adapter protein 1-like	-0.54	5.4226	21.6289	3.31E-06	1.30E-04
LOC107050463	-----	serine-aspartate repeat-containing protein F-like	-0.54	6.7541	27.8473	1.31E-07	8.64E-06
ABCG1	ENSGALG00000016164	ATP binding cassette subfamily G member 1	-0.54	3.1991	12.7739	3.51E-04	5.53E-03
PLEKHS1	ENSGALG00000020679	pleckstrin homology domain containing S1	-0.54	1.6665	9.6810	1.86E-03	1.91E-02
ENPP3	ENSGALG00000037587	ectonucleotide pyrophosphatase/phosphodiesterase 3	-0.54	2.6275	10.7029	1.07E-03	1.26E-02
TMF1	ENSGALG00000013408	TATA element modulatory factor 1	-0.54	6.1897	82.0966	1.30E-19	9.69E-17
PIK3IP1	ENSGALG00000006942	phosphoinositide-3-kinase interacting protein 1	-0.53	6.9640	50.4403	1.23E-12	3.02E-10
FRRS1L	ENSGALG00000025792	ferric chelate reductase 1 like	-0.53	5.7762	39.3639	3.52E-10	4.45E-08
XKR6	-----	XK related 6	-0.53	5.7456	14.6684	1.28E-04	2.51E-03
SLCO4A1	ENSGALG00000005460	solute carrier organic anion transporter family member 4A1	-0.53	3.3229	9.1598	2.47E-03	2.31E-02
LOC769704	-----	fatty acyl-CoA hydrolase precursor, medium chain-like	-0.53	2.0424	10.4554	1.22E-03	1.39E-02
CLIC6	ENSGALG00000016020	chloride intracellular channel 6	-0.53	2.5335	11.5601	6.74E-04	9.05E-03
KIAA1024	ENSGALG00000006519	KIAA1024	-0.53	3.5259	10.0064	1.56E-03	1.66E-02
ZNF226L	ENSGALG00000032405	zinc finger protein 226-like	-0.53	3.5949	16.2047	5.69E-05	1.33E-03
CAPNS2	-----	calpain small subunit 2	-0.53	1.9215	10.8837	9.70E-04	1.18E-02
LOC101748706	-----	ATP-dependent DNA helicase Q4-like	-0.53	6.3234	26.5524	2.56E-07	1.49E-05

TMEM79	ENSGALG00000039643	transmembrane protein 79-like	-0.53	1.8675	9.3379	2.24E-03	2.17E-02
MANBA	ENSGALG00000012308	mannosidase beta	-0.53	4.1394	19.8360	8.44E-06	2.86E-04
HIST1H110	ENSGALG00000031159	histone cluster 1, H1.10	-0.52	1.6294	7.7551	5.36E-03	4.00E-02
LOC107051764	-----	uncharacterized LOC107051764	-0.52	3.5693	25.0307	5.64E-07	2.98E-05
C1HXORF59	ENSGALG00000016268	chromosome 1 open reading frame, human CXORF59	-0.52	3.0858	7.8287	5.14E-03	3.89E-02
LOC112532476	-----	uncharacterized LOC112532476	-0.52	1.4191	9.4910	2.06E-03	2.06E-02
SLC9B2	ENSGALG00000012319	solute carrier family 9 member B2	-0.52	3.8477	20.8257	5.03E-06	1.86E-04
MCF2L2	ENSGALG00000008744	MCF.2 cell line derived transforming sequence-like 2	-0.52	3.5266	10.7167	1.06E-03	1.26E-02
GABRG2	ENSGALG00000038042	gamma-aminobutyric acid type A receptor gamma2 subunit	-0.52	2.3560	8.6895	3.20E-03	2.76E-02
RPS6KA2	ENSGALG00000011473	ribosomal protein S6 kinase A2	-0.52	2.4304	10.8793	9.72E-04	1.18E-02
EPHA10	ENSGALG00000001912	EPH receptor A10	-0.52	2.5897	9.2098	2.41E-03	2.27E-02
SMAD6	ENSGALG00000025898	SMAD family member 6	-0.52	4.5607	8.6904	3.20E-03	2.76E-02
GPC5	ENSGALG00000016902	glypican 5	-0.52	3.8805	9.9594	1.60E-03	1.70E-02
LOC101749699	-----	uncharacterized LOC101749699	-0.52	2.2077	7.3471	6.72E-03	4.70E-02
LOC112530196	-----	transmembrane protein 79-like	-0.52	2.6789	9.3725	2.20E-03	2.15E-02
HIST2H3D	ENSGALG00000035244	histone cluster 2 H3 family member d	-0.52	2.6356	8.5256	3.50E-03	2.95E-02
JADE2	ENSGALG00000006424	jade family PHD finger 2	-0.51	2.8534	12.4744	4.13E-04	6.26E-03
CCNG1	ENSGALG00000001718	cyclin G1	-0.51	6.8396	13.7974	2.04E-04	3.63E-03
GAS6	ENSGALG00000016820	growth arrest specific 6	-0.51	3.4361	10.9215	9.51E-04	1.16E-02
USH2A	ENSGALG00000009652	usherin	-0.51	1.1066	8.2376	4.10E-03	3.31E-02
ARAP2	ENSGALG00000041373	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	-0.51	2.8914	13.6591	2.19E-04	3.85E-03
FBLN1	ENSGALG00000014233	fibulin 1	-0.51	6.8284	29.3448	6.06E-08	4.37E-06
DGKG	ENSGALG00000005721	diacylglycerol kinase gamma	-0.51	1.7581	7.7876	5.26E-03	3.96E-02
PPP1R9A	ENSGALG00000009686	protein phosphatase 1 regulatory subunit 9A	-0.51	3.5129	12.4679	4.14E-04	6.27E-03
ADAMTS8	ENSGALG00000001370	ADAM metallopeptidase with thrombospondin type 1 motif, 8	-0.51	4.3106	11.9475	5.47E-04	7.77E-03
MAP10	ENSGALG00000049034	microtubule associated protein 10	-0.50	3.1927	15.9142	6.63E-05	1.51E-03
OGFOD3	ENSGALG00000001618	2-oxoglutarate and iron dependent oxygenase domain containing 3	-0.50	5.2003	29.4927	5.61E-08	4.12E-06
RERGL	ENSGALG00000013112	RERG like	-0.50	4.7617	12.8108	3.45E-04	5.46E-03
JARID2	ENSGALG00000012702	jumonji and AT-rich interaction domain containing 2	-0.50	7.0104	13.3239	2.62E-04	4.46E-03
APLN	ENSGALG00000054286	apelin	-0.50	2.0328	7.7075	5.50E-03	4.07E-02
LOC107052651	-----	uncharacterized LOC107052651	-0.50	3.5272	11.3268	7.64E-04	9.85E-03
MNR2	ENSGALG00000011349	homeodomain protein	-0.50	5.6768	7.4525	6.33E-03	4.53E-02
LOC112530211	-----	uncharacterized LOC112530211	-0.50	1.7194	8.3054	3.95E-03	3.22E-02
TEC	ENSGALG00000014124	tec protein tyrosine kinase	-0.50	1.8933	9.1109	2.54E-03	2.35E-02
NT5C1A	ENSGALG00000003816	5'-nucleotidase, cytosolic 1A	-0.49	2.4410	11.6818	6.31E-04	8.58E-03
AIFM2	ENSGALG00000004777	apoptosis inducing factor, mitochondria associated 2	-0.49	2.9145	8.3284	3.90E-03	3.19E-02
LOC112532097	-----	uncharacterized LOC112532097	-0.49	2.6873	10.9920	9.15E-04	1.13E-02
SLC36A4	ENSGALG00000017227	solute carrier family 36 member 4	-0.49	3.1699	17.2797	3.23E-05	8.27E-04
STK11IP	ENSGALG00000033515	serine/threonine kinase 11 interacting protein	-0.49	4.2130	22.7902	1.81E-06	7.75E-05
TRIM7.2	ENSGALG00000038278	Gallus gallus tripartite motif containing 7.2 (TRIM7.2), mRNA.	-0.49	5.5297	25.1390	5.33E-07	2.84E-05
NOL7	ENSGALG00000012695	nucleolar protein 7	-0.48	6.0179	45.5231	1.51E-11	2.82E-09
NACAD	ENSGALG00000050931	NAC alpha domain containing	-0.48	4.7965	12.8265	3.42E-04	5.44E-03
COLGALT2	ENSGALG00000038320	collagen beta(1-O)galactosyltransferase 1	-0.48	4.4140	10.5099	1.19E-03	1.36E-02
UNC80	ENSGALG00000041563	unc-80 homolog, NALCN activator	-0.48	3.6643	9.0244	2.66E-03	2.43E-02

LOC101751423	-----	uncharacterized LOC101751423	-0.48	6.7619	23.9539	9.87E-07	4.76E-05
LPIN1	ENSGALG00000016456	lipin 1	-0.48	4.6155	17.6077	2.71E-05	7.24E-04
FAM20C	ENSGALG00000038768	FAM20C, golgi associated secretory pathway kinase	-0.48	4.1433	8.2914	3.98E-03	3.24E-02
TFCP2L1	ENSGALG00000011635	transcription factor CP2 like 1	-0.48	4.4176	9.7177	1.82E-03	1.88E-02
SORBS2	ENSGALG00000013427	sorbin and SH3 domain containing 2	-0.48	4.8485	18.5248	1.68E-05	4.89E-04
LOC107054413	-----	uncharacterized LOC107054413	-0.47	3.7496	12.0633	5.14E-04	7.40E-03
LOC107051951	-----	uncharacterized LOC107051951	-0.47	2.3732	7.7675	5.32E-03	3.99E-02
DGKI	ENSGALG00000012890	diacylglycerol kinase iota	-0.47	2.0171	7.4340	6.40E-03	4.56E-02
PCDH15	ENSGALG00000002744	protocadherin related 15	-0.47	4.3080	8.2888	3.99E-03	3.24E-02
GDAP1L1	ENSGALG00000004309	ganglioside induced differentiation associated protein 1 like 1	-0.47	4.8989	33.5834	6.83E-09	6.21E-07
LOC422757	-----	uncharacterized LOC422757	-0.47	4.8054	14.3827	1.49E-04	2.82E-03
SULT6B1	ENSGALG00000046375	sulfotransferase family, cytosolic, 6B, member 1	-0.47	2.6071	10.6230	1.12E-03	1.30E-02
LOC107049262	-----	uncharacterized LOC107049262	-0.47	3.0852	10.7002	1.07E-03	1.26E-02
TRHDE	ENSGALG00000010200	thyrotropin releasing hormone degrading enzyme	-0.47	2.9299	11.6313	6.48E-04	8.78E-03
IFNGR1	ENSGALG00000013865	interferon gamma receptor 1	-0.47	5.1815	21.7961	3.03E-06	1.21E-04
COBL	ENSGALG00000013102	cordon-bleu WH2 repeat protein	-0.47	3.2638	7.3740	6.62E-03	4.65E-02
ITM2C	ENSGALG00000036111	integral membrane protein 2C	-0.47	3.4699	18.6850	1.54E-05	4.61E-04
NAV3	ENSGALG00000010311	neuron navigator 3	-0.47	3.5275	13.1817	2.83E-04	4.72E-03
MFSD9	-----	major facilitator superfamily domain containing 9	-0.46	4.5647	33.7425	6.29E-09	5.78E-07
GABRD	ENSGALG00000001282	gamma-aminobutyric acid type A receptor delta subunit	-0.46	1.8535	7.1934	7.32E-03	4.98E-02
TCTN1	ENSGALG00000041861	tectonic family member 1	-0.46	2.1608	11.6150	6.54E-04	8.83E-03
TAL2	ENSGALG00000054131	T-cell acute lymphocytic leukemia 2	-0.46	3.2324	7.5729	5.93E-03	4.30E-02
ARSI	ENSGALG00000005616	arylsulfatase family member I	-0.46	6.2115	13.1760	2.84E-04	4.72E-03
GPR1	ENSGALG00000008589	G protein-coupled receptor 1	-0.46	5.2440	39.8393	2.76E-10	3.63E-08
MSH4	ENSGALG00000011392	mutS homolog 4	-0.46	5.5881	21.4923	3.55E-06	1.38E-04
ARRDC1	ENSGALG00000008475	arrestin domain containing 1	-0.46	3.9230	15.7021	7.41E-05	1.65E-03
C1QTNF5	ENSGALG00000006758	C1q and tumor necrosis factor related protein 5	-0.46	2.3963	7.2264	7.18E-03	4.91E-02
TMEM173	ENSGALG00000041129	transmembrane protein 173	-0.46	2.5911	8.9860	2.72E-03	2.46E-02
SCG5	ENSGALG00000009725	secretogranin V	-0.46	2.6498	9.3771	2.20E-03	2.15E-02
DUSP27	ENSGALG00000015453	dual specificity phosphatase 27 (putative)	-0.46	3.0917	7.3207	6.82E-03	4.74E-02
RWDD2A	ENSGALG00000015851	RWD domain containing 2A	-0.46	3.2433	10.9203	9.51E-04	1.16E-02
ASCC2	ENSGALG00000008059	activating signal cointegrator 1 complex subunit 2	-0.46	5.8472	53.1190	3.14E-13	9.39E-11
RFT1	ENSGALG00000001945	RFT1 homolog	-0.45	5.5045	23.8357	1.05E-06	4.96E-05
ACAD6L	ENSGALG00000035994	probable acyl coa dehydrogenase 6-like	-0.45	4.1806	23.9311	9.98E-07	4.79E-05
LIMCH1	-----	LIM and calponin homology domains 1	-0.45	5.3642	18.7906	1.46E-05	4.40E-04
COL9A1	ENSGALG00000015970	collagen type IX alpha 1 chain	-0.45	4.7149	11.8294	5.83E-04	8.11E-03
OCLN	ENSGALG00000037316	occludin	-0.45	4.1083	23.7723	1.08E-06	5.07E-05
ADGRB2	ENSGALG00000043209	adhesion G protein-coupled receptor B2	-0.45	3.1762	7.7129	5.48E-03	4.07E-02
MAGI2	ENSGALG00000038834	membrane associated guanylate kinase, WW and PDZ domain containing 2	-0.44	4.1653	12.2622	4.62E-04	6.83E-03
MOB3C	ENSGALG00000025946	MOB kinase activator 3C	-0.44	2.4430	7.7181	5.47E-03	4.06E-02
STAMBPL1	ENSGALG00000006331	STAM binding protein like 1	-0.44	2.8035	10.6393	1.11E-03	1.29E-02
LOC112533257	-----	uncharacterized LOC112533257	-0.44	2.9611	8.6359	3.30E-03	2.83E-02
PSEN1	ENSGALG00000009320	presenilin 1	-0.44	5.9815	41.9252	9.48E-11	1.44E-08
AR	ENSGALG00000030879	androgen receptor	-0.44	4.6892	8.5818	3.40E-03	2.88E-02

CA10	ENSGALG00000002993	carbonic anhydrase 10	-0.44	3.6282	7.8180	5.17E-03	3.91E-02
SELENBP1	ENSGALG00000000866	selenium binding protein 1	-0.44	3.9044	11.8281	5.83E-04	8.11E-03
PQLC3	-----	PQ loop repeat containing 3	-0.44	4.4517	19.1756	1.19E-05	3.74E-04
GUCY1B4	ENSGALG00000005076	guanylate cyclase 1, soluble, beta 4	-0.44	3.0206	11.3608	7.50E-04	9.74E-03
ADRA2B	ENSGALG000000052016	adrenoceptor alpha 2B	-0.44	2.6648	7.3044	6.88E-03	4.77E-02
PASD1	ENSGALG000000009063	PAS domain containing 1	-0.44	3.3350	10.0901	1.49E-03	1.61E-02
POSTN	ENSGALG000000017046	periostin	-0.44	7.8263	21.7268	3.14E-06	1.24E-04
NQO2	ENSGALG000000025747	NAD(P)H quinone dehydrogenase 2	-0.44	4.1038	20.3135	6.57E-06	2.31E-04
LOC396224	-----	lamin A/C	-0.43	4.6344	19.3934	1.06E-05	3.42E-04
LOC107052740	-----	uncharacterized LOC107052740	-0.43	4.0481	25.3320	4.83E-07	2.60E-05
KIAA1143	ENSGALG000000035952	KIAA1143	-0.43	5.7346	22.2879	2.35E-06	9.73E-05
MEGF11	ENSGALG000000007631	multiple EGF like domains 11	-0.43	3.0974	8.6029	3.36E-03	2.87E-02
CPQ	ENSGALG000000030866	carboxypeptidase Q	-0.43	3.8750	8.3087	3.95E-03	3.22E-02
NTL	ENSGALG000000005156	neurotrypsin-like	-0.43	4.5426	22.2556	2.39E-06	9.87E-05
PPP1R17	ENSGALG000000036390	protein phosphatase 1 regulatory subunit 17	-0.43	4.7114	7.8748	5.01E-03	3.83E-02
DNAH1	ENSGALG000000004297	dynein axonemal heavy chain 1	-0.43	3.2262	8.4658	3.62E-03	3.03E-02
HS3ST3B1L	-----	heparan sulfate glucosamine 3-O-sulfotransferase 3B1-like	-0.43	4.9266	7.5576	5.98E-03	4.33E-02
LOC101747846	-----	uncharacterized LOC101747846	-0.43	2.6770	8.7903	3.03E-03	2.66E-02
LOC112529987	-----	uncharacterized LOC112529987	-0.43	2.9333	8.6517	3.27E-03	2.81E-02
SCUBE3	ENSGALG000000002675	signal peptide, CUB domain and EGF like domain containing 3	-0.43	6.8607	12.0043	5.31E-04	7.58E-03
PGGHG	ENSGALG000000004234	protein-glucosylgalactosylhydroxylysine glucosidase	-0.43	3.6153	16.5974	4.62E-05	1.12E-03
MYBL1	ENSGALG000000033304	MYB proto-oncogene like 1	-0.43	4.2112	13.2031	2.79E-04	4.67E-03
HELB	ENSGALG000000009885	DNA helicase B	-0.43	4.8840	33.7861	6.15E-09	5.69E-07
LOC107050995	-----	neuralized-like protein 4	-0.43	5.4411	33.9857	5.55E-09	5.19E-07
SYTL4	ENSGALG000000006786	synaptotagmin like 4	-0.43	4.4535	20.2812	6.69E-06	2.34E-04
CTBS	ENSGALG000000008780	chitobiase	-0.43	3.7617	15.0148	1.07E-04	2.16E-03
CACNA1D	ENSGALG000000005332	calcium voltage-gated channel subunit alpha1 D	-0.42	4.4649	10.9867	9.18E-04	1.13E-02
MAT2B	ENSGALG000000001750	methionine adenosyltransferase 2B	-0.42	5.5876	40.2989	2.18E-10	3.03E-08
RNF144B	ENSGALG000000012683	ring finger protein 144B	-0.42	1.8774	7.5805	5.90E-03	4.29E-02
TBC1D8	ENSGALG000000016776	TBC1 domain family member 8	-0.42	4.4025	17.2547	3.27E-05	8.37E-04
LOC112533441	-----	uncharacterized LOC112533441	-0.42	3.4200	13.4126	2.50E-04	4.30E-03
THBS4	ENSGALG000000014804	thrombospondin 4	-0.42	5.5646	20.1294	7.24E-06	2.50E-04
KLB	ENSGALG000000041663	klotho beta	-0.42	3.6054	13.5262	2.35E-04	4.09E-03
TATDN3	ENSGALG000000009811	TatD DNase domain containing 3	-0.42	4.1375	19.0457	1.28E-05	3.94E-04
MAP7D2	ENSGALG000000016415	MAP7 domain containing 2	-0.42	5.1146	19.7254	8.94E-06	2.98E-04
SLC7A2	ENSGALG000000013627	solute carrier family 7 member 2	-0.42	4.1304	14.7372	1.24E-04	2.43E-03
AKR1B10L3	ENSGALG000000019284	aldo-keto reductase family 1 member B10-like	-0.42	5.4831	13.0561	3.02E-04	4.95E-03
PROCR	ENSGALG000000006547	protein C receptor	-0.42	2.2834	9.3125	2.28E-03	2.19E-02
UVRAG	ENSGALG000000000845	UV radiation resistance associated	-0.42	4.2202	15.6901	7.46E-05	1.65E-03
MYH11	ENSGALG000000006520	myosin, heavy chain 11, smooth muscle	-0.42	5.5091	8.4461	3.66E-03	3.06E-02
LOC112531627	-----	small nucleolar RNA SNORA31	-0.42	2.7444	8.3634	3.83E-03	3.15E-02
ARHGAP40	ENSGALG000000003550	Rho GTPase activating protein 40	-0.42	4.4838	10.4207	1.25E-03	1.40E-02
ADAMTS3	ENSGALG000000011623	ADAM metallopeptidase with thrombospondin type 1 motif 3	-0.42	5.8559	24.5727	7.16E-07	3.65E-05
GPC6	ENSGALG000000016900	glypican 6	-0.42	2.6936	7.1938	7.32E-03	4.98E-02

LOC112532514	-----	golgin subfamily B member 1-like	-0.42	3.4478	12.1005	5.04E-04	7.30E-03
GRTP1	ENSGALG00000016828	growth hormone regulated TBC protein 1	-0.42	3.1535	10.7293	1.05E-03	1.25E-02
MICU2	ENSGALG00000017125	mitochondrial calcium uptake 2	-0.42	6.0676	59.8667	1.02E-14	3.88E-12
ABCG4	ENSGALG00000006795	ATP binding cassette subfamily G member 4	-0.42	3.3358	9.1394	2.50E-03	2.32E-02
SFI1	ENSGALG000000051488	SFI1 centrin binding protein	-0.41	5.1941	34.1279	5.16E-09	4.86E-07
UNC79	ENSGALG00000010874	unc-79 homolog (C. elegans)	-0.41	4.3139	7.7980	5.23E-03	3.95E-02
JMJD4	ENSGALG00000005417	jumonji domain containing 4	-0.41	6.4313	43.8155	3.61E-11	6.12E-09
TMEM106B	ENSGALG000000035140	transmembrane protein 106B	-0.41	5.5629	21.1296	4.29E-06	1.62E-04
PMLL	-----	promyelocytic leukemia-like	-0.41	2.7921	9.1806	2.45E-03	2.29E-02
SLX4	ENSGALG000000031841	SLX4 structure-specific endonuclease subunit homolog	-0.41	6.4257	23.9060	1.01E-06	4.82E-05
TBC1D19	ENSGALG000000029673	TBC1 domain family member 19	-0.41	4.4972	26.5718	2.54E-07	1.48E-05
GON4L	-----	gon-4 like	-0.41	6.3058	23.0314	1.59E-06	6.97E-05
ACADSB	ENSGALG000000041417	acyl-CoA dehydrogenase, short/branched chain	-0.41	5.7961	20.2059	6.95E-06	2.42E-04
ISPD	ENSGALG000000010795	isoprenoid synthase domain containing	-0.41	4.7572	19.1678	1.20E-05	3.75E-04
ZFAND2A	ENSGALG000000003122	zinc finger AN1-type containing 2A	-0.41	4.0705	9.4883	2.07E-03	2.07E-02
SLC16A14	ENSGALG000000002897	solute carrier family 16 member 14	-0.41	4.8796	9.7929	1.75E-03	1.82E-02
INF2	ENSGALG000000011608	inverted formin, FH2 and WH2 domain containing	-0.41	3.4949	10.2232	1.39E-03	1.52E-02
FAM84B	-----	family with sequence similarity 84 member B	-0.41	4.7994	9.7564	1.79E-03	1.85E-02
MPP3	ENSGALG000000042521	membrane palmitoylated protein 3	-0.40	4.4300	14.1825	1.66E-04	3.08E-03
SLC9A7	ENSGALG000000016734	solute carrier family 9 member A7	-0.40	3.3638	10.8592	9.83E-04	1.19E-02
DNASE2B	ENSGALG0000000028790	deoxyribonuclease 2 beta	-0.40	3.3624	13.0947	2.96E-04	4.88E-03
MANBAL15	-----	-----	-0.40	4.2546	10.9417	9.40E-04	1.15E-02
DGAT2	ENSGALG000000040418	diacylglycerol O-acyltransferase 2	-0.40	2.5207	7.7861	5.26E-03	3.96E-02
PHKA2	ENSGALG000000016518	phosphorylase kinase regulatory subunit alpha 2	-0.40	4.9122	27.1375	1.89E-07	1.17E-05
HEMK1	ENSGALG000000002253	HemK methyltransferase family member 1	-0.40	4.8224	14.2328	1.62E-04	3.00E-03
DERA	ENSGALG000000013095	deoxyribose-phosphate aldolase	-0.40	4.5685	11.6157	6.54E-04	8.83E-03
TMEM130	ENSGALG000000003569	transmembrane protein 130	-0.40	2.9258	12.0331	5.23E-04	7.50E-03
ACBD5	ENSGALG000000007519	acyl-CoA binding domain containing 5	-0.40	4.8245	19.4947	1.01E-05	3.27E-04
LOC107050437	-----	plectin-like	-0.40	3.0119	7.2476	7.10E-03	4.87E-02
AFMID	ENSGALG000000000109	arylformamidase	-0.40	5.5823	22.0910	2.60E-06	1.06E-04
NRDE2	ENSGALG000000010677	NRDE-2, necessary for RNA interference, domain containing	-0.39	5.5148	27.7599	1.37E-07	8.97E-06
TCP11L2	-----	-----	-0.39	5.1269	20.0174	7.67E-06	2.64E-04
NDRG4	ENSGALG000000043662	NDRG family member 4	-0.39	5.3637	18.7851	1.46E-05	4.40E-04
LHFPL3	ENSGALG000000043367	LHFPL tetraspan subfamily member 3	-0.39	3.2799	10.0652	1.51E-03	1.63E-02
SPRTN	ENSGALG000000011065	SprT-like N-terminal domain	-0.39	5.3259	23.3563	1.35E-06	6.09E-05
MT	-----	-----	-0.39	4.5123	12.2969	4.54E-04	6.73E-03
IL17RA	ENSGALG000000033887	interleukin 17 receptor A	-0.39	5.3280	18.2858	1.90E-05	5.41E-04
LOC107053353	-----	dispanin subfamily A member 2b-like	-0.39	3.3824	9.0777	2.59E-03	2.38E-02
CILP	ENSGALG000000007358	cartilage intermediate layer protein	-0.39	3.0687	9.3896	2.18E-03	2.14E-02
RAB4A	ENSGALG000000036218	RAB4A, member RAS oncogene family	-0.39	5.2281	23.3002	1.39E-06	6.21E-05
MMRN1	ENSGALG000000010391	multimerin 1	-0.38	3.7898	10.3267	1.31E-03	1.46E-02
IRF5	ENSGALG000000039982	interferon regulatory factor 5	-0.38	3.1202	9.8334	1.71E-03	1.78E-02
ANKRD52	ENSGALG000000031973	ankyrin repeat domain 52	-0.38	5.9130	18.5311	1.67E-05	4.89E-04
ZNF692	ENSGALG000000041845	zinc finger protein 692	-0.38	4.4944	7.8317	5.13E-03	3.89E-02

BAIAP2	ENSGALG000000042538	BAI1 associated protein 2	-0.38	4.6891	13.0654	3.01E-04	4.94E-03
IFT57	ENSGALG000000015356	intraflagellar transport 57	-0.38	4.8745	12.8621	3.35E-04	5.35E-03
MSRB3	ENSGALG000000026661	methionine sulfoxide reductase B3	-0.38	3.8680	9.3214	2.26E-03	2.18E-02
RIN3	ENSGALG000000010806	Ras and Rab interactor 3	-0.38	3.3086	10.1836	1.42E-03	1.55E-02
GALNT13	ENSGALG000000012536	polypeptide N-acetylgalactosaminyltransferase 13	-0.38	4.2972	9.7756	1.77E-03	1.83E-02
COG3	ENSGALG000000016980	component of oligomeric golgi complex 3	-0.38	5.5091	28.2393	1.07E-07	7.17E-06
BTN1	ENSGALG000000052240	B-butyrophilin 1	-0.38	4.5159	15.1194	1.01E-04	2.08E-03
CAPN2	ENSGALG000000009360	calpain 2	-0.38	3.9266	11.0946	8.66E-04	1.08E-02
LOC107057318	-----	uncharacterized LOC107057318	-0.38	4.9907	23.9444	9.92E-07	4.77E-05
LOC100858295	-----	uncharacterized LOC100858295	-0.37	4.0369	8.2615	4.05E-03	3.27E-02
AZIN2	ENSGALG000000003614	arginine decarboxylase	-0.37	3.6679	9.3427	2.24E-03	2.17E-02
TNFRSF11A	ENSGALG000000045642	TNF receptor superfamily member 11a	-0.37	3.4423	9.2078	2.41E-03	2.27E-02
NPNT	ENSGALG000000043555	nephronectin	-0.37	4.8912	9.5526	2.00E-03	2.01E-02
CHRD	ENSGALG000000026983	chordin	-0.37	3.3149	9.5537	2.00E-03	2.01E-02
BTBD11	ENSGALG000000039595	BTB domain containing 11	-0.37	4.9477	14.1235	1.71E-04	3.16E-03
CKLF	ENSGALG000000005254	chemokine like factor	-0.37	3.2512	9.4065	2.16E-03	2.12E-02
MED12L	ENSGALG000000010370	mediator complex subunit 12 like	-0.37	5.5303	22.4807	2.12E-06	8.90E-05
KIF21A	ENSGALG000000007098	kinesin family member 21A	-0.37	6.6450	25.4434	4.56E-07	2.49E-05
RMDN2	ENSGALG000000010554	regulator of microtubule dynamics 2	-0.37	2.8907	8.1792	4.24E-03	3.38E-02
LOC107052931	-----	uncharacterized LOC107052931	-0.37	3.0329	7.9462	4.82E-03	3.73E-02
RPS6KC1	ENSGALG000000009796	ribosomal protein S6 kinase C1	-0.37	5.5215	22.5318	2.07E-06	8.70E-05
KLHL42	ENSGALG000000017296	kelch like family member 42	-0.36	2.6081	7.7460	5.38E-03	4.02E-02
LYRM2	ENSGALG000000015762	LYR motif containing 2	-0.36	3.7619	12.5834	3.89E-04	6.00E-03
TTBK1	ENSGALG000000008627	tau tubulin kinase 1	-0.36	5.7080	19.3713	1.08E-05	3.45E-04
LAMA2	-----	laminin subunit alpha 2	-0.36	4.6300	12.2627	4.62E-04	6.83E-03
TTLL7	ENSGALG000000008850	tubulin tyrosine ligase like 7	-0.36	3.8677	11.6968	6.26E-04	8.54E-03
CNST	ENSGALG000000010649	consortin, connexin sorting protein	-0.36	4.4966	17.1610	3.43E-05	8.73E-04
FRRS1	ENSGALG000000005418	ferric chelate reductase 1	-0.36	4.4469	9.8776	1.67E-03	1.76E-02
KLHL14	ENSGALG000000036969	kelch like family member 14	-0.36	3.5778	9.4449	2.12E-03	2.09E-02
CGN	ENSGALG000000000920	cingulin	-0.36	4.1249	9.3477	2.23E-03	2.17E-02
EDNRB	ENSGALG000000016912	endothelin receptor type B	-0.36	4.8768	10.5301	1.17E-03	1.35E-02
CNTN3	ENSGALG000000007862	contactin 3	-0.36	3.4652	11.4529	7.14E-04	9.41E-03
PDLIM1	ENSGALG000000005422	PDZ and LIM domain 1	-0.36	4.0361	10.7630	1.04E-03	1.23E-02
ACSS3	ENSGALG000000010940	acyl-CoA synthetase short-chain family member 3	-0.36	4.1770	9.1520	2.48E-03	2.31E-02
C4HCXorf57	-----	-----	-0.36	4.1318	11.4956	6.98E-04	9.24E-03
TESK2	ENSGALG000000010230	testis-specific kinase 2	-0.36	3.9473	9.0911	2.57E-03	2.37E-02
LOC107051594	-----	uncharacterized LOC107051594	-0.36	3.3726	12.5571	3.95E-04	6.06E-03
MOGAT1	ENSGALG000000005217	monoacylglycerol O-acyltransferase 1	-0.36	2.8271	8.4457	3.66E-03	3.06E-02
FAM198A	-----	family with sequence similarity 198 member A	-0.36	4.5853	9.8718	1.68E-03	1.76E-02
DPH2	ENSGALG000000010089	DPH2 homolog	-0.36	4.2432	15.3306	9.02E-05	1.91E-03
LOC100858426	-----	uncharacterized LOC100858426	-0.36	3.2703	9.4362	2.13E-03	2.09E-02
FZD6	ENSGALG000000030626	frizzled class receptor 6	-0.36	5.5087	21.3737	3.78E-06	1.45E-04
PATJ	ENSGALG000000010934	PATJ, crumbs cell polarity complex component	-0.35	4.4341	11.2925	7.78E-04	9.99E-03
ZYG11B	-----	-----	-0.35	5.3889	24.5104	7.39E-07	3.73E-05

PLEKHA6	ENSGALG00000038399	pleckstrin homology domain containing A6	-0.35	5.3491	13.7630	2.07E-04	3.68E-03
ODF3L15	-----	-----	-0.35	6.3048	9.5987	1.95E-03	1.97E-02
ST3GAL2L	-----	-----	-0.35	3.3701	10.0253	1.54E-03	1.65E-02
PCK2	ENSGALG00000052014	phosphoenolpyruvate carboxykinase 2, mitochondrial	-0.35	5.6270	15.4048	8.68E-05	1.85E-03
TMOD2	ENSGALG00000004740	tropomodulin 2	-0.35	4.2813	9.4395	2.12E-03	2.09E-02
WWP1	ENSGALG00000041795	WW domain containing E3 ubiquitin protein ligase 1	-0.35	5.3182	14.5968	1.33E-04	2.57E-03
ZFYVE26	ENSGALG00000028762	zinc finger FYVE-type containing 26	-0.35	5.1024	16.0677	6.11E-05	1.41E-03
SMYD3	ENSGALG00000010653	SET and MYND domain containing 3	-0.35	3.4200	8.3774	3.80E-03	3.13E-02
CHRM4	ENSGALG00000008365	Gallus gallus cholinergic receptor muscarinic 4 (CHRM4), mRNA.	-0.35	4.6567	8.4300	3.69E-03	3.08E-02
LRP8	ENSGALG00000010692	LDL receptor related protein 8	-0.35	5.1100	14.3019	1.56E-04	2.92E-03
GNG11	-----	G protein subunit gamma 11	-0.35	3.3980	7.3316	6.78E-03	4.72E-02
RMND1	ENSGALG00000012968	required for meiotic nuclear division 1 homolog	-0.35	5.2107	33.3091	7.86E-09	6.95E-07
MBTPS2	ENSGALG00000016382	membrane bound transcription factor peptidase, site 2	-0.35	4.2655	14.6642	1.28E-04	2.51E-03
ZFYVE19	ENSGALG00000008460	zinc finger FYVE-type containing 19	-0.35	6.3979	15.0390	1.05E-04	2.15E-03
CSGALNACT1	ENSGALG00000010125	chondroitin sulfate N-acetylgalactosaminyltransferase 1	-0.35	3.1728	8.6192	3.33E-03	2.85E-02
PLTP	ENSGALG00000036686	phospholipid transfer protein	-0.35	4.5260	7.3004	6.89E-03	4.78E-02
ABCC3	ENSGALG00000007522	ATP binding cassette subfamily C member 3	-0.35	6.2814	13.1582	2.86E-04	4.76E-03
CUL9	-----	cullin 9	-0.35	5.2247	18.7738	1.47E-05	4.42E-04
PECR	ENSGALG00000011497	peroxisomal trans-2-enoyl-CoA reductase	-0.35	4.7793	20.5443	5.83E-06	2.10E-04
TFB1M	ENSGALG00000013647	transcription factor B1, mitochondrial	-0.35	4.3925	10.7359	1.05E-03	1.25E-02
MORC2	ENSGALG00000007512	MORC family CW-type zinc finger 1	-0.34	6.5408	20.8936	4.86E-06	1.81E-04
PIK3CD	ENSGALG00000002583	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta	-0.34	4.2282	11.9685	5.41E-04	7.70E-03
MYL12B	ENSGALG00000038635	myosin light chain 12B	-0.34	4.3564	11.1930	8.21E-04	1.04E-02
SIL1	ENSGALG00000002457	SIL1 nucleotide exchange factor	-0.34	3.5648	7.6233	5.76E-03	4.21E-02
ELMO3	ENSGALG00000030220	engulfment and cell motility 3	-0.34	3.4918	10.1332	1.46E-03	1.58E-02
ELP6	ENSGALG00000031227	elongator acetyltransferase complex subunit 6	-0.34	4.0837	7.2052	7.27E-03	4.96E-02
SOX11	ENSGALG00000016397	SRY-box 11	-0.34	6.8148	19.2698	1.13E-05	3.61E-04
ALCAM	ENSGALG00000015348	activated leukocyte cell adhesion molecule	-0.34	6.5977	8.5638	3.43E-03	2.91E-02
COL25A1	ENSGALG00000039411	collagen type XXV alpha 1 chain	-0.34	4.6909	10.3398	1.30E-03	1.45E-02
ISM2	-----	isthmin 2	-0.34	4.8959	11.1339	8.48E-04	1.06E-02
TBCEL	ENSGALG00000018819	tubulin folding cofactor E like	-0.34	4.6710	15.4800	8.34E-05	1.80E-03
LOC107057415	-----	uncharacterized LOC107057415	-0.34	5.0325	16.2245	5.63E-05	1.32E-03
DOCK10	ENSGALG00000005030	dedicator of cytokinesis 10	-0.33	4.5215	7.7672	5.32E-03	3.99E-02
RNF169	ENSGALG00000017309	ring finger protein 169	-0.33	4.0521	8.6539	3.26E-03	2.81E-02
STAGL	-----	-----	-0.33	5.8986	20.4456	6.14E-06	2.20E-04
SARAF	ENSGALG00000011395	store-operated calcium entry associated regulatory factor	-0.33	4.5391	12.7465	3.57E-04	5.60E-03
TUB	ENSGALG00000005986	tubby bipartite transcription factor	-0.33	5.4768	11.9080	5.59E-04	7.88E-03
MAN2B2	ENSGALG00000015537	mannosidase alpha class 2B member 2	-0.33	5.1245	12.5122	4.04E-04	6.19E-03
DHCR24	ENSGALG00000010798	24-dehydrocholesterol reductase	-0.33	6.1292	18.4770	1.72E-05	4.97E-04
TRAF4	ENSGALG00000003987	TNF receptor associated factor 4	-0.33	4.6865	17.6067	2.72E-05	7.24E-04
LOC107050300	-----	withdrawn	-0.33	3.2994	7.3372	6.75E-03	4.71E-02
CHST12	ENSGALG00000004276	carbohydrate sulfotransferase 12	-0.33	4.0865	10.6960	1.07E-03	1.26E-02
NUDT1	ENSGALG00000004245	nudix hydrolase 1	-0.33	6.0313	18.4377	1.76E-05	5.06E-04
C5H15orf57	ENSGALG00000029332	chromosome 5 C15orf57 homolog	-0.33	5.4589	17.2461	3.28E-05	8.39E-04

TMEM169	ENSGALG00000011493	transmembrane protein 169	-0.33	6.3634	16.0795	6.07E-05	1.41E-03
PRICKLE4	ENSGALG00000028262	prickle planar cell polarity protein 4	-0.33	4.0108	12.7415	3.58E-04	5.60E-03
PIEZO2	ENSGALG00000042134	piezo type mechanosensitive ion channel component 2	-0.33	4.4422	9.4298	2.13E-03	2.10E-02
NUDT9	ENSGALG00000010932	nudix hydrolase 9	-0.33	4.4305	10.7485	1.04E-03	1.24E-02
OGFRL1	ENSGALG00000015951	opioid growth factor receptor like 1	-0.32	4.4471	11.1239	8.52E-04	1.07E-02
RGN	ENSGALG00000016724	regucalcin	-0.32	4.6717	9.4450	2.12E-03	2.09E-02
ATR	ENSGALG00000002663	ATR serine/threonine kinase	-0.32	6.5894	15.4467	8.49E-05	1.82E-03
MRPL43	ENSGALG00000034352	mitochondrial ribosomal protein L43	-0.32	4.7641	7.9381	4.84E-03	3.74E-02
NUMBL	-----	----	-0.32	4.4197	11.2697	7.88E-04	1.01E-02
JMJD7	ENSGALG00000026846	jumonji domain containing 7	-0.32	3.5424	10.5474	1.16E-03	1.34E-02
COBLL1	ENSGALG00000011068	cordon-bleu WH2 repeat protein like 1	-0.32	4.2411	9.8469	1.70E-03	1.78E-02
LOC107051290	-----	withdrawn	-0.32	7.2330	9.7300	1.81E-03	1.87E-02
CADM2	ENSGALG00000043393	cell adhesion molecule 2	-0.32	3.7571	7.5434	6.02E-03	4.35E-02
PDPR	ENSGALG00000002690	pyruvate dehydrogenase phosphatase regulatory subunit	-0.32	5.9581	19.8494	8.38E-06	2.84E-04
PCTP	ENSGALG00000003099	phosphatidylcholine transfer protein	-0.32	5.0152	8.1833	4.23E-03	3.38E-02
DNAJC27	ENSGALG00000028967	DnaJ heat shock protein family (Hsp40) member C27	-0.32	4.1258	11.1299	8.49E-04	1.07E-02
ANAPC5	ENSGALG00000004179	anaphase promoting complex subunit 5	-0.32	5.7588	14.8582	1.16E-04	2.30E-03
TOR3A	ENSGALG00000004216	torsin family 3 member A	-0.32	3.9954	11.3830	7.41E-04	9.66E-03
CECR1	ENSGALG00000013031	cat eye syndrome chromosome region, candidate 1	-0.32	3.2515	7.5977	5.84E-03	4.26E-02
GSTO1	-----	----	-0.32	5.5020	16.7873	4.18E-05	1.03E-03
MFS4B	ENSGALG00000049668	major facilitator superfamily domain containing 4B	-0.32	5.5123	19.7487	8.83E-06	2.97E-04
LOC101750715	-----	uncharacterized LOC101750715	-0.32	4.7197	13.2928	2.66E-04	4.52E-03
TOP1MT	ENSGALG00000029572	DNA topoisomerase I mitochondrial	-0.31	5.5375	23.0606	1.57E-06	6.91E-05
DYNC1I1	ENSGALG00000009722	dynein cytoplasmic 1 intermediate chain 1	-0.31	4.6788	7.4814	6.23E-03	4.47E-02
IMPA1	ENSGALG00000034487	inositol monophosphatase 1	-0.31	5.5301	12.5498	3.96E-04	6.08E-03
LOC107057416	-----	uncharacterized LOC107057416	-0.31	4.7135	8.5812	3.40E-03	2.88E-02
PRKAA2	ENSGALG00000010826	protein kinase AMP-activated catalytic subunit alpha 2	-0.31	3.6220	7.5043	6.16E-03	4.43E-02
NEXN	ENSGALG00000008945	nexilin F-actin binding protein	-0.31	5.2389	9.3525	2.23E-03	2.17E-02
GLYCTK	ENSGALG00000054430	glycerate kinase	-0.31	5.3033	10.8459	9.90E-04	1.19E-02
LOC101751615	-----	uncharacterized LOC101751615	-0.31	3.0496	7.2759	6.99E-03	4.82E-02
SLC25A30	ENSGALG00000016979	solute carrier family 25 member 30	-0.31	4.4331	8.3764	3.80E-03	3.13E-02
CMTM6	ENSGALG00000011490	CKLF like MARVEL transmembrane domain containing 6	-0.31	5.5229	17.3119	3.17E-05	8.18E-04
DMXL2	ENSGALG00000039924	Dmx like 2	-0.31	4.6979	9.1730	2.46E-03	2.30E-02
NFKBIZ	ENSGALG00000015346	NFKB inhibitor zeta	-0.31	3.8525	8.9906	2.71E-03	2.46E-02
CCDC80	ENSGALG00000015193	coiled-coil domain containing 80	-0.31	6.7096	15.0940	1.02E-04	2.10E-03
VASN	ENSGALG00000047356	vasorin	-0.31	6.1328	17.8565	2.38E-05	6.52E-04
FKBP9	ENSGALG00000037669	FK506 binding protein 9	-0.31	8.2219	16.3297	5.32E-05	1.26E-03
PEX26	ENSGALG00000019286	peroxisomal biogenesis factor 26	-0.31	4.9790	19.7337	8.90E-06	2.98E-04
LMINA	-----	----	-0.30	4.0567	8.2559	4.06E-03	3.28E-02
KIF5C	ENSGALG00000012462	kinesin family member 5C	-0.30	6.5978	13.5054	2.38E-04	4.12E-03
TECPR1	ENSGALG00000003507	tectonin beta-propeller repeat containing 1	-0.30	3.9104	7.9427	4.83E-03	3.74E-02
CTSB	ENSGALG00000030016	cathepsin B	-0.30	5.8936	14.0589	1.77E-04	3.24E-03
SNAPIN	ENSGALG00000026796	SNAP associated protein	-0.30	5.0482	23.0055	1.62E-06	7.03E-05
EVC2	ENSGALG00000015029	EvC ciliary complex subunit 2	-0.30	4.4756	13.2557	2.72E-04	4.59E-03

MIOS	ENSGALG00000010699	meiosis regulator for oocyte development	-0.30	5.9045	13.1562	2.87E-04	4.76E-03
TCP11L1	ENSGALG00000011688	t-complex 11 like 1	-0.30	5.3672	12.4812	4.11E-04	6.25E-03
TMEM60	ENSGALG00000008330	transmembrane protein 60	-0.30	4.3556	9.0775	2.59E-03	2.38E-02
C24H11orf57	-----	-----	-0.30	5.1565	18.8050	1.45E-05	4.37E-04
TTPAL	ENSGALG00000004244	alpha tocopherol transfer protein like	-0.30	5.1976	17.9440	2.27E-05	6.27E-04
GALNT5	-----	polypeptide N-acetylgalactosaminyltransferase 5	-0.30	3.8254	8.4217	3.71E-03	3.09E-02
CDKL2	ENSGALG00000010119	cyclin dependent kinase like 2	-0.30	3.8495	7.6630	5.64E-03	4.15E-02
OSGIN2	ENSGALG00000042840	oxidative stress induced growth inhibitor family member 2	-0.30	4.4740	8.5422	3.47E-03	2.93E-02
LOC420294	-----	cyldromatosis-like	-0.30	4.6614	13.6099	2.25E-04	3.93E-03
DNAJC12	ENSGALG00000002769	DnaJ heat shock protein family (Hsp40) member C12	-0.30	4.8539	15.0186	1.06E-04	2.16E-03
TRADD	ENSGALG00000003195	TNFRSF1A associated via death domain	-0.30	4.5141	12.3736	4.35E-04	6.53E-03
DNAJC5G	-----	DnaJ heat shock protein family (Hsp40) member C5 gamma	-0.30	3.4616	7.3468	6.72E-03	4.70E-02
AATK	ENSGALG00000006901	apoptosis associated tyrosine kinase	-0.30	5.0542	10.5799	1.14E-03	1.32E-02
PMVK	ENSGALG00000046656	phosphomevalonate kinase	-0.30	4.8774	11.9800	5.38E-04	7.66E-03
CTPS2	ENSGALG00000016549	CTP synthase 2	-0.30	3.8226	10.6587	1.10E-03	1.28E-02
ARMC1	ENSGALG00000036567	armadillo repeat containing 1	-0.30	5.2941	9.7777	1.77E-03	1.83E-02
PCMTD2	ENSGALG00000005901	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	-0.29	5.2991	15.7821	7.11E-05	1.60E-03
PLCD1	ENSGALG00000005805	phospholipase C delta 1	-0.29	5.9543	9.1407	2.50E-03	2.32E-02
KIAA1147	-----	-----	-0.29	4.4351	10.6631	1.09E-03	1.28E-02
IFNAR2	ENSGALG00000041867	interferon alpha and beta receptor subunit 2	-0.29	5.4003	19.1793	1.19E-05	3.74E-04
PLEKHA7	ENSGALG00000029679	pleckstrin homology domain containing A7	-0.29	5.6426	8.6286	3.31E-03	2.84E-02
FBXO25	ENSGALG00000016359	F-box protein 25	-0.29	3.8647	8.4802	3.59E-03	3.01E-02
FBXL8	ENSGALG00000003201	F-box and leucine rich repeat protein 8	-0.29	3.6948	7.6510	5.67E-03	4.17E-02
DAP	ENSGALG00000013002	death associated protein	-0.29	5.8910	18.8222	1.43E-05	4.34E-04
AFG1L	ENSGALG00000015303	lactation elevated 1	-0.29	4.1142	10.2978	1.33E-03	1.48E-02
IRAK4	ENSGALG00000009586	interleukin 1 receptor associated kinase 4	-0.29	3.6889	8.8778	2.89E-03	2.58E-02
TRPC1	ENSGALG00000002639	transient receptor potential cation channel subfamily C member 1	-0.29	5.7582	20.6940	5.39E-06	1.97E-04
ITPR2	ENSGALG00000014071	inositol 1,4,5-trisphosphate receptor type 2	-0.29	6.1582	7.2860	6.95E-03	4.80E-02
APPL1	ENSGALG00000005527	adaptor protein, phosphotyrosine interacting with PH domain and leucine zipper 1	-0.29	5.7678	11.5593	6.74E-04	9.05E-03
TTC12	ENSGALG00000007833	tetratricopeptide repeat domain 12	-0.29	4.5829	11.4304	7.23E-04	9.50E-03
RECQL	ENSGALG00000013174	RecQ like helicase	-0.29	5.1476	15.9709	6.43E-05	1.47E-03
ELMO1	ENSGALG00000035492	engulfment and cell motility 1	-0.29	4.3862	9.8680	1.68E-03	1.76E-02
UNC5B	ENSGALG00000004569	unc-5 netrin receptor B	-0.28	5.5500	7.9794	4.73E-03	3.68E-02
NOX5	ENSGALG00000008063	NADPH oxidase 5	-0.28	6.2767	8.2626	4.05E-03	3.27E-02
PTGES3L	ENSGALG00000038129	prostaglandin E synthase 3 (cytosolic)-like	-0.28	4.1798	9.8403	1.71E-03	1.78E-02
LOC425117	-----	uncharacterized LOC425117	-0.28	6.4418	15.5016	8.24E-05	1.79E-03
PLK3	ENSGALG00000010129	polo like kinase 3	-0.28	4.5311	10.0570	1.52E-03	1.63E-02
EPG5	-----	ectopic P-granules autophagy protein 5 homolog	-0.28	5.2362	9.3471	2.23E-03	2.17E-02
SLC7A6	-----	solute carrier family 7 member 6	-0.28	5.1823	11.3300	7.63E-04	9.85E-03
TMEM170A	ENSGALG00000002861	transmembrane protein 170A	-0.28	4.7436	10.7258	1.06E-03	1.25E-02
BBS5	ENSGALG00000009846	Bardet-Biedl syndrome 5	-0.28	5.0702	10.4139	1.25E-03	1.41E-02
TMX4	ENSGALG00000028587	thioredoxin related transmembrane protein 4	-0.28	5.9879	12.8237	3.42E-04	5.44E-03
CEP350	ENSGALG00000003955	centrosomal protein 350	-0.28	6.2836	13.2324	2.75E-04	4.61E-03
FANCG	ENSGALG00000002009	Fanconi anemia complementation group G	-0.28	5.2517	7.8378	5.12E-03	3.88E-02

RCAN1	ENSGALG00000016014	regulator of calcineurin 1	-0.28	4.3664	7.6844	5.57E-03	4.11E-02
C10H15orf40	-----	C15ORF40 homolog	-0.28	4.3805	8.1766	4.24E-03	3.39E-02
TIAM1	ENSGALG00000015842	T-cell lymphoma invasion and metastasis 1	-0.28	6.4095	9.7036	1.84E-03	1.89E-02
BLOC1S3	-----	iogenesis of lysosomal organelles complex-1, subunit 3	-0.28	5.9283	8.5920	3.38E-03	2.88E-02
HIST1H2B5L	ENSGALG00000054287	histone cluster 1, H2B-V-like	-0.28	6.3293	17.4625	2.93E-05	7.68E-04
DFNA5	ENSGALG00000010997	DFNA5, deafness associated tumor suppressor	-0.28	5.7902	8.6033	3.36E-03	2.87E-02
ZBTB38	ENSGALG00000036543	zinc finger and BTB domain containing 38	-0.28	4.5363	7.7620	5.34E-03	3.99E-02
VPS37A	ENSGALG00000013646	VPS37A, ESCRT-I subunit	-0.27	4.1444	9.3753	2.20E-03	2.15E-02
NAT9	ENSGALG00000007723	N-acetyltransferase 9 (putative)	-0.27	4.8714	14.0590	1.77E-04	3.24E-03
AVL9	ENSGALG00000041568	AVL9 cell migration associated	-0.27	4.8185	8.8723	2.90E-03	2.58E-02
SCARF2	ENSGALG00000034560	scavenger receptor class F, member 2	-0.27	7.0539	15.0618	1.04E-04	2.13E-03
YAE1D1	ENSGALG00000043636	Yae1 domain containing 1	-0.27	3.9226	9.3467	2.23E-03	2.17E-02
TCEA2	ENSGALG00000005976	transcription elongation factor A2	-0.27	6.0340	18.1206	2.07E-05	5.78E-04
BAZ2B	ENSGALG00000012579	bromodomain adjacent to zinc finger domain 2B	-0.27	7.1472	12.3155	4.49E-04	6.69E-03
LOC107049545	-----	cytochrome c oxidase subunit 5B	-0.27	6.0338	10.4897	1.20E-03	1.37E-02
INTS7	ENSGALG00000009843	integrator complex subunit 7	-0.27	6.0375	11.8978	5.62E-04	7.89E-03
PRKAB1	ENSGALG00000007373	protein kinase AMP-activated non-catalytic subunit beta 1	-0.27	6.2090	18.2138	1.97E-05	5.58E-04
ALAS1	ENSGALG00000003948	5'-aminolevulinate synthase 1	-0.27	5.6723	7.4433	6.37E-03	4.54E-02
SPOCK3	ENSGALG00000009568	SPARC/osteonectin, cwcw and kazal like domains proteoglycan 3	-0.27	6.4278	12.8123	3.44E-04	5.46E-03
KRIT1	ENSGALG00000042651	KRIT1, ankyrin repeat containing	-0.27	5.7797	22.7633	1.83E-06	7.83E-05
MERTK	ENSGALG00000008257	MER proto-oncogene, tyrosine kinase	-0.27	5.1761	13.2459	2.73E-04	4.59E-03
ROBO1	ENSGALG00000015511	roundabout guidance receptor 1	-0.27	6.8791	14.0632	1.77E-04	3.24E-03
TK2	ENSGALG00000034216	thymidine kinase 2, mitochondrial	-0.27	7.0559	10.3189	1.32E-03	1.46E-02
PRR5L	ENSGALG00000007920	proline rich 5 like	-0.27	5.2611	10.5825	1.14E-03	1.32E-02
USP30	ENSGALG00000040265	ubiquitin specific peptidase 30	-0.27	5.3636	14.4442	1.44E-04	2.76E-03
MIEN1	ENSGALG00000026328	migration and invasion enhancer 1	-0.27	5.1399	14.4551	1.44E-04	2.75E-03
HARS2	ENSGALG00000029346	histidyl-tRNA synthetase 2, mitochondrial	-0.27	4.2768	7.6377	5.72E-03	4.19E-02
ABCG2	ENSGALG00000030677	ATP binding cassette subfamily G member 2 (Junior blood group)	-0.27	3.5482	7.2874	6.94E-03	4.80E-02
CCDC173	ENSGALG00000031069	coiled-coil domain containing 173	-0.27	6.4063	12.4868	4.10E-04	6.24E-03
GLUD1	-----	-----	-0.27	5.7915	21.7123	3.17E-06	1.25E-04
LOC112530288	-----	proline-rich receptor-like protein kinase PERK2	-0.27	4.4495	7.2854	6.95E-03	4.80E-02
FRMPD4	ENSGALG00000033541	FERM and PDZ domain containing 4	-0.26	3.6611	7.7232	5.45E-03	4.05E-02
SPPL2B	-----	-----	-0.26	6.6749	8.0868	4.46E-03	3.52E-02
GPATCH1	ENSGALG00000004839	G-patch domain containing 1	-0.26	5.5999	13.9799	1.85E-04	3.35E-03
RHPN2	ENSGALG00000004814	rhophilin Rho GTPase binding protein 2	-0.26	4.5231	8.8653	2.91E-03	2.58E-02
RFTN2	ENSGALG00000036471	raftlin family member 2	-0.26	6.2042	9.4118	2.16E-03	2.12E-02
MFN1	ENSGALG00000041873	mitofusin 1	-0.26	7.0836	18.1637	2.03E-05	5.69E-04
CELSR3	ENSGALG00000036763	cadherin EGF LAG seven-pass G-type receptor 3	-0.26	6.5574	12.2927	4.55E-04	6.74E-03
TRAF3IP2	ENSGALG00000015026	TRAF3 interacting protein 2	-0.26	4.9824	9.2310	2.38E-03	2.26E-02
RNF217	ENSGALG00000013651	ring finger protein 217	-0.26	6.3671	12.0575	5.16E-04	7.41E-03
NANP	ENSGALG00000047977	N-acetylneuraminic acid phosphatase	-0.26	5.2581	12.6148	3.83E-04	5.91E-03
SELENOS	ENSGALG00000007162	selenoprotein S	-0.26	5.8177	10.8588	9.83E-04	1.19E-02
PLA2G10	ENSGALG00000021314	phospholipase A2 group X	-0.26	4.8347	9.6913	1.85E-03	1.90E-02
SYNE1	ENSGALG00000013505	spectrin repeat containing, nuclear envelope 1	-0.26	5.7772	9.5404	2.01E-03	2.02E-02

XPO1p	ENSGALG00000038549	exportin 1, transcribed pseudogene	-0.26	3.7298	7.3952	6.54E-03	4.62E-02
RREB1	ENSGALG00000012799	ras responsive element binding protein 1	-0.26	5.3452	7.7213	5.46E-03	4.05E-02
KIAA0930	ENSGALG00000014226	KIAA0930	-0.26	5.3241	11.7579	6.06E-04	8.34E-03
RNF149	ENSGALG00000016779	ring finger protein 149	-0.26	5.8404	15.7769	7.13E-05	1.60E-03
TBL3	ENSGALG00000005558	transducin beta like 3	-0.26	7.2349	18.5439	1.66E-05	4.88E-04
FAM83H	ENSGALG00000033118	family with sequence similarity 83 member H	-0.26	4.1850	7.7599	5.34E-03	4.00E-02
CDIP1	ENSGALG00000036502	cell death-inducing p53 target 1	-0.26	5.0583	10.3051	1.33E-03	1.47E-02
MSRB1	ENSGALG00000005414	methionine sulfoxide reductase B1	-0.26	4.6937	7.4292	6.42E-03	4.57E-02
ZNF512B	ENSGALG00000006013	zinc finger protein 512B	-0.25	6.5257	25.4157	4.62E-07	2.51E-05
VPS37B	ENSGALG00000003743	VPS37B, ESCRT-I subunit	-0.25	6.3651	18.2178	1.97E-05	5.58E-04
NOCT	ENSGALG00000032957	nocturnin	-0.25	4.3777	9.4509	2.11E-03	2.09E-02
ICK	ENSGALG00000016321	intestinal cell kinase	-0.25	6.0281	15.1545	9.91E-05	2.05E-03
MAML1	-----	mastermind like transcriptional coactivator 1	-0.25	5.8221	10.0953	1.49E-03	1.61E-02
LOC101748694	-----	dentin sialophosphoprotein-like	-0.25	5.6915	11.7003	6.25E-04	8.54E-03
SEMA5B	ENSGALG00000011686	semaphorin 5B	-0.25	8.0429	14.9920	1.08E-04	2.17E-03
AGA	ENSGALG00000010716	aspartylglucosaminidase	-0.25	5.7214	12.8759	3.33E-04	5.32E-03
L2HGDH	ENSGALG00000012282	L-2-hydroxyglutarate dehydrogenase	-0.25	4.8378	9.4606	2.10E-03	2.08E-02
MCF2L	ENSGALG00000016834	MCF.2 cell line derived transforming sequence like	-0.25	5.1371	8.7998	3.01E-03	2.65E-02
ISCU	ENSGALG00000004869	iron-sulfur cluster assembly enzyme	-0.25	6.8065	15.7488	7.23E-05	1.62E-03
TMEM38A	ENSGALG00000003778	transmembrane protein 38A	-0.25	5.3101	12.3612	4.38E-04	6.56E-03
LETM2	ENSGALG00000036049	leucine zipper and EF-hand containing transmembrane protein 2	-0.25	4.5601	11.0503	8.87E-04	1.10E-02
VCPKMT	ENSGALG00000012269	valosin containing protein lysine methyltransferase	-0.25	4.3761	7.8801	5.00E-03	3.83E-02
ALMS1	ENSGALG00000044620	ALMS1, centrosome and basal body associated protein	-0.25	6.8736	12.1267	4.97E-04	7.23E-03
TMEM150C	ENSGALG00000011175	transmembrane protein 150C	-0.25	4.9603	8.1614	4.28E-03	3.40E-02
PRMT8	ENSGALG00000013272	protein arginine methyltransferase 1	-0.25	4.8158	7.7737	5.30E-03	3.98E-02
NCKIPSD	ENSGALG00000005713	NCK interacting protein with SH3 domain	-0.25	5.5631	8.3025	3.96E-03	3.22E-02
AXIN2	ENSGALG00000039200	axin 2	-0.25	5.3737	7.2716	7.01E-03	4.83E-02
FAAH2	ENSGALG00000028084	fatty acid amide hydrolase 2	-0.24	5.5503	14.7205	1.25E-04	2.45E-03
C4HXorf56	-----	-----	-0.24	6.1445	12.9782	3.15E-04	5.11E-03
LDLRAD3	ENSGALG00000038913	low density lipoprotein receptor class A domain containing 3	-0.24	7.1575	7.2098	7.25E-03	4.94E-02
SDC2	ENSGALG00000031424	syndecan 2	-0.24	6.4457	10.7110	1.07E-03	1.26E-02
INTS6L	ENSGALG00000006157	integrator complex subunit 6 like	-0.24	6.1823	13.4956	2.39E-04	4.14E-03
PTDSS1	ENSGALG00000030185	phosphatidylserine synthase 1	-0.24	6.1719	16.0357	6.22E-05	1.43E-03
ZDHC20	ENSGALG00000017126	zinc finger DHHC-type containing 20	-0.24	6.6535	19.0978	1.24E-05	3.84E-04
CCBL1	-----	-----	-0.24	4.4544	9.3677	2.21E-03	2.15E-02
SLC39A11	ENSGALG00000004413	solute carrier family 39 member 11	-0.24	5.0172	11.1726	8.30E-04	1.05E-02
PLEKHG3	-----	pleckstrin homology and RhoGEF domain containing G3	-0.24	5.4747	7.2357	7.15E-03	4.89E-02
SIN3A	ENSGALG00000001644	SIN3 transcription regulator family member A	-0.24	7.2455	16.3272	5.33E-05	1.26E-03
TMEM181	ENSGALG00000013737	transmembrane protein 181	-0.24	5.1592	7.6604	5.64E-03	4.16E-02
NCLN	ENSGALG00000013369	nicalin	-0.24	6.7790	16.7502	4.26E-05	1.05E-03
RLIM	ENSGALG00000007750	ring finger protein, LIM domain interacting	-0.24	6.9172	16.9535	3.83E-05	9.61E-04
MAN1B1	ENSGALG00000037375	mannosidase alpha class 1B member 1	-0.24	5.8033	8.6848	3.21E-03	2.77E-02
MVK	ENSGALG00000013848	mevalonate kinase	-0.24	5.8181	12.4298	4.23E-04	6.38E-03
ATF7IP	ENSGALG00000011814	activating transcription factor 7 interacting protein	-0.24	6.6857	11.9591	5.44E-04	7.73E-03

KIF13B	ENSGALG000000016639	kinesin family member 13B	-0.24	5.4384	9.1078	2.55E-03	2.36E-02
FAM20B	ENSGALG000000004227	FAM20B, glycosaminoglycan xylosylkinase	-0.24	5.5172	13.9024	1.93E-04	3.47E-03
GTF2F2	ENSGALG000000016974	general transcription factor IIF subunit 2	-0.24	7.2035	15.2815	9.26E-05	1.95E-03
MPHOSPH9	-----	M-phase phosphoprotein 9	-0.24	5.2130	9.9175	1.64E-03	1.73E-02
CNOT6L	ENSGALG000000010333	CCR4-NOT transcription complex subunit 6 like	-0.24	5.3242	9.7023	1.84E-03	1.89E-02
PIKFYVE	ENSGALG000000008842	phosphoinositide kinase, FYVE-type zinc finger containing	-0.24	6.3719	9.8933	1.66E-03	1.74E-02
TTC17	ENSGALG000000039558	tetratricopeptide repeat domain 17	-0.23	5.8890	12.0218	5.26E-04	7.53E-03
RAB11FIP5	ENSGALG000000047393	RAB11 family interacting protein 5	-0.23	4.9828	8.0539	4.54E-03	3.56E-02
TNFRSF1A	ENSGALG000000039461	TNF receptor superfamily member 1A	-0.23	4.5355	7.5509	6.00E-03	4.33E-02
PARP12	ENSGALG000000046187	poly(ADP-ribose) polymerase family member 12	-0.23	4.7084	8.6752	3.23E-03	2.78E-02
C1GALT1C1	ENSGALG000000008513	C1GALT1 specific chaperone 1	-0.23	4.3078	7.2174	7.22E-03	4.93E-02
PROS1	ENSGALG000000015409	protein S (alpha)	-0.23	6.8792	16.1589	5.82E-05	1.35E-03
CBL	ENSGALG000000029077	Cbl proto-oncogene	-0.23	6.4465	14.9845	1.08E-04	2.18E-03
RBM15	ENSGALG000000000401	RNA binding motif protein 15	-0.23	6.6983	8.8649	2.91E-03	2.58E-02
B4GALT4	ENSGALG000000015069	beta-1,4-galactosyltransferase 4	-0.23	5.1586	10.4591	1.22E-03	1.38E-02
GPATCH2	ENSGALG000000009627	G-patch domain containing 2	-0.23	5.5154	11.5097	6.92E-04	9.20E-03
SPINT1	ENSGALG000000008469	serine peptidase inhibitor, Kunitz type 1	-0.23	5.8626	9.3622	2.22E-03	2.16E-02
LNPK	ENSGALG000000037944	lunapark, ER junction formation factor	-0.23	5.5839	13.2438	2.73E-04	4.59E-03
DHX35	ENSGALG000000003658	DEAH-box helicase 35	-0.23	4.6799	9.8605	1.69E-03	1.77E-02
GCLC	ENSGALG000000016313	glutamate-cysteine ligase catalytic subunit	-0.23	5.3399	7.3141	6.84E-03	4.75E-02
NBEAL2	ENSGALG000000039120	neurobeachin like 2	-0.23	5.7322	11.6181	6.53E-04	8.83E-03
LOC101749469	-----	uncharacterized LOC101749469	-0.23	7.5329	9.2440	2.36E-03	2.25E-02
TRMT61A	ENSGALG000000011522	tRNA methyltransferase 61A	-0.23	5.7684	9.5196	2.03E-03	2.04E-02
BMP7	ENSGALG000000007668	bone morphogenetic protein 7	-0.23	5.8962	10.0461	1.53E-03	1.64E-02
IDI1	-----	----	-0.23	6.1165	7.4677	6.28E-03	4.50E-02
MDM2	ENSGALG000000009942	MDM2 proto-oncogene	-0.23	6.4703	8.8718	2.90E-03	2.58E-02
USP20	ENSGALG000000041104	ubiquitin specific peptidase 20	-0.22	6.0375	11.4865	7.01E-04	9.27E-03
DOCK9	ENSGALG000000016883	dedicator of cytokinesis 9	-0.22	5.0869	8.0500	4.55E-03	3.57E-02
MGARP	ENSGALG000000046580	mitochondria localized glutamic acid rich protein	-0.22	5.5878	8.1872	4.22E-03	3.38E-02
ZBTB26	ENSGALG000000042762	zinc finger and BTB domain containing 26	-0.22	5.7410	8.7884	3.03E-03	2.66E-02
CDC42EP1	ENSGALG000000038556	CDC42 effector protein 1	-0.22	7.0204	13.1934	2.81E-04	4.69E-03
CAMSAP1	ENSGALG000000001692	calmodulin regulated spectrin associated protein 1	-0.22	6.4631	10.3679	1.28E-03	1.44E-02
RD3	ENSGALG000000009861	retinal degeneration 3	-0.22	4.8471	9.1693	2.46E-03	2.30E-02
GCC1	ENSGALG000000033149	GRIP and coiled-coil domain containing 1	-0.22	4.9203	9.7960	1.75E-03	1.82E-02
PSKH1	ENSGALG000000001647	protein serine kinase H1	-0.22	5.6429	9.6597	1.88E-03	1.93E-02
FOXN2	ENSGALG000000008942	forkhead box N2	-0.22	5.7749	7.9854	4.72E-03	3.67E-02
N6AMT1	ENSGALG000000015802	N-6 adenine-specific DNA methyltransferase 1 (putative)	-0.22	4.9812	7.8615	5.05E-03	3.84E-02
ZBTB47	ENSGALG000000005287	zinc finger and BTB domain containing 47	-0.22	5.6995	8.8203	2.98E-03	2.63E-02
BCS1L	ENSGALG000000011386	BCS1 homolog, ubiquinol-cytochrome c reductase complex chaperone	-0.22	4.8420	7.4329	6.40E-03	4.56E-02
ANO5	ENSGALG000000003748	anoctamin 5	-0.22	6.5501	14.1707	1.67E-04	3.09E-03
YOD1	ENSGALG000000037597	YOD1 deubiquitinase	-0.22	6.1802	10.7439	1.05E-03	1.24E-02
MAPKAPK5	ENSGALG000000004743	mitogen-activated protein kinase-activated protein kinase 5	-0.22	6.2773	12.9882	3.13E-04	5.11E-03
LOC420992	-----	uncharacterized LOC420992	-0.22	5.9674	11.2504	7.96E-04	1.02E-02
ZC2HC1A	ENSGALG000000035932	zinc finger, C2HC-type containing 1A	-0.22	5.7628	12.3527	4.40E-04	6.59E-03

WDR6	ENSGALG00000006936	WD repeat domain 6	-0.22	5.0309	8.1713	4.26E-03	3.39E-02
TANC1	ENSGALG00000012570	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	-0.22	6.2596	9.6706	1.87E-03	1.92E-02
CTTNBP2	ENSGALG00000009134	cortactin binding protein 2	-0.22	5.0996	7.3334	6.77E-03	4.72E-02
INO80C	ENSGALG000000051335	INO80 complex subunit C	-0.22	6.0060	10.2133	1.39E-03	1.53E-02
RAB11FIP1	ENSGALG00000003129	RAB11 family interacting protein 1	-0.22	5.5137	9.9277	1.63E-03	1.72E-02
PDIA5	ENSGALG00000011689	protein disulfide isomerase family A member 5	-0.22	6.3500	12.6882	3.68E-04	5.74E-03
PGM3	ENSGALG00000015854	phosphoglucomutase 3	-0.22	5.3264	8.5087	3.53E-03	2.97E-02
UBE3B	ENSGALG00000013851	ubiquitin protein ligase E3B	-0.21	6.0024	10.1643	1.43E-03	1.56E-02
UGGT1	ENSGALG00000002141	UDP-glucose glycoprotein glucosyltransferase 1	-0.21	6.9309	8.2680	4.03E-03	3.27E-02
SYNE3	ENSGALG00000011076	spectrin repeat containing nuclear envelope family member 3	-0.21	6.2863	9.3443	2.24E-03	2.17E-02
GNS	ENSGALG00000009856	glucosamine (N-acetyl)-6-sulfatase	-0.21	6.6696	15.4242	8.59E-05	1.84E-03
NPLOC4	ENSGALG00000004583	NPL4 homolog, ubiquitin recognition factor	-0.21	6.7924	9.0485	2.63E-03	2.41E-02
GOLGA3	ENSGALG00000002158	golgin A3	-0.21	5.6928	9.2127	2.40E-03	2.27E-02
CAMK1	ENSGALG00000029912	calcium/calmodulin dependent protein kinase I	-0.21	5.2561	9.0422	2.64E-03	2.41E-02
RFC2	ENSGALG00000029449	replication factor C subunit 2	-0.21	6.2614	9.4749	2.08E-03	2.07E-02
CCDC92	ENSGALG00000003146	coiled-coil domain containing 92	-0.21	5.5542	7.5934	5.86E-03	4.27E-02
PANX2	ENSGALG00000000003	pannexin 2	-0.21	5.6368	7.7268	5.44E-03	4.05E-02
MDM4	ENSGALG00000000636	MDM4, p53 regulator	-0.21	7.4226	10.7888	1.02E-03	1.22E-02
LGALS1	ENSGALG00000027096	galectin like	-0.21	4.6639	8.4149	3.72E-03	3.10E-02
TTYH3	ENSGALG00000004310	tweety family member 3	-0.21	8.4824	11.8335	5.82E-04	8.11E-03
TMEM248	ENSGALG00000033954	transmembrane protein 248	-0.21	6.5879	11.9961	5.33E-04	7.61E-03
OSBP2	ENSGALG00000007758	oxysterol binding protein 2	-0.21	5.1127	8.3006	3.96E-03	3.22E-02
CLIP2	ENSGALG00000030450	CAP-GLY domain containing linker protein 2	-0.21	7.2871	9.3694	2.21E-03	2.15E-02
LOC776273	ENSGALG00000036085	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-1-like	-0.21	7.3000	15.3073	9.14E-05	1.93E-03
AFG3L2	ENSGALG00000013853	AFG3 like matrix AAA peptidase subunit 2	-0.21	6.8375	17.6423	2.67E-05	7.15E-04
SMYD5	ENSGALG00000022920	SMYD family member 5	-0.21	5.0026	7.7674	5.32E-03	3.99E-02
CORO7	ENSGALG00000038325	coronin 7	-0.21	5.1163	7.3497	6.71E-03	4.70E-02
ARL6IP4	ENSGALG00000003682	ADP ribosylation factor like GTPase 6 interacting protein 4	-0.21	5.8407	13.8573	1.97E-04	3.54E-03
COG2	ENSGALG00000011114	component of oligomeric golgi complex 2	-0.21	5.2859	11.5397	6.81E-04	9.10E-03
P3H3	ENSGALG00000014490	prolyl 3-hydroxylase 3	-0.21	5.4666	7.4145	6.47E-03	4.60E-02
TUBGCP6	ENSGALG00000032156	tubulin gamma complex associated protein 6	-0.21	5.0536	7.8279	5.14E-03	3.89E-02
GZF1	ENSGALG00000053640	GNDF inducible zinc finger protein 1	-0.20	5.6733	7.8766	5.01E-03	3.83E-02
SIN3B	ENSGALG00000003771	SIN3 transcription regulator family member B	-0.20	6.1070	8.8556	2.92E-03	2.59E-02
SUCLG2	ENSGALG00000007652	succinate-CoA ligase GDP-forming beta subunit	-0.20	6.9411	8.3994	3.75E-03	3.11E-02
YIPF3	ENSGALG000000041037	Yip1 domain family member 3	-0.20	5.9614	13.1601	2.86E-04	4.76E-03
CHCHD5	ENSGALG00000030457	coiled-coil-helix-coiled-coil-helix domain containing 5	-0.20	6.4152	10.4930	1.20E-03	1.37E-02
ASB6	ENSGALG00000004378	ankyrin repeat and SOCS box containing 6	-0.20	5.5897	7.6804	5.58E-03	4.12E-02
SLC25A24	ENSGALG00000001938	solute carrier family 25 member 24	-0.20	5.3139	8.7493	3.10E-03	2.70E-02
FKBP15	ENSGALG00000008838	FK506 binding protein 15	-0.20	6.2928	13.0632	3.01E-04	4.94E-03
PISD	ENSGALG00000006872	phosphatidylserine decarboxylase	-0.20	5.9242	7.8356	5.12E-03	3.88E-02
POLH	ENSGALG00000010317	DNA polymerase eta	-0.20	5.3014	8.8707	2.90E-03	2.58E-02
WDR26	ENSGALG000000043081	WD repeat domain 26	-0.20	6.7943	15.2557	9.39E-05	1.97E-03
HEY1	ENSGALG00000035031	hes related family bHLH transcription factor with YRPW motif 1	-0.20	6.1767	7.7795	5.28E-03	3.97E-02
CENPI	ENSGALG00000005038	centromere protein I	-0.20	5.9279	10.9143	9.54E-04	1.16E-02

ZBTB17	ENSGALG00000035352	zinc finger and BTB domain containing 17	-0.20	5.5238	9.9429	1.61E-03	1.71E-02
SYT11	ENSGALG00000014646	synaptotagmin 11	-0.20	7.7367	11.1444	8.43E-04	1.06E-02
E2F4	ENSGALG00000001722	E2F transcription factor 4	-0.20	6.4078	11.4987	6.96E-04	9.23E-03
ACSL1	ENSGALG00000010628	acyl-CoA synthetase long-chain family member 1	-0.20	5.9203	7.6696	5.62E-03	4.14E-02
DENND4A	ENSGALG00000041403	DENN domain containing 4A	-0.20	6.5107	8.1386	4.33E-03	3.44E-02
PLOD2	ENSGALG00000006783	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	-0.20	7.5922	11.0846	8.70E-04	1.08E-02
BOD1L1	ENSGALG00000026470	biorientation of chromosomes in cell division 1 like 1	-0.20	6.8387	7.8098	5.20E-03	3.92E-02
PLEKHO1	ENSGALG00000037540	pleckstrin homology domain containing O1	-0.20	6.1886	8.5705	3.42E-03	2.90E-02
DIS3L	ENSGALG00000007643	DIS3 like exosome 3'-5' exoribonuclease	-0.20	4.9449	7.2225	7.20E-03	4.92E-02
FAM160B1	ENSGALG00000031404	family with sequence similarity 160 member B1	-0.20	6.0890	11.9071	5.59E-04	7.88E-03
EMC3	ENSGALG00000003738	ER membrane protein complex subunit 3	-0.20	5.4547	10.5854	1.14E-03	1.32E-02
CTSD	ENSGALG00000006613	cathepsin D	-0.20	6.3516	8.9783	2.73E-03	2.47E-02
C3H1ORF198	-----	-----	-0.20	7.0214	13.9237	1.90E-04	3.44E-03
IQCE	-----	IQ motif containing E	-0.19	6.7900	10.2704	1.35E-03	1.49E-02
VPS4B	ENSGALG00000012879	vacuolar protein sorting 4 homolog B	-0.19	5.9254	8.6233	3.32E-03	2.84E-02
ZBED1	ENSGALG00000016681	dehydrogenase/reductase X-linked	-0.19	4.7626	7.2235	7.20E-03	4.92E-02
SNAPC4	ENSGALG00000044726	small nuclear RNA activating complex polypeptide 4	-0.19	5.5412	7.3927	6.55E-03	4.62E-02
PNN	ENSGALG00000010167	pinin, desmosome associated protein	-0.19	8.0080	10.1819	1.42E-03	1.55E-02
PHACTR2	ENSGALG00000013768	phosphatase and actin regulator 2	-0.19	6.3553	8.9431	2.79E-03	2.51E-02
RIT1	ENSGALG00000014647	Ras like without CAAX 1	-0.19	7.7333	8.7888	3.03E-03	2.66E-02
SCFD2	ENSGALG00000039168	sec1 family domain containing 2	-0.19	5.9459	7.9246	4.88E-03	3.76E-02
GPATCH4	ENSGALG00000048365	G-patch domain containing 4	-0.19	5.9615	7.2029	7.28E-03	4.96E-02
RNF25	ENSGALG00000011375	ring finger protein 25	-0.19	5.6819	9.4637	2.10E-03	2.08E-02
CASD1	ENSGALG00000009653	CAS1 domain containing 1	-0.19	5.6799	11.0571	8.83E-04	1.09E-02
WASHC4	ENSGALG00000028254	WASH complex subunit 4	-0.19	6.0403	11.6834	6.31E-04	8.58E-03
SSH1	-----	-----	-0.19	5.4368	7.4100	6.49E-03	4.60E-02
HGSNAT	ENSGALG00000010136	heparan-alpha-glucosaminide N-acetyltransferase	-0.19	5.5631	10.8259	1.00E-03	1.20E-02
SGF29	ENSGALG00000020590	SAGA complex associated factor 29	-0.19	6.5443	10.4453	1.23E-03	1.39E-02
RB1CC1	ENSGALG00000015259	RB1 inducible coiled-coil 1	-0.19	5.7344	8.4153	3.72E-03	3.10E-02
TELO2	ENSGALG00000009297	telomere maintenance 2	-0.18	5.3252	9.6243	1.92E-03	1.96E-02
CLCN7	ENSGALG00000030826	chloride voltage-gated channel 7	-0.18	5.5771	8.8143	2.99E-03	2.64E-02
IGDCC4	ENSGALG00000007410	immunoglobulin superfamily DCC subclass member 4	-0.18	7.0035	7.2602	7.05E-03	4.85E-02
ARFIP2	ENSGALG00000037839	ADP ribosylation factor interacting protein 2	-0.18	6.0981	10.3729	1.28E-03	1.43E-02
SLC22A5	ENSGALG00000036920	solute carrier family 22 member 5	-0.18	6.7246	11.4229	7.25E-04	9.52E-03
PCF11	ENSGALG00000017249	PCF11 cleavage and polyadenylation factor subunit	-0.18	7.2874	8.3178	3.93E-03	3.21E-02
SMIM14	ENSGALG00000014321	small integral membrane protein 14	-0.18	5.6410	7.5799	5.90E-03	4.29E-02
ATPAF1	ENSGALG00000010444	ATP synthase mitochondrial F1 complex assembly factor 1	-0.18	5.2283	7.5906	5.87E-03	4.27E-02
IREB2	ENSGALG00000035462	iron responsive element binding protein 2	-0.18	7.6632	11.4149	7.29E-04	9.53E-03
SEC61A1	ENSGALG00000005966	Sec61 translocon alpha 1 subunit	-0.18	8.1082	9.6172	1.93E-03	1.96E-02
LIPA	ENSGALG00000006378	lipase A, lysosomal acid type	-0.18	5.7719	8.8151	2.99E-03	2.64E-02
TMEM209	ENSGALG00000008036	transmembrane protein 209	-0.18	5.8948	8.4334	3.68E-03	3.07E-02
BTG1	ENSGALG00000011276	BTG anti-proliferation factor 1	-0.18	7.2913	11.2515	7.96E-04	1.02E-02
MIA3	ENSGALG00000041034	MIA family member 3, ER export factor	-0.18	6.7623	11.9298	5.52E-04	7.84E-03
SLC25A20	ENSGALG00000028227	solute carrier family 25 member 20	-0.18	7.1363	10.6443	1.10E-03	1.29E-02

LOC107050717	-----	calumenin-like	-0.18	6.0546	7.7250	5.45E-03	4.05E-02
USP44	ENSGALG000000011400	ubiquitin specific peptidase 44	-0.17	6.7124	7.2634	7.04E-03	4.84E-02
LIMK2	ENSGALG000000006950	LIM domain kinase 2	-0.17	5.7644	7.3332	6.77E-03	4.72E-02
STRADA	ENSGALG000000000550	STE20-related kinase adaptor alpha	-0.17	6.7915	8.6211	3.32E-03	2.85E-02
FAM98B	ENSGALG000000009744	family with sequence similarity 98 member B	-0.17	7.0277	7.9021	4.94E-03	3.80E-02
ATP6V1E1	ENSGALG000000013036	ATPase H+ transporting V1 subunit E1	-0.17	5.8730	7.5095	6.14E-03	4.42E-02
FMNL2	ENSGALG000000012525	formin like 2	-0.17	6.9978	8.6995	3.18E-03	2.75E-02
EPB41L1	ENSGALG000000034171	erythrocyte membrane protein band 4.1 like 1	-0.17	6.6353	9.5191	2.03E-03	2.04E-02
GATAD2A	ENSGALG000000042900	GATA zinc finger domain containing 2A	-0.17	7.6874	10.9402	9.41E-04	1.15E-02
CLCN3	ENSGALG000000009674	chloride voltage-gated channel 3	-0.17	6.5591	10.2295	1.38E-03	1.52E-02
TWF2	ENSGALG000000003977	twincillin actin binding protein 2	-0.17	7.2063	7.6669	5.62E-03	4.15E-02
PRPF4	ENSGALG000000008857	pre-mRNA processing factor 4	-0.17	6.1693	9.1313	2.51E-03	2.33E-02
NRAS	ENSGALG000000026692	neuroblastoma RAS viral oncogene homolog	-0.17	6.3362	9.4535	2.11E-03	2.09E-02
TCEB3	ENSGALG000000034625	transcription elongation factor B subunit 3	-0.16	5.7617	8.3751	3.80E-03	3.13E-02
FZD1	ENSGALG000000009064	frizzled class receptor 1	-0.16	7.4481	7.7681	5.32E-03	3.99E-02
GMPPA	ENSGALG000000002417	GDP-mannose pyrophosphorylase A	-0.16	6.1277	8.7730	3.06E-03	2.68E-02
MIER2	ENSGALG000000001108	MIER family member 2	-0.16	5.7777	8.9512	2.77E-03	2.50E-02
ST7L	ENSGALG000000001538	suppression of tumorigenicity 7 like	-0.16	5.5877	7.7772	5.29E-03	3.98E-02
PDSS1	ENSGALG000000007559	prenyl (decaprenyl) diphosphate synthase, subunit 1	-0.16	5.3148	7.5474	6.01E-03	4.34E-02
MVB12B	ENSGALG000000000950	multivesicular body subunit 12B	-0.16	7.0264	11.9003	5.61E-04	7.89E-03
SLC39A9	ENSGALG000000009438	solute carrier family 39 member 9	-0.16	6.8457	8.4361	3.68E-03	3.07E-02
GTF2H5	ENSGALG000000013733	general transcription factor IIF subunit 5	-0.16	6.9059	7.7408	5.40E-03	4.03E-02
NUP133	ENSGALG000000011091	nucleoporin 133	-0.16	6.9068	7.4123	6.48E-03	4.60E-02
BAZ1A	-----	bromodomain adjacent to zinc finger domain 1A	-0.15	6.4957	9.2488	2.36E-03	2.25E-02
SCAP	ENSGALG000000035768	SREBF chaperone	-0.15	7.1686	7.6460	5.69E-03	4.18E-02
PRCC	ENSGALG000000040696	papillary renal cell carcinoma (translocation-associated)	-0.15	6.8223	7.4012	6.52E-03	4.61E-02
TMEM57	ENSGALG000000001067	transmembrane protein 57	-0.15	6.3874	10.3007	1.33E-03	1.48E-02
GNA11	ENSGALG000000003238	G protein subunit alpha 11	-0.15	6.3483	7.4479	6.35E-03	4.54E-02
RGL1	ENSGALG000000004728	ral guanine nucleotide dissociation stimulator like 1	-0.15	7.2066	8.8781	2.89E-03	2.58E-02
SGPL1	ENSGALG000000004553	sphingosine-1-phosphate lyase 1	-0.14	6.6678	7.3730	6.62E-03	4.65E-02
LOC428335	-----	hyperpolarization activated cyclic nucleotide-gated potassium channel 2	-0.14	7.1072	8.7309	3.13E-03	2.72E-02
TSN	ENSGALG000000011652	translin	-0.14	7.2902	7.3414	6.74E-03	4.71E-02
NDST1	ENSGALG000000004581	N-deacetylase and N-sulfotransferase 1	-0.14	6.8812	7.2614	7.05E-03	4.84E-02
SMAP2	ENSGALG000000029244	small ArfGAP2	-0.14	6.5502	7.2516	7.08E-03	4.86E-02
KCTD10	ENSGALG000000005138	potassium channel tetramerization domain containing 10	-0.13	6.8974	8.0583	4.53E-03	3.56E-02