Table S1: A list of CRTC1-MAML2 fusion-regulated genes in fusion-positive H3118 MEC cells. Gene expression profiling analyses were performed on fusion/MAML2-knockdown H3118 cells and MAML2-knockdown HSY cells in comparison with their corresponding control cells. Differentially expressed genes with absolute fold change >= 2 and p<0.05 were identified. The differentially expressed genes in fusion/MAML2 knockdown H3118 cells showing the same regulated direction in MAML2 knockdown HSY cells were filtered out. The "positive" and "negative" signs denote up-regulated or down-regulated genes in KD compared to control groups, respectively. The asterisk indicates the common gene in different regulatory direction between HSY and H3118.

Gene Symbol	Gene Title	Fold change Fusion&MAML2 KD/Control (H3118)	p-value (H3118)	Fold change MAML2 KD/Control (HSY)	p-value (HSY)
LINC00473	chromosome 6 open reading frame 176	-37.12	0	-1.03	0.87
DMBT1	deleted in malignant brain tumors 1	-35.73	0	1.16	0.52
STC1	stanniocalcin 1	-21.74	0	1.03	0.83
LOC100288985	Hypothetical protein LOC100288985	-17.73	0	1.01	0.96
NR4A3	nuclear receptor subfamily 4, group A, member 3	-16.29	1.00E-05	1.02	0.95
AW302848	---	-12.93	0.00013	-1.33	0.43432
ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	-10.68	0	-1.1	0.56
KIAA1199	KIAA1199	-10.29	0.00094	-1.09	0.85
OSBP2	oxysterol binding protein 2	-9.52	1.00E-05	1.04	0.84
SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	-9.25	0.00011	-1.29	0.41
CAPN14	calpain 14	-9.04	0	-1.13	0.43
PLEKHH1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	-8.80	0	-1.15	0.30
NR4A2	nuclear receptor subfamily 4, group A, member 2	-8.67	2.00E-05	-1.05	0.82
SORBS2	sorbin and SH3 domain containing 2	-8.42	6.00E-04	-1.22	0.60
PDE4B	phosphodiesterase 4B, cAMP-specific	-8.41	0	1.09	0.58
C2CD4A	C2 calcium-dependent domain containing 4A	-7.84	0.00011	-1.03	0.91
ARG2	arginase, type II	-7.79	5.00E-05	1.1	0.70
AL355689	---	-7.04	8.00E-05	-1.18	0.51225
FAM176C	family with sequence similarity 176, member	-7.01	1.00E-05	-1	1.00
LUM	lumican	-6.98	0.00061	1.19	0.63
PECAM1	platelet/endothelial cell adhesion molecule	-6.92	0	2.01	0.00
UBE2QL1	ubiquitin-conjugating enzyme E2Q family-like 1	-6.81	0	-1.04	0.79
HAL	histidine ammonia-lyase	-6.79	2.00E-05	1.28	0.25
AGXT2L1	alanine-glyoxylate aminotransferase 2-like 1	-6.76	0.00068	1.17	0.65
SMOC1	SPARC related modular calcium binding 1	-6.47	0	-1.01	0.93
BC027448	---	-6.45	0.00045	-1.15	0.65648
BC020911	---	-6.44	0.00377	1.5	0.38979
PPP2R1B	protein phosphatase 2, regulatory subunit A, beta	-6.44	0	-1.22	0.20
NR4A1	nuclear receptor subfamily 4, group A, member 1	-6.14	4.00E-05	1.05	0.80
T79639	---	-6.06	0.02185	-1.15	0.8231
AA523939	---	-6.00	1.00E-05	-1.01	0.9645

NPR3	natriuretic peptide receptor C/guanylate cycla	-6.00	0.00019	1.02	0.93
CREG2	cellular repressor of E1A-stimulated genes 2	-5.91	2.00E-05	-1.08	0.69
LSAMP	limbic system-associated membrane protein	-5.83	6.00E-05	-1.34	0.21
PCSK1	proprotein convertase subtilisin/kexin type 1	-5.70	0.00048	1.22	0.52
RHOBTB2	Rho-related BTB domain containing 2	-5.68	0	1.06	0.66
N29850	---	-5.55	0.00118	-1.09	0.801
CHL1-AS2	CHL1 antisense RNA 2	-5.54	0.00083	-1.15	0.66
AW960100	---	-5.52	0.01095	1.06	0.90602
LGSN	lengsin, lens protein with glutamine synthetase domain	-5.27	2.00E-05	-1.38	0.10
GREM1	gremlin 1	-5.21	0.00105	-1.3	0.43
AA700206	---	-5.02	2.00E-05	-1.19	0.31209
H12214	---	-4.97	3.00E-05	-1	0.99957
MFSD2A	major facilitator superfamily domain containing 2A	-4.96	5.00E-05	-1.01	0.96
RUNX3	runt-related transcription factor 3	-4.88	0.00034	1.03	0.92
AI476341	---	-4.87	0.00659	-1.03	0.9506
DUSP1	dual specificity phosphatase 1	-4.81	0.00017	-1.03	0.89
AI141861	---	-4.75	0.00023	1.1	0.69989
SLC8A1-AS1	SLC8A1 antisense RNA 1	-4.75	0.00808	1.15	0.75
AK024800	---	-4.72	0.01546	-1.02	0.96439
M31157	---	-4.64	0.00116	-1.12	0.70413
A2M	alpha-2-macroglobulin	-4.62	0.00102	1.53	0.18
C19orf77	chromosome 19 open reading frame 77	-4.59	3.00E-05	1.09	0.63
GFRA1	GDNF family receptor alpha 1	-4.56	0.00966	-1.37	0.49
AK022474	---	-4.51	0.01964	-1.09	0.86726
CHL1	Cell adhesion molecule with homology to L1CAM	-4.47	0.00163	-1.43	0.28
EHD3	EH-domain containing 3	-4.45	0.00061	1.18	0.54
ZNF331	zinc finger protein 331	-4.24	8.00E-05	1.01	0.95
IL20	interleukin 20	-4.23	0.00345	-1.19	0.61
AI452799	---	-4.20	0.02557	-1.12	0.83286
ENO3	enolase 3 (beta, muscle)	-4.14	0.00033	-1.1	0.69
EOMES	eomesodermin	-4.10	1.00E-05	1.07	0.62
AI806183	---	-4.10	0.00016	1.01	0.96464
SLAIN1	SLAIN motif family, member 1	-4.08	0	1.07	0.60
QRFPR	pyroglutamylated RFamide peptide receptor	-4.07	0.00011	1	0.99
SIK2	salt-inducible kinase 2	-4.06	0	-1.01	0.94
PNLDC1	poly(A)-specific ribonuclease (PARN)-like domain containing 1	-4.00	4.00E-05	1.1	0.56
GREM2	gremlin 2	-3.95	0.00271	-1.04	0.91
SRGN	serglycin	-3.95	0.00518	1.22	0.59
DUSP4	dual specificity phosphatase 4	-3.93	0.00155	-1	0.99
NM_024853	---	-3.92	0.00013	-1.09	0.6543
PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	-3.89	0	1.31	0.04
PTHLH	parathyroid hormone-like hormone	-3.82	0.00035	1.35	0.20
AV702787	---	-3.81	0.00075	1.03	0.90859
FZD10	frizzled homolog 10 (Drosophila)	-3.79	0.00034	1.1	0.67
LINC00323	long intergenic non-protein coding RNA 323	-3.72	0.00249	-1.06	0.84
WDR66	WD repeat domain 66	-3.65	0.0036	1.2	0.57
CREB5	cAMP responsive element binding protein 5	-3.63	0.01072	-1.18	0.68
ENOX1	ecto-NOX disulfide-thiol exchanger 1	-3.59	6.00E-05	1.08	0.65

BG112263	---	-3.55	3.00E-05	1.06	0.69217
TMCO7	transmembrane and coiled-coil domains 7	-3.54	7.00E-05	1.03	0.84
AK026914	---	-3.52	0.00237	-1.14	0.64894
AK021804	---	-3.52	0.0043	1.03	0.92584
TMEM229B	transmembrane protein 229B	-3.51	6.00E-05	1.05	0.75
CALCA	calcitonin-related polypeptide alpha	-3.49	0.00643	1.13	0.72
AL831884	---	-3.47	0.00902	1.12	0.75966
SLCO4A1	solute carrier organic anion transporter family, member 4A1	-3.46	0	1.02	0.87
MCAM	melanoma cell adhesion molecule	-3.45	7.00E-05	1.07	0.68789
RPS2P45	Ribosomal protein S2 pseudogene 45	-3.44	0.04081	-1.13	0.81
MIR100HG	mir-100-let-7a-2 cluster host gene (non-protei	-3.42	0.00064	1.02	0.92
AIG1	androgen-induced 1	-3.42	1.00E-05	1.23	0.11
N90870	---	-3.39	0.00122	-1.11	0.66954
FAM184A	family with sequence similarity 184, member A	-3.38	8.00E-05	1.45	0.04
AI343000	---	-3.38	0.00097	-1.25	0.35792
CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	-3.38	0.00044	-1.07	0.74
AA699346	---	-3.36	0.00511	-1.1	0.76413
IL6	interleukin 6 (interferon, beta 2)	-3.35	0.00259	1.03	0.92
MCF2L-AS1	MCF2L antisense RNA 1	-3.35	0.00045	-1.14	0.53
NCALD	neurocalcin delta	-3.34	5.00E-05	1.22	0.19
PDE10A	phosphodiesterase 10A	-3.32	1.00E-04	-1.08	0.63
TECPR2	tectonin beta-propeller repeat containing 2	-3.31	0.00012	-1.09	0.62
AL832253	---	-3.28	0.00031	-1.19	0.38218
AW138143	---	-3.26	0.00025	-1.04	0.84646
AW979271	---	-3.25	0.01939	-1.12	0.78505
TNFRSF19	tumor necrosis factor receptor superfamily, member 19	-3.24	0.00183	1.05	0.84
GRAMD1B	GRAM domain containing 1B	-3.24	0.00167	-1.03	0.91
LOC100506870	hypothetical LOC100506870	-3.24	0.00071	1.13	0.58
AL832681	---	-3.22	0.00278	1.01	0.98174
SLC2A14	solute carrier family 2 (facilitated glucose transporter), member 14	-3.20	0.00037	1.03	0.87
BF508839	---	-3.19	0.00463	-1.13	0.68957
LOC283713	hypothetical protein LOC283713	-3.19	0.01709	-1.32	0.49
FAM83A	family with sequence similarity 83, member A	-3.18	0.00238	1.01	0.97
MSI2	musashi homolog 2 (Drosophila)	-3.17	0.00012	1.17	0.34
AA416756	---	-3.16	0.00578	1.09	0.77465
HAVCR2	hepatitis A virus cellular receptor 2	-3.16	5.00E-05	1.06	0.66
SFRP1	secreted frizzled-related protein 1	-3.12	0.00018	1.42	0.06
F2RL2	coagulation factor II (thrombin) receptor-like 2	-3.11	0.00039	1.28	0.22
PLD1	phospholipase D1, phosphatidylcholine-specific	-3.11	0.00164	-1.05	0.82
FUCA1	fucosidase, alpha-L- 1, tissue	-3.09	0.0048	1.12	0.71
MGC39372	serpin peptidase inhibitor, clade B (ovalbumin), member 9 pseudogene	-3.09	0.00106	1.14	0.55
AI075770	---	-3.07	0.00108	-1.17	0.48147
TPRG1	tumor protein p63 regulated 1	-3.06	3.00E-05	1.48	0.01
RAB3A	RAB3A, member RAS oncogene family	-3.05	0.00377	1.13	0.65

RASD1	RAS, dexamethasone-induced 1	-3.05	1.00E-04	1.02	0.89
LPPR4	lipid phosphate phosphatase-related protein type 4	-3.04	0.00051	-1.28	0.23
E2F2	E2F transcription factor 2	-3.03	0.0024	-1.03	0.90
STEAP4	STEAP family member 4	-3.03	0.00022	1.11	0.55
SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	-2.98	0.00472	1.53	0.16
FAM111B	family with sequence similarity 111, member B	-2.97	0.01626	-1.12	0.76
SYT12	synaptotagmin XII	-2.97	0.00015	-1.06	0.73
SMOX	spermine oxidase	-2.95	0.01324	-1.02	0.95
AW291714	---	-2.95	0.00177	-1.05	0.84341
PDE4D	phosphodiesterase 4D, cAMP-specific	-2.93	0.00034	1.05	0.79
MDS2	myelodysplastic syndrome 2 translocation associated	-2.93	0.002	-1.05	0.83
ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit a4	-2.90	0.00544	-1.42	0.23
AI082004	---	-2.90	0.00275	-1.19	0.48172
AW138815	---	-2.90	0.00162	1.13	0.58513
TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	-2.89	0.00018	-1.11	0.50
XDH	xanthine dehydrogenase	-2.87	0.02018	-1.33	0.45
BC037339	---	-2.86	0.00021	1.09	0.59679
NFASC	neurofascin	-2.85	0.00054	1.16	0.43
AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	-2.84	0.01948	1.3	0.48
LOC338651	hypothetical LOC338651	-2.82	0.04575	-1.11	0.81
PTGES	prostaglandin E synthase	-2.81	0.0132	1.07	0.83
C1QTNF6	C1q and tumor necrosis factor related protein 6	-2.81	0.00023	1.02	0.89
USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	-2.80	0.00813	1.09	0.76
FSIP1	fibrous sheath interacting protein 1	-2.80	0.00272	-1.06	0.81
TESC	tescalcin	-2.80	0.00029	-1.07	0.67
BICD2	bicaudal D homolog 2 (Drosophila)	-2.79	0.00096	1.28	0.24
COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	-2.79	0.00211	-1.12	0.63
FLJ31485	hypothetical LOC440119	-2.79	0.01063	-1.09	0.79
SEMA3B	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	-2.78	0.00031	-1.13	0.45
CA9	carbonic anhydrase IX	-2.77	0.00402	1.2	0.47
XPR1	xenotropic and polytropic retrovirus receptor	-2.77	0.00322	-1.24	0.3881
AI973099	---	-2.76	5.00E-04	1.06	0.75676
CLDN18	claudin 18	-2.76	0.00058	1.19	0.34
AA927995	---	-2.74	0.00047	-1.26	0.20483
AL833742	---	-2.74	0.01416	1.12	0.72257
PON3	paraoxonase 3	-2.74	0.00314	-1.07	0.78
RAET1E	retinoic acid early transcript 1E	-2.72	0.02536	1.21	0.61
MAGIX	MAGI family member, X-linked	-2.71	0.00432	1.23	0.43
SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	-2.70	0.01542	1.17	0.64
N55072	---	-2.70	0.00341	-1.16	0.53791
AFF3	AF4/FMR2 family, member 3	-2.69	0.00072	-1.07	0.72

KSR1	kinase suppressor of ras 1	-2.69	0.00355	1.16	0.53
ZNF462	zinc finger protein 462	-2.69	0.00885	1.21	0.51
AI078033	---	-2.68	0.00037	-1.17	0.35915
ULBP2	UL16 binding protein 2	-2.67	0.00021	-1.04	0.80
IRX4	iroquois homeobox 4	-2.67	0.00233	-1.36	0.19
LOC401317	hypothetical LOC401317	-2.67	0.01249	-1.03	0.92
CGA	glycoprotein hormones, alpha polypeptide	-2.66	0.00011	1.48	0.02
SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-2.65	0.00144	1.03	0.88
MPPED2	metallophosphoesterase domain containing 2	-2.65	0.00261	-1.35	0.21
CLMP	CXADR-like membrane protein	-2.63	7.00E-05	-1.03	0.80
KYNU	kynureninase (L-kynurenine hydrolase)	-2.63	0.00098	-1.08	0.70
BF433037	---	-2.62	0.00046	-1.12	0.49457
BF590850	---	-2.60	4.00E-05	1.13	0.30427
IGFN1	immunoglobulin-like and fibronectin type III domain containing 1	-2.60	0.00162	-1.2	0.38
C20orf132	chromosome 20 open reading frame 132	-2.58	0.00086	1.14	0.48
SLC35G2	solute carrier family 35, member G2	-2.57	0.00077	-1.04	0.81
DUSP2	dual specificity phosphatase 2	-2.57	0.00032	1.26	0.16
BC043169	---	-2.56	0.00745	1.05	0.85744
IL13RA2	interleukin 13 receptor, alpha 2	-2.55	0.01144	1.09	0.76
GAS1	growth arrest-specific 1	-2.55	0.00158	1.03	0.90
AW843302	---	-2.54	0.02473	-1.15	0.68565
MPRIP	myosin phosphatase Rho interacting protein	-2.54	0.00113	1.05	0.80
ODC1	ornithine decarboxylase 1	-2.54	0.0019	-1.06	0.79
PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	-2.54	0.00187	1	0.98
OTUD7A	OTU domain containing 7A	-2.54	0.00062	-1.05	0.77
ANKRD9	ankyrin repeat domain 9	-2.52	0.00135	-1.01	0.96
GPR133	G protein-coupled receptor 133	-2.52	0.00279	-1.11	0.63
LOC283140	hypothetical protein LOC283140	-2.52	1.00E-04	-1.09	0.49
ST6GALNAC3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	-2.51	6.00E-05	-1.13	0.29
ANO3	anoctamin 3	-2.50	0.00317	1.05	0.83
PIGH	phosphatidylinositol glycan anchor biosynthesis, class H	-2.50	0.00017	1.02	0.91
BF590769	---	-2.49	0.00036	1.05	0.73378
NID2	nidogen 2 (osteonidogen)	-2.49	0.00011	1.18	0.21
TGFB2	transforming growth factor, beta 2	-2.48	0.00244	1.21	0.37
ALDH3B1	aldehyde dehydrogenase 3 family, member B1	-2.48	9.00E-05	1.11	0.40
EXT1	exostosin 1	-2.48	0.00074	1.03	0.88
ONECUT2	one cut homeobox 2	-2.47	0.00124	-1.09	0.63
PSD3	pleckstrin and Sec7 domain containing 3	-2.47	0.03327	1.26	0.53
AVPI1	arginine vasopressin-induced 1	-2.47	0.00015	-1.01	0.95
FAM43A	family with sequence similarity 43, member A	-2.47	0.00646	1.01	0.97
NM_024912	---	-2.46	0.0057	1.21	0.43952
EYA1	eyes absent homolog 1 (Drosophila)	-2.46	0.00041	1.27	0.14
AI289774	---	-2.46	0.01229	-1.08	0.78157
RASSF10	Ras association (RalGDS/AF-6) domain family (N-terminal) member 10	-2.45	0.00684	-1.34	0.26

AW500340	---	-2.45	0.00511	1.43	0.15117
LOC100506834	hypothetical LOC100506834	-2.45	0.00317	-1.14	0.55
LOC100128653	hypothetical LOC100128653	-2.44	0.00019	1.06	0.64
TSPAN8	tetraspanin 8	-2.43	0.0296	-1	1.00
CPVL	carboxypeptidase, vitellogenic-like	-2.43	0.00902	1.09	0.74
FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	-2.42	9.00E-05	1.03	0.77
DZIP1L	DAZ interacting protein 1-like	-2.42	0.00033	1.16	0.32
SSH1	slingshot homolog 1 (Drosophila)	-2.42	0.00079	-1	0.98
BF751607	---	-2.41	0.01425	1.17	0.57802
PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	-2.41	0.02817	-1.04	0.90
ATP8B4	ATPase, class I, type 8B, member 4	-2.41	0.00865	1.3	0.32
CENPV	centromere protein V	-2.40	0.00211	-1.03	0.89
KLF9	Kruppel-like factor 9	-2.40	0.00169	1.24	0.26
PDK3	pyruvate dehydrogenase kinase, isozyme 3	-2.40	0.03499	1.06	0.86
RNF157-AS1	RNF157 antisense RNA 1	-2.40	0.01288	1.04	0.89863
AI761207	---	-2.39	0.00236	1.05	0.79811
SOBP	sine oculis binding protein homolog (Drosophila)	-2.38	0.03683	1.1	0.78
AL833050	---	-2.38	0.04945	-1.07	0.86593
BMP8B	bone morphogenetic protein 8b	-2.38	0.00438	1.1	0.66
H79303	---	-2.38	0.04488	-1.06	0.87769
CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	-2.37	1.00E-04	-1	0.97
BE219187	---	-2.36	0.04447	-1.08	0.82833
SNX25	sorting nexin 25	-2.36	0.01993	-1.08	0.79
WDR76	WD repeat domain 76	-2.35	0.00499	1.03	0.89
MKX	mohawk homeobox	-2.35	0.00244	-1.03	0.89
BE271180	---	-2.34	0.00459	1.1	0.6514
NFIA	Nuclear factor I/A	-2.34	0.02628	1.04	0.90
AL038725	---	-2.34	0.028	-1.09	0.79988
BCAR3	breast cancer anti-estrogen resistance 3	-2.34	0.00029	1.01	0.92
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	-2.34	0.02471	1.71	0.12
CASP9	caspase 9, apoptosis-related cysteine peptidase	-2.33	0.00016	1	0.99
RND2	Rho family GTPase 2	-2.32	0.00173	1.37	0.11
EPYC	epiphycan	-2.31	0.00142	1.16	0.39
C11orf86	chromosome 11 open reading frame 86	-2.31	0.00125	1.07	0.68
ZNF367	zinc finger protein 367	-2.31	0.00111	1.02	0.92
HDAC5	histone deacetylase 5	-2.30	0.00216	1	0.99
TRIM2	tripartite motif-containing 2	-2.30	0.00157	1.02	0.89
LOC728431	hypothetical LOC728431	-2.30	0.00174	-1	0.98
SLC25A45	solute carrier family 25, member 45	-2.30	0.01443	-1.09	0.75
PCDH20	protocadherin 20	-2.30	0.00226	-1.12	0.55
BTBD16	BTB (POZ) domain containing 16	-2.29	0.00114	1.1	0.58
RHOB	ras homolog gene family, member B	-2.29	0.00081	1.1	0.56
PER1	period homolog 1 (Drosophila)	-2.28	0.00018	1.03	0.82
W57613	---	-2.28	0.00354	1.21	0.35353

MYCL1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	-2.28	0.00965	1.09	0.71
IL24	interleukin 24	-2.27	0.04771	1.25	0.54
RNF150	ring finger protein 150	-2.27	0.00026	1.25	0.11
AW611560	---	-2.26	0.00519	-1.13	0.56794
AW207701	---	-2.26	0.02039	-1.21	0.50162
AA702409	---	-2.25	0.02683	1.17	0.6053
AI686793	---	-2.25	0.00066	1.1	0.50697
BDH1	3-hydroxybutyrate dehydrogenase, type 1	-2.25	0.00152	1.07	0.71
NEK4	NIMA (never in mitosis gene a)-related kinase 4	-2.25	0.02606	-1.03	0.93
MAP3K13	Mitogen-activated protein kinase kinase kinase 13	-2.24	0.01821	-1.59	0.12
NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	-2.23	0.00261	-1.04	0.82
ARPC5L	actin related protein 2/3 complex, subunit 5-like	-2.23	0.00244	-1.4	0.09
GYG2	glycogenin 2	-2.23	0.00261	-1.04	0.81
ZC3H12B	zinc finger CCCH-type containing 12B	-2.23	0.00143	-1	0.98
AREG	amphiregulin	-2.23	0.04495	1.11	0.84172
BF445387	---	-2.23	0.0027	-1.15	0.45183
EDNRB	endothelin receptor type B	-2.23	0.00037	-1.15	0.32
MBD5	methyl-CpG binding domain protein 5	-2.23	0.00097	-1.13	0.42
RSPO3	R-spondin 3 homolog (Xenopus laevis)	-2.23	0.04989	-1.42	0.34
KIAA1549	flavin containing monooxygenase 4	-2.22	0.00013	-1.3	0.04
B4GALT1	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	-2.21	0.0161	1.07	0.79
CLCNKB	chloride channel Kb	-2.21	0.02339	-1.27	0.41
AL109691	---	-2.20	0.00964	-1.11	0.64838
STAMBPL1	STAM binding protein-like 1	-2.20	0.0049	-1.06	0.79
ZBTB38	zinc finger and BTB domain containing 38	-2.19	0.04405	-1.04	0.90
MCM10	minichromosome maintenance complex component 10	-2.19	0.04848	1.01	0.97
SLC35F3	solute carrier family 35, member F3	-2.19	0.02181	1.05	0.86
ARID5B	AT rich interactive domain 5B (MRF1-like)	-2.18	0.00052	1.05	0.72
DNASE1L3	deoxyribonuclease I-like 3	-2.18	0.00419	-1.13	0.52
AU157716	---	-2.18	0.00082	1.03	0.85413
AI274981	---	-2.18	0.03251	-1	0.99629
AU155091	---	-2.17	0.01259	-1.02	0.94603
FAM87A	family with sequence similarity 87, member A	-2.17	0.00349	-1.02	0.90
KBTBD11	kelch repeat and BTB (POZ) domain containing 11	-2.17	0.0063	1.11	0.63
LOC100507455	hypothetical LOC100507455	-2.17	0.00013	1.23	0.09
KIAA1430	KIAA1430	-2.17	0.0074	1.09	0.68
PC	pyruvate carboxylase	-2.17	0.00064	1.04	0.78
PHF17	PHD finger protein 17	-2.17	0.00385	1.08	0.70
FAM216A	family with sequence similarity 216, member	-2.16	0.00016	-1.03	0.79
AW969265	---	-2.16	0.01838	-1	0.98722
LOC100505498	uncharacterized LOC100505498	-2.16	0.00894	-1.48	0.11
PRKCH	protein kinase C, eta	-2.16	0.00061	1.56	0.01
SAMD13	sterile alpha motif domain containing 13	-2.16	0.03066	-1.44	0.25
AW263539	---	-2.16	0.04293	1.09	0.79281

PXDC1	PX domain containing 1	-2.16	0.00584	-1.16	0.47
BM664532	---	-2.15	0.01996	1	0.99844
ALDH6A1	aldehyde dehydrogenase 6 family, member A1	-2.15	0.01516	1.3	0.32
AI434789	---	-2.15	0.0293	1.09	0.77744
EPHX4	epoxide hydrolase 4	-2.15	0.00106	-1.22	0.21
AA778565	---	-2.15	0.01204	1.01	0.9611
SMIM2	small integral membrane protein 2	-2.15	0.02342	1.05	0.85
SH3GL2	SH3-domain GRB2-like 2	-2.15	0.00032	1.03	0.81
AI300077	---	-2.15	0.00412	1.42	0.09748
BRI3BP	BRI3 binding protein	-2.15	0.0253	1.13	0.67
LOC100506021	hypothetical LOC100506021	-2.15	0.01054	-1.05	0.84
DLGAP1-AS1	DLGAP1 antisense RNA 1	-2.14	0.04809	-1.28	0.46
GLS2	glutaminase 2 (liver, mitochondrial)	-2.14	0.01315	1.05	0.83
ITPR1	inositol 1,4,5-triphosphate receptor, type 1	-2.14	0.00162	-1.01	0.95
ZNF141	zinc finger protein 141	-2.13	0.00661	-1.05	0.80
FKBP7	FK506 binding protein 7	-2.13	0.00893	1.11	0.63
ZNF280D	zinc finger protein 280D	-2.13	0.00421	-1.4	0.11
MCF2L	MCF.2 cell line derived transforming sequence-like	-2.13	0.00022	-1.08	0.50
WIPF1	WAS/WASL interacting protein family, member 1	-2.13	0.00149	-1.03	0.86
CMIP	c-Maf inducing protein	-2.12	0.00036	1.04	0.72796
PTP4A1	protein tyrosine phosphatase type IVA, member 1	-2.12	0.00068	1.02	0.91
DST	dystonin	-2.11	0.03694	-1.38	0.30
LOC158696	hypothetical LOC158696	-2.11	0.00213	-1.02	0.88
TYMS	thymidylate synthetase	-2.10	0.02143	-1.03	0.90
SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	-2.10	0.00061	-1.19	0.21
BCL7A	B-cell CLL/lymphoma 7A	-2.10	0.00085	1.12	0.42
MSX2	msh homeobox 2	-2.10	0.01319	1.71	0.05
BC042893	---	-2.09	0.0284	-1.06	0.84067
EN2	engrailed homeobox 2	-2.09	0.01431	1.03	0.91
AW293012	---	-2.09	0.00093	-1.16	0.30585
MCTP2	multiple C2 domains, transmembrane 2	-2.09	0.00189	1.03	0.84
FNDC3A	Fibronectin type III domain containing 3A	-2.09	0.04589	-1.48	0.24
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-2.08	0.00621	1.38	0.14
LOC100287676	Hypothetical protein LOC100287676	-2.08	0.00125	1.03	0.86
AA088388	---	-2.08	0.04262	-1.32	0.37818
AA057437	---	-2.08	0.00985	-1.26	0.31258
AI935541	---	-2.07	0.00942	-1.14	0.55583
CDK6	cyclin-dependent kinase 6	-2.07	0.00134	1.02	0.88
GPR98	G protein-coupled receptor 98	-2.07	0.01515	1.16	0.53
ORF1	hypothetical protein, clone pT-Adv JuaX22	-2.07	0.01191	1.15	0.53
CYFIP2	cytoplasmic FMR1 interacting protein 2	-2.07	0.0021	1.43	0.05
ZNF275	zinc finger protein 275	-2.07	0.04737	1.25	0.48
DPY19L2P2	dpy-19-like 2 pseudogene 2 (C. elegans)	-2.07	0.01003	-1.16	0.51
MDM2	Mdm2 p53 binding protein homolog (mouse)	-2.07	0.00477	1.1	0.63
AL049245	---	-2.06	0.00369	-1.07	0.70243
PRTG	protogenin	-2.06	0.0091	1	1.00

TOB1	transducer of ERBB2, 1	-2.06	0.03573	-1.03	0.92
SSFA2	sperm specific antigen 2	-2.05	0.00073	-1.21	0.17
LINC00521	long intergenic non-protein coding RNA 521	-2.05	0.00885	-1.1	0.65
ANKH	ankylosis, progressive homolog (mouse)	-2.05	0.01833	-1.35	0.24
ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1	-2.05	0.00097	-1.33	0.07
HCG11	HLA complex group 11	-2.04	0.00878	1.08	0.72
LOC100505974	uncharacterized LOC100505974	-2.04	0.00592	-1.05	0.81
PLLP	plasmolipin	-2.04	0.00578	-1.07	0.73
NCAM1	Neural cell adhesion molecule 1	-2.04	0.00845	-1.49	0.08
REEP1	receptor accessory protein 1	-2.04	0.00111	-1	1.00
NAV2	neuron navigator 2	-2.04	0.00061	-1.41	0.03
SMAD2	SMAD family member 2	-2.04	0.00215	-1	0.98
TMEM231	transmembrane protein 231	-2.03	0.02144	-1.01	0.98
VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	-2.03	0.01998	1.05	0.84
CAMK2B	calcium/calmodulin-dependent protein kinase II beta	-2.03	0.00028	1	0.99
KRT23	keratin 23 (histone deacetylase inducible)	-2.03	0.0272	-1.29	0.35
C11orf96	chromosome 11 open reading frame 96	-2.03	0.01409	-1.42	0.15
RGCC	regulator of cell cycle	-2.03	0.03419	1.08	0.79
ADAMTS8	ADAM metallopeptidase with thrombospondin type 1 motif, 8	-2.02	0.00352	-1.12	0.52
BC041941	---	-2.02	0.04639	-1.11	0.73358
ATOH8	Atonal homolog 8 (Drosophila)	-2.02	0.03864	1.16	0.61
RORA	RAR-related orphan receptor A	-2.02	0.00052	-1.16	0.25
LYAR	Ly1 antibody reactive homolog (mouse)	-2.01	0.00091	-1.17	0.25
SNAPC1	small nuclear RNA activating complex, polypeptide 1, 43kDa	-2.01	0.00323	1.11	0.53
TRAF3IP3	TRAF3 interacting protein 3	-2.01	0.00273	1.28	0.16
UQCRB	ubiquinol-cytochrome c reductase binding protein	-2.01	0.00074	-1.19	0.21
ACSBG1	acyl-CoA synthetase bubblegum family member 1	-2.01	0.0213	-1.29	0.31
ERGIC1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	-2.01	0.00621	-1.04	0.84
PRKAG2-AS1	PRKAG2 antisense RNA 1	-2.01	0.01612	1.15	0.54
DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	-2.01	0.0169	-1.03	0.91
NOS1	nitric oxide synthase 1 (neuronal)	-2.01	0.01753	-1.04	0.87
DLX6-AS1	DLX6 antisense RNA 1	-2.00	0.02707	-1.28	0.36
AXL	AXL receptor tyrosine kinase	-2.00	0.00608	1.01	0.98
LINC00313	long intergenic non-protein coding RNA 313	-2.00	0.01814	1.13	0.60
BU789637	---	2.00	0.01924	-1.1	0.68819
CDH8	cadherin 8, type 2	2.00	0.03039	1.53	0.14
G6PD	glucose-6-phosphate dehydrogenase	2.00	0.01192	1.08	0.71
ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	2.00	0.01198	-1.1	0.65
W87626	---	2.00	0.01801	-1.18	0.48782
MEX3B	mex-3 homolog B (C. elegans)	2.01	0.00195	1.26	0.16
NREP	neuronal regeneration related protein homolo	2.01	0.04319	-1.37	0.30
IL17RD	interleukin 17 receptor D	2.01	0.00123	1.1	0.52
HOXA10	homeobox A10	2.01	0.00161	1.37	0.06
ITPKC	inositol 1,4,5-trisphosphate 3-kinase C	2.01	0.01452	1.17	0.50
TPRXL	tetra-peptide repeat homeobox-like	2.01	0.01069	-1.24	0.32

GNG2	guanine nucleotide binding protein (G protein), gamma 2	2.01	0.00163	-1.07	0.64
FAT2	FAT tumor suppressor homolog 2 (Drosophila)	2.01	0.02442	1.14	0.62
PDZK1IP1	PDZK1 interacting protein 1	2.02	0.01489	1.24	0.35
PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	2.02	0.01614	1.01	0.96
CMTM7	CKLF-like MARVEL transmembrane domain containing 7	2.02	0.04259	1.33	0.35
RRAS	related RAS viral (r-ras) oncogene homolog	2.02	6.00E-04	-1.01	0.93
BF724621	---	2.02	0.00546	-1.25	0.25831
DGKH	diacylglycerol kinase, eta	2.02	0.00133	-1.17	0.30
GAL3ST4	galactose-3-O-sulfotransferase 4	2.02	0.00027	1.09	0.45
APOL6	apolipoprotein L, 6	2.02	0.02016	1.27	0.34
DYSF	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)	2.03	0.00116	-1.12	0.43
HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	2.03	0.02889	-1.34	0.30
FLJ42709	hypothetical LOC441094	2.03	0.01393	1.05	0.82
PADI3	peptidyl arginine deiminase, type III	2.03	0.00887	-1.2	0.39
PHLDB1	pleckstrin homology-like domain, family B, member 1	2.03	0.00347	1.03	0.88
RARRES3	retinoic acid receptor responder (tazarotene induced) 3	2.03	0.04827	1.06	0.84
LOC100126784	hypothetical LOC100126784	2.03	0.00581	-1.04	0.82
ROR1	receptor tyrosine kinase-like orphan receptor 1	2.03	0.0211	1.7	0.06
PRKCA	protein kinase C, alpha	2.04	0.00066	1.02	0.88
MIR205HG	MIR205 host gene (non-protein coding)	2.04	0.03495	-1.15	0.63
LOC100506621	hypothetical LOC100506621	2.04	0.03095	1.14	0.63
ENDOD1	endonuclease domain containing 1	2.04	0.00857	-1.16	0.47
AA644178	---	2.04	0.00168	1.01	0.95939
DFNB31	deafness, autosomal recessive 31	2.04	0.01215	-1.05	0.83
GPR161	G protein-coupled receptor 161	2.04	0.03426	-1.01	0.98
IRS1	insulin receptor substrate 1	2.05	0.04193	1.13	0.69
JAKMIP2	janus kinase and microtubule interacting protein 2	2.05	0.01565	-1.09	0.72
GRIK2	glutamate receptor, ionotropic, kainate 2	2.05	0.00074	1.03	0.83
AKR1C2	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	2.05	0.04602	-1.21	0.54
FOXL1	forkhead box L1	2.05	0.0219	-1.15	0.59
PLCB4	phospholipase C, beta 4	2.05	0.02032	1.03	0.91
CRABP2	cellular retinoic acid binding protein 2	2.05	0.00825	-1.03	0.88
GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	2.05	0.02429	-1.03	0.92
LOC100507164	hypothetical LOC100507164	2.06	0.01102	1.12	0.60
CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	2.06	0.00038	-1.27	0.08
NOX4	NADPH oxidase 4	2.06	0.01202	-1.42	0.15

CCDC80	coiled-coil domain containing 80	2.06	0.00254	1.34	0.11
GRIA2	glutamate receptor, ionotropic, AMPA 2	2.06	0.00059	-1.24	0.12
PDE5A	phosphodiesterase 5A, cGMP-specific	2.06	0.02609	-1	1.00
STON2	Stonin 2	2.06	0.0371	1	0.99
AA809487	---	2.06	0.00884	1.16	0.49235
ACPP	acid phosphatase, prostate	2.06	0.00135	1.51	0.02
GBP4	guanylate binding protein 4	2.07	0.00809	-1.13	0.57
IVNS1ABP	influenza virus NS1A binding protein	2.07	0.00016	1.1	0.36
AW953794	---	2.07	0.01007	1.02	0.94143
WNT9A	wingless-type MMTV integration site family, member 9A	2.07	0.00489	-1.08	0.68
AK021505	---	2.08	0.002	-1.06	0.71778
PI3	peptidase inhibitor 3, skin-derived	2.08	0.03815	1.02	0.94
SYNPO	synaptopodin	2.08	0.00921	-1.05	0.83
GREB1	growth regulation by estrogen in breast cancer 1	2.08	0.00014	1.13	0.26
NGEF	neuronal guanine nucleotide exchange factor	2.08	0.00323	1.24	0.25
RASL11B	RAS-like, family 11, member B	2.08	0.00127	-1.07	0.63
TP53I3	tumor protein p53 inducible protein 3	2.09	0.00058	1.04	0.74
ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	2.09	0.00895	1.01	0.95
CIITA	class II, major histocompatibility complex, transactivator	2.09	0.01009	-1	0.98
SYNPO2	synaptopodin 2	2.09	0.00858	-1.12	0.59
DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	2.09	0.00312	-1.04	0.80
IRAK2	interleukin-1 receptor-associated kinase 2	2.10	0.00105	1.45	0.03
CAMK2D	calcium/calmodulin-dependent protein kinase II delta	2.10	0.00099	1.11	0.46
CYBASC3	cytochrome b, ascorbate dependent 3	2.10	0.00236	1.03	0.88
PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	2.11	0.00514	1.11	0.59
GBP3	guanylate binding protein 3	2.11	0.00464	1.17	0.41
FRMD4B	FERM domain containing 4B	2.11	0.01174	1.3	0.27
ALOX5AP	arachidonate 5-lipoxygenase-activating protein	2.11	0.00802	-1.09	0.70
REPS2	RALBP1 associated Eps domain containing 2	2.12	0.00074	-1.08	0.59
PITPNM3	PITPNM family member 3	2.12	0.00107	1.01	0.93
CLSTN2	calsyntenin 2	2.13	0.00077	1.01	0.96
GADD45B	Growth arrest and DNA-damage-inducible, beta	2.13	0.0233	1.35	0.29
KIAA0226L	KIAA0226-like	2.13	0.01072	1.04	0.88
LINC00626	long intergenic non-protein coding RNA 626	2.13	0.00133	-1.3	0.12
NGB	neuroglobin	2.13	0.00131	1.02	0.88
TMCC2	transmembrane and coiled-coil domain family 2	2.13	0.0035	1.08	0.69
RDH16	retinol dehydrogenase 16 (all-trans)	2.14	0.00598	-1.16	0.48
BEAN1	brain expressed, associated with NEDD4, 1	2.14	0.00478	1.12	0.56
CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	2.14	0.00679	1.07	0.76
AW292830	---	2.14	0.00133	1.02	0.91966
DDX60L	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	2.14	0.02071	1.09	0.75

FBLIM1	filamin binding LIM protein 1	2.14	0.01025	-1.01	0.95
WFDC2	WAP four-disulfide core domain 2	2.14	0.00652	1.15	0.50
KIAA1841	KIAA1841	2.15	0.00068	-1.06	0.66
IGSF9	immunoglobulin superfamily, member 9	2.15	0.00934	1.04	0.88
AU151465	---	2.15	0.00373	-1.22	0.31827
ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	2.17	0.00029	-1.02	0.86
AW044663	---	2.17	0.01897	1.12	0.67908
GFPT2	glutamine-fructose-6-phosphate transaminase 2	2.17	0.02835	-1.08	0.80
SERTAD4	SERTA domain containing 4	2.17	0.00122	-1.1	0.54
MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	2.17	0.01207	-1.06	0.81
WNT10A	Wingless-type MMTV integration site family, member 10A	2.17	0.00265	-1.2	0.33
LOC728978	uncharacterized LOC728978	2.18	0.00056	1	0.99
MARCKS	myristoylated alanine-rich protein kinase C substrate	2.18	0.00228	1.13	0.50
HRH1	histamine receptor H1	2.18	0.00533	1.2	0.39
TFEB	transcription factor EB	2.18	0.00165	-1.16	0.39
ATP6V0D2	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2	2.18	0.02069	-1.39	0.25
SGK223	homolog of rat pragma of Rnd2	2.19	0.00839	1.17	0.48
ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	2.19	0.01555	1.12	0.67
KIF3C	kinesin family member 3C	2.19	0.00127	1.13	0.46
PDGFB	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	2.19	0.00056	1.04	0.76
LOC100292680	hypothetical LOC100292680	2.19	0.00376	-1.16	0.45
AI935710	---	2.20	0.00784	-1.31	0.24662
CDK15	cyclin-dependent kinase 15	2.20	0.01575	-1.24	0.42
CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	2.21	0.0361	1.12	0.73
LYST	lysosomal trafficking regulator	2.21	0.00093	1.19	0.26
NLRC5	NLR family, CARD domain containing 5	2.21	0.00966	1.13	0.60
FN1	fibronectin 1	2.23	0.00031	-1.29	0.08
LOX	lysyl oxidase	2.23	0.00388	1.02	0.91
PRR5L	proline rich 5 like	2.23	0.00145	-1	0.99
RPRM	reprimo, TP53 dependent G2 arrest mediator candidate	2.23	0.00472	-1.13	0.55
PTGER4	prostaglandin E receptor 4 (subtype EP4)	2.23	0.04292	-1.07	0.85
GLIPR1	GLI pathogenesis-related 1	2.23	0.03537	1.08	0.80
LOC643792	contactin associated protein-like 3 pseudogene	2.23	0.00128	1.17	0.36
RUNDC3B	RUN domain containing 3B	2.23	0.03495	1.04	0.91
PLEKHG1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	2.24	0.00093	1.08	0.62
NAV3	neuron navigator 3	2.24	0.01017	-1.03	0.89
CA430162	---	2.25	0.00075	1.15	0.36079
HOMER2	homer homolog 2 (Drosophila)	2.25	0.00028	1.04	0.74
COL6A3	collagen, type VI, alpha 3	2.25	0.00034	-1.11	0.45
R20640	---	2.25	0.00275	-1.42	0.09416

GBP6	guanylate binding protein family, member 6	2.25	0.00273	1.15	0.47
KALRN	kalirin, RhoGEF kinase	2.26	0.01337	1.01	0.96
C8orf48	chromosome 8 open reading frame 48	2.27	0.01136	-1	1.00
SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	2.27	0.02918	1.14	0.68
CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	2.27	0.00873	1.01	0.98
SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	2.27	0.00614	-1	1.00
AI936724	---	2.27	0.00302	-1.29	0.21124
FRMD6	FERM domain containing 6	2.28	0.00078	1.19	0.28
ST8SIA1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	2.28	0.00262	-1.03	0.90
FMO4	flavin containing monooxygenase 4	2.28	0.00582	1.7	0.04
HMGA2	high mobility group AT-hook 2	2.28	0.0189	-1.17	0.58
SHB	Src homology 2 domain containing adaptor protein B	2.28	0.02295	-1	1.00
ROS1	c-ros oncogene 1 , receptor tyrosine kinase	2.28	0.00038	-1	0.99
CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	2.29	0.0261	1.1	0.77
MLPH	melanophilin	2.29	0.0174	1.16	0.59
SAA4	serum amyloid A4, constitutive	2.30	0.00614	1.17	0.49
ALPK2	alpha-kinase 2	2.30	0.00231	-1.17	0.41
RASD2	RASD family, member 2	2.30	0.00523	-1.18	0.47
CNTNAP3	contactin associated protein-like 3	2.30	0.00013	1.26	0.08
AW189097	---	2.30	0.01593	-1.07	0.80029
RUNX1	runt-related transcription factor 1	2.30	0.00957	-1.47	0.15
TLR2	toll-like receptor 2	2.30	0.02504	-1.04	0.90
MAMDC2	MAM domain containing 2	2.31	0.01338	1.15	0.61
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	2.31	0.01038	1.02	0.93
N73742	---	2.31	0.00379	1.13	0.54978
LRRC7	leucine rich repeat containing 7	2.31	0.02334	1.26	0.46
LOXL2	lysyl oxidase-like 2	2.32	0.0121	1.19	0.52
ADM	adrenomedullin	2.32	0.00796	1.19	0.48
ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	2.33	0.04535	-1.03	0.94
EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	2.33	0.00082	-1	0.98
DUSP10	dual specificity phosphatase 10	2.33	0.00032	-1.22	0.17
PLA2R1	phospholipase A2 receptor 1, 180kDa	2.33	0.00637	1.03	0.88508
RHBDL2	rhomboid, veinlet-like 2 (Drosophila)	2.33	0.00279	1	0.99
AI223854	---	2.34	0.00425	1.13	0.57936
BC040310	---	2.34	0.00044	1.03	0.85012
MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	2.34	0.00665	1.19	0.47
PLAC2	placenta-specific 2 (non-protein coding)	2.34	0.00424	1.09	0.70
ANKRD55	Ankyrin repeat domain 55	2.34	0.03682	-1.06	0.87
BF110268	---	2.35	0.02002	1.01	0.9638
UAP1L1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	2.35	0.00283	-1.15	0.49
CAMK2A	calcium/calmodulin-dependent protein kinase II alpha	2.35	0.00052	1	0.98

HERC5	hect domain and RLD 5	2.36	0.00028	1.03	0.83
AW292765	---	2.37	0.00376	1.11	0.61664
MTMR11	myotubularin related protein 11	2.37	0.00138	1.08	0.67
IFITM10	interferon induced transmembrane protein 10	2.38	0.04561	1.06	0.88
OPTN	optineurin	2.38	4.00E-04	1.08	0.60
CAV1	caveolin 1, caveolae protein, 22kDa	2.38	0.03554	-1.02	0.96
APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	2.39	0.00196	1.21	0.34
LAMC2	laminin, gamma 2	2.39	0.01315	-1.03	0.90
UPP1	uridine phosphorylase 1	2.39	0.02813	-1.04	0.90
FTH1	ferritin, heavy polypeptide 1	2.39	0.00426	1.06	0.79
BC041915 *	---	2.41	0.00502	-2.89	0.0018
SLIT3	slit homolog 3 (Drosophila)	2.41	0.00012	1.02	0.8795
COL5A1	collagen, type V, alpha 1	2.41	0.00067	-1.09	0.59
DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	2.41	0.00374	1.16	0.50
NMNAT2	nicotinamide nucleotide adenylyltransferase 2	2.41	0.01638	1.17	0.60
ZEB1	zinc finger E-box binding homeobox 1	2.41	0.0028	1.17	0.45
TRIM47	tripartite motif-containing 47	2.42	0.00066	-1.03	0.86
AA702930	---	2.43	0.02414	-1.18	0.61656
CA442342	---	2.43	0.00012	1.02	0.84539
LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	2.44	0.00201	-1.08	0.70
SLC2A12	solute carrier family 2 (facilitated glucose transporter), member 12	2.44	0.00246	-1.07	0.73
IGFBP5	insulin-like growth factor binding protein 5	2.45	0.00098	1.69	0.02
AF339789	---	2.46	0.0366	1.14	0.71273
MMP10	matrix metallopeptidase 10 (stromelysin 2)	2.46	0.01733	-1.08	0.80
TNF	tumor necrosis factor	2.46	0.00053	-1.01	0.96
KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3	2.46	0.00231	1.13	0.56
C1orf116	chromosome 1 open reading frame 116	2.47	0.00197	1.01	0.97
TGFB1I1	transforming growth factor beta 1 induced transcript 1	2.47	0.01473	1.02	0.96
TFCP2L1	transcription factor CP2-like 1	2.47	0.00346	-1.1	0.66
KLF7	Kruppel-like factor 7 (ubiquitous)	2.47	0.00165	1.07	0.74
LCP1	lymphocyte cytosolic protein 1 (L-plastin)	2.47	0.0248	-1.42	0.31
VGLL3	vestigial like 3 (Drosophila)	2.48	0.04286	1.61	0.24
NUAK2	NUAK family, SNF1-like kinase, 2	2.49	0.00441	1.3	0.28
CTHRC1	collagen triple helix repeat containing 1	2.49	0.00273	1.02	0.94
PAX5	paired box 5	2.49	6.00E-05	-1.74	0.00
RUNX1-IT1	RUNX1 intronic transcript 1 (non-protein codir	2.50	0.02351	1.16	0.67
BC020897	---	2.50	0.01663	-1.02	0.95992
MAN1A1	mannosidase, alpha, class 1A, member 1	2.52	0.00193	1.55	0.06
PPAP2B	phosphatidic acid phosphatase type 2B	2.52	0.01711	1.24	0.49
SCN3B	sodium channel, voltage-gated, type III, beta	2.52	0.00298	1.1	0.66
BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	2.52	0.00412	1.02	0.94
GLIS1	GLIS family zinc finger 1	2.52	0.001	1.19	0.34
SLC6A20	solute carrier family 6 (proline IMINO transporter), member 20	2.52	0.00993	-1.13	0.67
CNPY3	canopy 3 homolog (zebrafish)	2.53	0.00913	-1.13	0.65
EMP1	epithelial membrane protein 1	2.53	0.00554	-1.01	0.96
NKAIN4	Na+/K+ transporting ATPase interacting 4	2.54	0.00059	1.06	0.71

IL32	interleukin 32	2.54	0.00512	-1.04	0.88
BM873997	---	2.54	0.00723	-1.08	0.76795
PROC	protein C (inactivator of coagulation factors Va and VIIIa)	2.55	0.00161	-1.11	0.59
SEMA3E	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	2.55	0.03018	-1.06	0.87
SCN2A	sodium channel, voltage-gated, type II, alpha subunit	2.56	0.04753	-1.55	0.30
CYP27C1	cytochrome P450, family 27, subfamily C, polypeptide 1	2.58	0.02897	1.02	0.95
ARHGEF28	Rho guanine nucleotide exchange factor (GEF)	2.58	4.00E-05	-1.05	0.66
BF508849	---	2.58	0.00127	-1.02	0.93729
CAPN6	calpain 6	2.59	0.00064	-1.46	0.06
PLCE1	phospholipase C, epsilon 1	2.60	0.00048	1.05	0.75
BM992214	---	2.60	0.00428	1.1	0.70284
GULP1	GULP, engulfment adaptor PTB domain containing 1	2.60	0.00093	1.16	0.43
TMEM200A	transmembrane protein 200A	2.60	0.0012	1.07	0.72
C10orf10	chromosome 10 open reading frame 10	2.60	0.02025	1.42	0.31
IL16	interleukin 16 (lymphocyte chemoattractant factor)	2.60	0.00629	1.06	0.83
W23691	---	2.60	0.00139	-1.07	0.73078
ARL4C	ADP-ribosylation factor-like 4C	2.61	5.00E-05	1.08	0.49
TEAD2	TEA domain family member 2	2.61	0.01421	1.05	0.87
CD44	CD44 molecule (Indian blood group)	2.62	0.00099	1.07	0.71
LOXL4	lysyl oxidase-like 4	2.63	0.00381	1.04	0.86
SYT1	synaptotagmin I	2.63	0.00153	-1.06	0.77
CSF1R	colony stimulating factor 1 receptor	2.63	0.00231	-1.65	0.05
HS3ST2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	2.64	0.00102	1.16	0.45
PSG1	pregnancy specific beta-1-glycoprotein 1	2.64	0.03158	-1.05	0.90
R71596	---	2.64	0.00974	-1.06	0.83822
MALL	mal, T-cell differentiation protein-like	2.65	0.00358	1.26	0.34
DSG3	desmoglein 3	2.66	7.00E-05	1.04	0.74
STRA6	stimulated by retinoic acid gene 6 homolog (mouse)	2.66	0.00108	1.08	0.68
C20orf160	chromosome 20 open reading frame 160	2.66	0.0102	-1.02	0.96
LGALS3	lectin, galactoside-binding, soluble, 3	2.66	0.00032	1.02	0.90
BC025343	---	2.68	0.03919	-1.15	0.73487
CTSS	cathepsin S	2.70	0.00603	1.23	0.45
C3orf52	chromosome 3 open reading frame 52	2.72	0.00756	-1.06	0.8312
NID1	nidogen 1	2.72	0.00362	-1.15	0.57
CORO2B	coronin, actin binding protein, 2B	2.72	0.0018	-1.11	0.63
AI245300	---	2.73	0.00861	-1.15	0.64071
BF110534	---	2.73	1.00E-04	-1.33	0.06382
LURAP1L	leucine rich adaptor protein 1-like	2.73	0.00655	1.03	0.90
MARK1	MAP/microtubule affinity-regulating kinase 1	2.74	0.00072	1.02	0.91
KIAA1211L	KIAA1211-like	2.75	0.00177	1.15	0.52
L1CAM	L1 cell adhesion molecule	2.75	0.01583	-1.06	0.87
PLK2	polo-like kinase 2	2.75	0.00141	1.27	0.28
DSC2	desmocollin 2	2.76	0.00066	1.23	0.29
IVL	involucrin	2.77	7.00E-05	-1.19	0.21
SEC14L2	SEC14-like 2 (S. cerevisiae)	2.78	0.00167	1.14	0.55

LRRN1	leucine rich repeat neuronal 1	2.79	8.00E-05	-1.62	0.01
SFN	stratifin	2.79	0.00106	-1.03	0.88
MIAT	myocardial infarction associated transcript (non-protein coding)	2.81	0.00368	-1.06	0.81
AI733336	---	2.82	0.00076	-1.08	0.69344
ZNF365	zinc finger protein 365	2.83	0.00018	-1.02	0.88
DAPL1	death associated protein-like 1	2.83	0.00749	1.45	0.23
SCN3A	sodium channel, voltage-gated, type III, alpha subunit	2.84	0.02159	-1.86	0.13
SAMD9L	sterile alpha motif domain containing 9-like	2.84	0.01154	1.21	0.56
FAM49A	family with sequence similarity 49, member A	2.84	9.00E-05	1.33	0.07
KRT6B	keratin 6B	2.84	0.00038	1.07	0.70
BTBD19	BTB (POZ) domain containing 19	2.85	0.04713	1.16	0.74
BC028670	---	2.85	0.00075	1.15	0.4797
HDAC9	histone deacetylase 9	2.86	0.00363	1.28	0.35
KRT14	keratin 14	2.86	0.00215	-1.11	0.65
FILIP1L	filamin A interacting protein 1-like	2.86	0.00308	1.08	0.77
IFIT2	interferon-induced protein with tetratricopeptide repeats 2	2.86	0.00031	1.29	0.16
AF009316	---	2.87	0.00383	-1.31	0.32074
TSHZ3	teashirt zinc finger homeobox 3	2.88	0.00219	1.1	0.68
DUSP5P	dual specificity phosphatase 5 pseudogene	2.89	5.00E-04	-1.07	0.71
GPER	G protein-coupled estrogen receptor 1	2.89	8.00E-05	1.08	0.56
RSAD2	radical S-adenosyl methionine domain containing 2	2.90	0.00155	-1.44	0.13
UNC5CL	unc-5 homolog C (C. elegans)-like	2.90	0.00036	-1.01	0.95
AACSP1	acetoacetyl-CoA synthetase pseudogene 1	2.91	0.00358	1.01	0.97
GBP2	guanylate binding protein 2, interferon-inducible	2.91	0.01575	1.24	0.55
PLXDC1	plexin domain containing 1	2.91	0.00125	1.1	0.67
ALDH1A3	aldehyde dehydrogenase 1 family, member A3	2.92	0.00026	1.1	0.56
HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	2.92	0.0414	1.29	0.57
TUBA1A	tubulin, alpha 1a	2.94	0.00044	1.01	0.96
THBD	thrombomodulin	2.96	0.00033	1.02	0.92
KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	2.97	0.00436	-1.35	0.30
STK32A	serine/threonine kinase 32A	2.97	0.00116	1.06	0.80
CLEC7A	C-type lectin domain family 7, member A	2.99	0.01612	-1.03	0.93
AK026743	---	2.99	0.01533	-1.16	0.68377
AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	3.00	0.00137	-1.03	0.91
MAP7D2	MAP7 domain containing 2	3.00	3.00E-05	1.11	0.40
RASSF6	Ras association (RalGDS/AF-6) domain family member 6	3.01	0.00019	1.14	0.45
CXCL10	chemokine (C-X-C motif) ligand 10	3.01	0.00484	-1.04	0.88
BLNK	B-cell linker	3.03	0.0093	1.02	0.96
APCDD1L-AS1	APCDD1L antisense RNA 1	3.04	0.00017	-1.37	0.08
KRT16	keratin 16	3.04	0.00032	-1.18	0.37
RTTN	rotatin	3.06	0.00032	-1.05	0.79

ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	3.06	2.00E-05	1.25	0.10
AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	3.06	0.00128	1.28	0.30
UGT1A1	UDP glucuronosyltransferase 1 family, polypeptide A1	3.06	0.00336	1.61	0.11
SLAMF7	SLAM family member 7	3.08	3.00E-04	1.08	0.65
MYLK	myosin light chain kinase	3.09	0.00691	1.06	0.85
TAGLN	transgelin	3.10	0.04019	1.26	0.62
MERTK	c-mer proto-oncogene tyrosine kinase	3.13	0.0346	1.13	0.79
AF339813	---	3.13	0.04392	-1.88	0.21725
TNFAIP3	tumor necrosis factor, alpha-induced protein 3	3.13	0.00128	1.34	0.23
NANOS1	nanos homolog 1 (Drosophila)	3.14	0.00516	1.24	0.48061
RIMS2	regulating synaptic membrane exocytosis 2	3.15	0.00195	-1.37	0.23
SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	3.17	0.00085	-1	0.99
LPAR5	lysophosphatidic acid receptor 5	3.18	6.00E-05	1.05	0.71
PAMR1	peptidase domain containing associated with muscle regeneration 1	3.20	0.00053	-1.33	0.19
MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	3.20	0.01557	1.04	0.91
PDZK1	PDZ domain containing 1	3.21	0.0207	-1	0.99
ADAM12	ADAM metallopeptidase domain 12	3.22	0.00035	1.02	0.92
TNFSF15	tumor necrosis factor (ligand) superfamily, me	3.22	0.00739	1.64	0.15862
LRRC4C	leucine rich repeat containing 4C	3.22	0.00111	-1.81	0.03
OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	3.25	0.00216	1.24	0.42
BF509371	---	3.26	0.00287	1.29	0.36837
TNFAIP2	tumor necrosis factor, alpha-induced protein 2	3.26	0.00256	1.05	0.87
CTSH	cathepsin H	3.27	9.00E-05	-1.03	0.83
PIM1	pim-1 oncogene	3.29	1.00E-05	1.05	0.67
ATP13A2	ATPase type 13A2	3.29	0.00037	-1.02	0.92
CSF1	colony stimulating factor 1 (macrophage)	3.30	0.00859	1.39	0.36
ITGB6	integrin, beta 6	3.34	0.00944	-1.07	0.84
TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	3.34	0.00567	1.14	0.69
DLX2	distal-less homeobox 2	3.34	0.00143	1.27	0.35
R83322	---	3.35	0.00277	-1.48	0.19026
APCDD1L	adenomatosis polyposis coli down-regulated 1-like	3.37	7.00E-05	-1.02	0.89
GSTA4	glutathione S-transferase alpha 4	3.38	0.00147	1.1	0.69
MMP9	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	3.42	0.00353	1.23	0.50
PSG4	pregnancy specific beta-1-glycoprotein 4	3.44	0.01617	-1.03	0.94
IFIT3	interferon-induced protein with tetratricopeptide repeats 3	3.45	2.00E-05	1.23	0.13
GPR115	G protein-coupled receptor 115	3.48	1.00E-04	1.03	0.87
AU155234	---	3.50	0.00096	-1.32	0.2709
IFIT1	interferon-induced protein with tetratricopeptide repeats 1	3.50	0.00049	1.16	0.50
PSG7	pregnancy specific beta-1-glycoprotein 7 (gene/pseudogene)	3.51	0.02646	-1.41	0.47
PLAU	plasminogen activator, urokinase	3.55	0.00081	-1.01	0.95

AF318340	---	3.57	0.00437	-1.35	0.3674
AHNAK2	AHNAK nucleoprotein 2	3.58	0.00281	1.04	0.89
NRP1	neuropilin 1	3.61	0.01165	-1.16	0.71
SLC47A2	solute carrier family 47, member 2	3.61	0.00311	1.21	0.54
BC033184	---	3.61	0.01033	-1.59	0.25325
IGFL1	IGF-like family member 1	3.62	0.00797	1.39	0.38
VTCN1	V-set domain containing T cell activation inhibitor 1	3.62	0.00121	1.39	0.23
OASL	2'-5'-oligoadenylate synthetase-like	3.66	0.00153	-1	0.99
HES2	hairy and enhancer of split 2 (Drosophila)	3.67	0.01278	-1.18	0.69
BHLHE41	basic helix-loop-helix family, member e41	3.70	0.00104	-1.09	0.75
LOC100506374	uncharacterized LOC100506374	3.70	0.00108	1.2	0.48
VSNL1	visinin-like 1	3.72	0.00093	-1.08	0.76
PRLR	prolactin receptor	3.74	0.0016	1.08	0.79
LY96	lymphocyte antigen 96	3.83	0.00309	-1.01	0.97
SH3RF2	SH3 domain containing ring finger 2	3.83	2.00E-05	1.05	0.76
IFI44L	interferon-induced protein 44-like	3.83	0.0069	-1.17	0.67
MFAP2	microfibrillar-associated protein 2	3.87	0.00492	1.12	0.74
TGM5	transglutaminase 5	3.87	0.00299	1.1	0.77
SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	3.87	0.00374	-1.37	0.36
RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	3.88	4.00E-05	-1.01	0.97
MX2	myxovirus (influenza virus) resistance 2 (mouse)	3.91	0	1.02	0.82
KLK6	kallikrein-related peptidase 6	3.98	2.00E-05	-1.05	0.74
SNCAIP	synuclein, alpha interacting protein	4.03	0.00597	-1.15	0.71
SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter), member 3	4.12	2.00E-05	1.07	0.63
CXCL14	chemokine (C-X-C motif) ligand 14	4.13	0.0139	1.09	0.85
ARL14	ADP-ribosylation factor-like 14	4.13	0.00047	-1.25	0.37
ERC1	ELKS/RAB6-interacting/CAST family member 1	4.15	9.00E-05	1.21	0.33
MAP2	microtubule-associated protein 2	4.21	1.00E-04	1.29	0.21
ABLIM3	actin binding LIM protein family, member 3	4.23	0.00021	1.22	0.38
MMP28	matrix metallopeptidase 28	4.23	0.00033	1.03	0.91
HMOX1	heme oxygenase (decycling) 1	4.24	0.00012	1.05	0.82
IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	4.25	0.00021	-1.02	0.93
KLK10	kallikrein-related peptidase 10	4.27	1.00E-04	1.2	0.37
EPHA4	EPH receptor A4	4.30	0.00042	-1.02	0.94
WNT5B	wingless-type MMTV integration site family, member 5B	4.31	2.00E-05	1.27	0.16
ADTRP	androgen-dependent TFPI-regulating protein	4.37	5.00E-05	1.23	0.28
TCHH	trichohyalin	4.40	1.00E-04	-1.05	0.79
LYPD1	LY6/PLAUR domain containing 1	4.42	2.00E-04	1.05	0.82
P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	4.42	0	-1.05	0.71
FABP4	fatty acid binding protein 4, adipocyte	4.45	0.01837	1.49	0.45
SLITRK6	SLIT and NTRK-like family, member 6	4.46	1.00E-05	-1.32	0.08
SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	4.54	0.01435	1.06	0.90

C18orf1	chromosome 18 open reading frame 1	4.58	0.0013	1.08	0.81
AI694413	---	4.61	0.02425	-1.1	0.86638
GPR39	G protein-coupled receptor 39	4.64	0.00029	1.34	0.26
CLCA2	chloride channel accessory 2	4.68	0.00369	1.08	0.83
ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	4.70	2.00E-05	1.06	0.72
MTSS1	metastasis suppressor 1	4.83	0.00047	1.04	0.90
AI819863	---	4.87	0.00019	1.1	0.67672
KRT75	keratin 75	4.93	0.00057	1.15	0.63
NEURL3	neuralized homolog 3 (Drosophila) pseudogene	5.03	0	-1.1	0.48
CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	5.08	0.00545	1	1.00
C4orf26	chromosome 4 open reading frame 26	5.16	0	1.16	0.26
PHEX	phosphate regulating endopeptidase homolog, X-linked	5.21	0.0014	-1.01	0.98
KRT6A	keratin 6A	5.22	4.00E-05	1.24	0.27
KLK7	kallikrein-related peptidase 7	5.24	0.00023	1.37	0.23
CXCL12	chemokine (C-X-C motif) ligand 12	5.33	0.01159	-1.1	0.86
BG010493	---	5.34	0.002	-1.08	0.84059
SPRR1B	small proline-rich protein 1B	5.39	6.00E-05	1.01	0.98
SPOCD1	SPOC domain containing 1	5.54	0.00084	-1.18	0.61
C6orf141	chromosome 6 open reading frame 141	5.57	0	1.01	0.96
KRT6C	keratin 6C	5.58	3.00E-05	-1.09	0.65
GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	5.65	6.00E-05	-1.02	0.93
DACT1	dapper, antagonist of beta-catenin, homolog 1	5.65	0.00065	1.89	0.07
FBXO32	F-box protein 32	5.68	0.00022	1.39	0.23
TNC	tenascin C	5.68	9.00E-05	-1.04	0.85
AL389956	---	5.70	0.00055	1.03	0.92538
BF244402	---	5.75	1.00E-05	1.74	0.00616
SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	5.78	0.00155	-1.45	0.33
MMP13	matrix metallopeptidase 13 (collagenase 3)	5.84	0.00162	-1.14	0.72
AI333596	---	5.88	0.00143	1.02	0.96015
CST6	cystatin E/M	5.90	1.00E-05	1.05	0.79
MMP12	matrix metallopeptidase 12 (macrophage elastase)	6.06	0.00429	-1.12	0.80
TRIM22	tripartite motif-containing 22	6.10	8.00E-04	1.01	0.97
TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	6.38	0.00206	-1.11	0.80
SCN9A	sodium channel, voltage-gated, type IX, alpha subunit	6.49	0	-1.03	0.86
KRT15	keratin 15	6.65	0.00113	1.48	0.31
IFI44	Interferon-induced protein 44	7.11	0.00021	1.02	0.94
VAV3	vav 3 guanine nucleotide exchange factor	7.17	0.00034	1.22	0.53
FLG-AS1	FLG antisense RNA 1	7.24	2.00E-05	-1.1	0.65
KLK5	kallikrein-related peptidase 5	7.66	0	-1.04	0.81
GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	7.82	0.0038	1.14	0.80
FYB	FYN binding protein	8.14	0.00032	1.22	0.56
TSPAN2	tetraspanin 2	8.66	3.00E-05	1.18	0.50
GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	9.73	6.00E-05	-1.01	0.97

MMP1	matrix metallopeptidase 1 (interstitial collagenase)	11.48	7.00E-05	-1.5	0.22
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	15.77	0	-1.05	0.79
GPNMB	glycoprotein (transmembrane) nmb	16.00	2.00E-05	1.17	0.58
KANK4	KN motif and ankyrin repeat domains 4	16.06	0	1.02	0.94
MMP3	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	16.38	0.00023	-1.08	0.86
CCL2	chemokine (C-C motif) ligand 2	42.02	0	1.04	0.88

Table S2. A list of differentially regulated genes affected by CREB depletion in human fusion-positive MEC, but not fusion-negative cells. The The differentially expressed genes after CREB was depleted were identified in both fusion-positive MEC H3118 cells and fusion-negative HSY cells. Those CREB-regulated genes in H3118 cells showing the same regulated direction in fusion-negative HSY were then filtered out. The “positive” and “negative” signs denote up-regulated or down-regulated genes in KD compared to control groups, respectively. The asterisk indicates the common gene in different regulatory direction between HSY and H3118 cells.

Gene Symbol	Gene Title	Fold change CREB KD/Control (H3118)	p-value (H3118)	Fold change CREB KD/Control (HSY)	p-value (HSY)
LOC100288985	Hypothetical protein LOC100288985	-41.04	8.00E-05	1.34	0.63291
STC1	stanniocalcin 1	-26.98	2.00E-05	1.07	0.88257
SMOX	spermine oxidase	-21.45	0	-1.57	0.08883
BCAT1	branched chain amino-acid transaminase 1, cytosolic	-21.11	1.00E-05	1.12	0.7643
DUSP6	dual specificity phosphatase 6	-20.44	0	-1.02	0.9561
AREG	amphiregulin	-18.34	0	-1.04	0.91531
NGFR	nerve growth factor receptor	-16.22	0	-1.11	0.56875
GPC6	glypican 6	-14.21	0	1.13	0.51143
ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit a4	-13.97	0	1.02	0.94703
PLAT	plasminogen activator, tissue	-13.61	1.00E-05	-1.35	0.39202
AI093492	---	-12.24	0.00023	-2.44	0.07764
GDF15	growth differentiation factor 15	-10.63	0.00361	-1.47	0.55723
CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	-10.61	6.00E-05	-2.02	0.08082
UGT8	UDP glycosyltransferase 8	-10.45	1.00E-05	-1.06	0.83301
IL1B	interleukin 1, beta	-10.32	7.00E-05	-1.09	0.8173
CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	-10.27	0	-1.32	0.31101
BC027448	---	-10.18	0	1.04	0.85824
HBEGF	heparin-binding EGF-like growth factor	-10.15	3.00E-05	-1.33	0.40938
MFSD2A	major facilitator superfamily domain containing 2A	-10.08	0	-1.55	0.12522
LOC100506870	uncharacterized LOC100506870	-10.04	0.00016	-1.78	0.17859
STC2	stanniocalcin 2	-9.91	0.01089	1.11	0.88649
LIF	leukemia inhibitory factor	-9.77	4.00E-05	-1.16	0.67491
HAL	histidine ammonia-lyase	-9.33	0	1.16	0.27135
PSAT1	phosphoserine aminotransferase 1	-9.13	2.00E-04	-1.96	0.11804
DMBT1	deleted in malignant brain tumors 1	-8.39	5.00E-05	-1.02	0.95146
CYP24A1	cytochrome P450, family 24, subfamily A, polypeptide 1	-8.31	0.00013	-1.04	0.92083
CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)	-8.30	0.0188	-1.3	0.73814
PNMA2	paraneoplastic Ma antigen 2	-8.08	3.00E-05	1.11	0.73676
SLCO4A1	solute carrier organic anion transporter family, member 4A1	-7.92	6.00E-05	-1.01	0.97645
IL11	interleukin 11	-7.62	7.00E-05	1.71	0.12442
JAM3	junctional adhesion molecule 3	-7.59	0	-1.14	0.56748
PPP1R3C	protein phosphatase 1, regulatory subunit 3C	-7.28	1.00E-05	-1.2	0.49605
HPCAL4	hippocalcin like 4	-7.20	0	-1.22	0.28761
PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	-7.16	9.00E-05	-1.89	0.07106
DHRS2 *	dehydrogenase/reductase (SDR family) member 2	-7.12	0.00051	4.02	0.00531
ELOVL6	ELOVL fatty acid elongase 6	-7.06	0	-1.34	0.16912
CTSL2	cathepsin L2	-6.95	0.00071	-1.21	0.65159

IL8	interleukin 8	-6.83	0	1.94	0.00775
SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	-6.82	0	-1.04	0.86809
AREGB	Amphiregulin B	-6.68	0	-1.07	0.74896
FOS	FBJ murine osteosarcoma viral oncogene homolog	-6.66	3.00E-05	-1.51	0.16137
AI936034	---	-6.65	6.00E-05	-1.06	0.83556
SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	-6.58	1.00E-05	-1.01	0.9801
PLAU	plasminogen activator, urokinase	-6.56	0	-1.04	0.81734
ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	-6.51	0.00015	1.21	0.56536
DUSP5	dual specificity phosphatase 5	-6.50	0	1.09	0.68515
AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	-6.50	0.00013	-1.58	0.17957
LOC541471	uncharacterized LOC541471	-6.43	0	-1.14	0.28764
KLF9	Kruppel-like factor 9	-6.30	0.00242	-1.18	0.72463
KYNU	kynureninase	-6.23	0	-1.68	0.02918
NR4A3	nuclear receptor subfamily 4, group A, member 3	-6.19	3.00E-05	-1.2	0.48638
SPRY4	sprouty homolog 4 (Drosophila)	-6.03	0	-1.15	0.52646
ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	-5.95	4.00E-05	-1.67	0.07485
CHL1-AS2	CHL1 antisense RNA 2 (non-protein coding)	-5.91	2.00E-05	-1.23	0.405
HIST1H3A	histone cluster 1, H3a	-5.89	9.00E-05	-1.94	0.04225
DESI1	desumoylating isopeptidase 1	-5.86	5.00E-04	-3.64	0.00435
KIF21B	kinesin family member 21B	-5.83	1.00E-04	-1.36	0.3111
KCNQ5	potassium voltage-gated channel, KQT-like subfamily, member 5	-5.82	0	1.06	0.71397
CA12	carbonic anhydrase XII	-5.81	0.00027	1.15	0.67697
TIMP1	TIMP metallopeptidase inhibitor 1	-5.76	0.00025	-1.79	0.10017
SH3GL3	SH3-domain GRB2-like 3	-5.76	0.00054	1.16	0.68034
AL049245	---	-5.75	0	-1.05	0.7761
PCOLCE2	procollagen C-endopeptidase enhancer 2	-5.72	0	1.08	0.70474
IL1A	interleukin 1, alpha	-5.65	4.00E-05	1.14	0.62626
F2RL2	coagulation factor II (thrombin) receptor-like 2	-5.63	0.00428	1.59	0.35014
TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	-5.62	0.00027	1.13	0.70417
SPP1	secreted phosphoprotein 1	-5.59	0.00028	1.03	0.93498
ANO3	anoctamin 3	-5.59	0	-1.5	0.05304
LOC100653010	uncharacterized LOC100653010	-5.58	0.02428	-1.45	0.57858
FSTL1	follistatin-like 1	-5.57	1.00E-05	-1.81	0.01931
CBLC	Cbl proto-oncogene, E3 ubiquitin protein ligase C	-5.55	1.00E-05	-1.19	0.41841
IGFBP7	insulin-like growth factor binding protein 7	-5.48	0	-1.54	0.02086
CDC45	cell division cycle 45 homolog (S. cerevisiae)	-5.43	0.00073	-1.18	0.65399
FAM101B	family with sequence similarity 101, member B	-5.41	0.00092	1.34	0.44382
SAA1	serum amyloid A1	-5.34	0.00149	-1.38	0.4275
PECAM1	platelet/endothelial cell adhesion molecule 1	-5.33	8.00E-05	-1.25	0.41692
KIF15	kinesin family member 15	-5.23	0.00205	-1.55	0.30368
DUSP4	dual specificity phosphatase 4	-5.23	0	-1.31	0.11602
SKA3	spindle and kinetochore associated complex subunit 3	-5.22	0.00665	-1.4	0.50876
TRIB3	tribbles homolog 3 (Drosophila)	-5.20	0.02592	-1.29	0.69487
CTGF	connective tissue growth factor	-5.16	2.00E-05	-1.18	0.49192
BU955063	---	-5.15	2.00E-04	1.01	0.97263

FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	-5.11	0	-1.4	0.09444
FAM216A	family with sequence similarity 216, member A	-5.08	0.00011	-1.73	0.06788
HTRA3	HtrA serine peptidase 3	-5.05	0	-1.2	0.30938
TSPAN12	tetraspanin 12	-5.05	0.01751	-2.85	0.09684
MELK	maternal embryonic leucine zipper kinase	-5.04	0.00751	-1.11	0.83668
COL4A1	collagen, type IV, alpha 1	-5.01	2.00E-05	-1.13	0.58963
FGF2	fibroblast growth factor 2 (basic)	-4.96	5.00E-05	1.1	0.70631
RASD1	RAS, dexamethasone-induced 1	-4.96	2.00E-05	1.05	0.8222
SLC9A7	solute carrier family 9, subfamily A (NHE7, cation proton antiporter 7), member 7	-4.92	0.00171	-1.03	0.94709
BC043357	---	-4.87	6.00E-05	-1.05	0.85858
SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	-4.85	8.00E-04	-1.05	0.88585
SFRP1	secreted frizzled-related protein 1	-4.85	4.00E-05	-1.18	0.49084
SYT12	synaptotagmin XII	-4.85	1.00E-05	-1.3	0.21144
TMCC3	transmembrane and coiled-coil domain family 3	-4.85	0.00034	-1.71	0.10433
EXO1	exonuclease 1	-4.83	4.00E-05	-1.08	0.75247
KCNG1	potassium voltage-gated channel, subfamily G, member 1	-4.82	1.00E-05	-1.1	0.65882
SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	-4.81	0.00034	-1.22	0.52294
CENPQ	centromere protein Q	-4.80	0.00204	-1.59	0.25458
PAQR5	progestin and adipoQ receptor family member V	-4.77	7.00E-05	1.25	0.39312
TGFB2	transforming growth factor, beta 2	-4.76	0.00034	-1.21	0.53776
CKAP2L	cytoskeleton associated protein 2-like	-4.74	0.00111	-1.49	0.27735
LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	-4.73	0.00032	1.27	0.43833
SPRY2	sprouty homolog 2 (Drosophila)	-4.67	0.00054	-1.17	0.61829
CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	-4.67	0.00032	1.21	0.5261
MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2	-4.65	0.0036	1.05	0.90275
SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	-4.65	0.00044	-1.07	0.83686
SLC9A1	solute carrier family 9, subfamily A (NHE1, cation proton antiporter 1), member 1	-4.65	1.00E-05	-1.75	0.01078
LOC100507307	uncharacterized LOC100507307	-4.63	0	-1.47	0.05153
PLEK2	pleckstrin 2	-4.60	0.00022	1.47	0.19332
ABCA12	ATP-binding cassette, sub-family A (ABC1), member 12	-4.59	0.00018	-1.13	0.65965
MIR17HG	MIR17 host gene (non-protein coding)	-4.59	3.00E-05	-1.95	0.01178
IL27RA	interleukin 27 receptor, alpha	-4.54	0.00111	1.15	0.6816
KCNK5	potassium channel, subfamily K, member 5	-4.54	0.00062	-1.41	0.29856
C11orf82	chromosome 11 open reading frame 82	-4.53	0.00019	-1.39	0.25196
IL20	interleukin 20	-4.53	0.0017	-1.1	0.7965
ADORA2B	adenosine A2b receptor	-4.52	8.00E-05	-1.07	0.77319
CLGN	calmegin	-4.51	0.00913	1.02	0.97307
CLDN10	claudin 10	-4.50	0	-1.01	0.96027
SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	-4.50	1.00E-05	-1.32	0.16415
GALNT12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)	-4.47	8.00E-05	-1.85	0.02656

GRAMD1B	GRAM domain containing 1B	-4.47	5.00E-05	1.26	0.33164
CTH *	cystathionase (cystathionine gamma-lyase)	-4.45	0.00113	2.38	0.0172
MCM6	minichromosome maintenance complex component 6	-4.45	0.00083	-1.08	0.81474
MKI67	antigen identified by monoclonal antibody Ki-67	-4.45	0.00115	-1.5	0.25198
BC015429	---	-4.39	0.00034	-1.07	0.82733
PTPRE	protein tyrosine phosphatase, receptor type, E	-4.38	1.00E-05	-1.23	0.2796
SLC39A8	solute carrier family 39 (zinc transporter), member 8	-4.36	7.00E-05	-1.68	0.04818
C11orf86	chromosome 11 open reading frame 86	-4.34	0.00013	1.03	0.89948
ADAM23	ADAM metallopeptidase domain 23	-4.34	0.00016	1.18	0.53925
ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	-4.33	0.0113	1.37	0.52752
RMI2	RMI2, RecQ mediated genome instability 2, homolog (S. cerevisiae)	-4.33	0.00544	-1.02	0.95803
STEAP4	STEAP family member 4	-4.27	0.00091	-1.99	0.0536
BEND6	BEN domain containing 6	-4.27	2.00E-05	-1.42	0.10304
DEPDC1	DEP domain containing 1	-4.25	0.01146	-1.33	0.55778
ZNF697	zinc finger protein 697	-4.24	0.00231	-1.46	0.31807
SORBS2	sorbin and SH3 domain containing 2	-4.23	0.00779	-1.05	0.91115
SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-4.22	0.00034	1.45	0.20854
TPRG1	tumor protein p63 regulated 1	-4.22	0.00033	1.2	0.51485
PHF20L1	PHD finger protein 20-like 1	-4.19	0.01178	-1.7	0.28264
HIST1H1D	histone cluster 1, H1d	-4.18	0	-1.07	0.67885
PHGDH	phosphoglycerate dehydrogenase	-4.18	0.00044	1.06	0.83981
DLGAP5	discs, large (Drosophila) homolog-associated protein 5	-4.17	0.02027	-1.76	0.30433
GJA3	gap junction protein, alpha 3, 46kDa	-4.17	0.01423	-1.11	0.83517
CHSY3	chondroitin sulfate synthase 3	-4.16	0.00028	-1.13	0.65437
LUM	lumican	-4.16	0.03358	-1.33	0.63405
MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	-4.16	1.00E-05	-1.35	0.11375
TRAF5	TNF receptor-associated factor 5	-4.14	0	1.62	0.00257
HOXD-AS1	HOXD cluster antisense RNA 1 (non-protein coding)	-4.14	0.00449	-2.62	0.03358
XPR1	xenotropic and polytropic retrovirus receptor 1	-4.14	0.00657	-1.47	0.37781
LAPTM5	lysosomal protein transmembrane 5	-4.14	0	-1.03	0.80679
BCL3	B-cell CLL/lymphoma 3	-4.12	1.00E-05	-1.06	0.72639
FNDC3B	fibronectin type III domain containing 3B	-4.12	0.00773	-1.92	0.15967
GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	-4.10	0.00012	-1.01	0.95903
ERRFI1	ERBB receptor feedback inhibitor 1	-4.08	1.00E-04	-1.84	0.02463
CDT1	Chromatin licensing and DNA replication factor 1	-4.08	0.02336	-1.17	0.76838
EGR1	early growth response 1	-4.08	1.00E-05	-2.26	0.00114
DKK1	dickkopf 1 homolog (Xenopus laevis)	-4.06	0.00966	-1.56	0.33531
AA938184	---	-4.06	0.02191	1.07	0.90576
BF590917	---	-4.06	1.00E-04	1.02	0.9321
UBE2V2	ubiquitin-conjugating enzyme E2 variant 2	-4.05	0.00781	-3.57	0.01315
ALDH1A3	aldehyde dehydrogenase 1 family, member A3	-4.04	0.00105	-1.29	0.4377
SLCO2A1	solute carrier organic anion transporter family, member 2A1	-4.04	0.00095	-1.35	0.34924
CDCA7	cell division cycle associated 7	-4.03	0.00118	-1.11	0.738
RNF165	ring finger protein 165	-4.02	1.00E-05	-1.76	0.01058

FOSL1	FOS-like antigen 1	-4.01	0.00018	-1.26	0.36281
PSRC1	proline/serine-rich coiled-coil 1	-4.01	0.00592	-2.11	0.0922
IER3	immediate early response 3	-4.00	0	-1.1	0.55523
MAP1B	microtubule-associated protein 1B	-4.00	0.00822	1.16	0.73494
VLDLR	very low density lipoprotein receptor	-3.99	0.00422	-1	0.99744
DLGAP1-AS2	DLGAP1 antisense RNA 2	-3.99	9.00E-05	-1.57	0.06964
AI926924	---	-3.93	0.01003	-1.46	0.40675
ZNF239	zinc finger protein 239	-3.92	0.00015	-1.19	0.48845
JPH1	junctophilin 1	-3.92	0.0011	1.25	0.48168
CHRM3	cholinergic receptor, muscarinic 3	-3.92	0.00085	-1.07	0.83136
BLMH	bleomycin hydrolase	-3.91	1.00E-04	-1.29	0.27753
SH3KBP1	SH3-domain kinase binding protein 1	-3.90	0.00018	-1.27	0.34487
SHISA2	shisa homolog 2 (Xenopus laevis)	-3.89	0.00035	1.14	0.61964
KLHL8	kelch-like 8 (Drosophila)	-3.89	0.00637	-2.16	0.0815
MAP3K9	mitogen-activated protein kinase kinase kinase 9	-3.88	1.00E-04	1.02	0.93607
MARC1	mitochondrial amidoxime reducing component 1	-3.88	0.00127	-1.15	0.66513
FYN	FYN oncogene related to SRC, FGR, YES	-3.87	0.00025	-1.11	0.69561
NR4A2 *	nuclear receptor subfamily 4, group A, member 2	-3.86	0.00041	2.17	0.01446
SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	-3.85	0.00018	1.09	0.72033
TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A	-3.85	0.00162	-1.35	0.36653
AI743753	---	-3.85	0.00102	-1.93	0.05111
GLB1L2	galactosidase, beta 1-like 2	-3.83	0.00101	-1.26	0.45423
EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	-3.83	0.00085	-1.17	0.59764
RAD51AP1	RAD51 associated protein 1	-3.82	0.03328	1.17	0.77625
NTN4	netrin 4	-3.82	0.001	-1.95	0.04646
GEM	GTP binding protein overexpressed in skeletal muscle	-3.82	0.00416	-1.02	0.94967
TRPA1	transient receptor potential cation channel, subfamily A, member 1	-3.81	0.0023	-1.08	0.81279
PALD1	phosphatase domain containing, paladin 1	-3.81	3.00E-05	1.2	0.34561
PGF	placental growth factor	-3.81	0.00459	-1.13	0.74268
BQ024490	---	-3.80	0.00026	-1.14	0.60793
FAM132B	family with sequence similarity 132, member B	-3.79	0.00015	-1.03	0.89889
SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	-3.79	0.00491	1.06	0.8723
CDCA5	cell division cycle associated 5	-3.78	0.04824	-1.29	0.67428
LAMA1	laminin, alpha 1	-3.78	7.00E-05	1.06	0.7756
CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotrans	-3.75	0.00028	-1.61	0.08158
ZNF331	zinc finger protein 331	-3.73	1.00E-05	-1.04	0.79857
PRKCH	protein kinase C, eta	-3.73	0.00024	1.22	0.42117
LPAR3	lysophosphatidic acid receptor 3	-3.71	1.00E-05	-1.1	0.54784
LOC100507564	uncharacterized LOC100507564	-3.70	0.00018	1.13	0.59692
SARS	seryl-tRNA synthetase	-3.69	0.00314	-1.13	0.72791
ARL13B	ADP-ribosylation factor-like 13B	-3.68	0.0106	-1.72	0.22489
CTNNAL1	catenin (cadherin-associated protein), alpha-like 1	-3.68	0.0018	1.21	0.55403
E2F8	E2F transcription factor 8	-3.68	0.00376	-1.04	0.91717
NID2	nidogen 2 (osteonidogen)	-3.68	0.00591	1	0.99963
NOG	noggin	-3.67	0.00015	-1.27	0.31226
PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	-3.67	0.02668	1.46	0.47116
UBASH3B	ubiquitin associated and SH3 domain containing B	-3.66	3.00E-05	1.44	0.07612

PBK	PDZ binding kinase	-3.65	0.03004	-1.15	0.79546
LGSN	lengsin, lens protein with glutamine synthetase domain	-3.65	0.02779	1.01	0.98181
DEPDC1B	DEP domain containing 1B	-3.65	0.02583	-1.3	0.60783
LOC100506918	hypothetical LOC100506918	-3.63	0.00107	-1.82	0.06307
SPAG4	sperm associated antigen 4	-3.62	0.00425	-1.03	0.92528
TCF19	transcription factor 19	-3.62	0.017	1.17	0.73299
EGF	epidermal growth factor	-3.62	4.00E-05	-1.42	0.08946
NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-3.61	0.0157	-1.3	0.57088
OSMR	oncostatin M receptor	-3.60	0.00092	-1.21	0.50367
LINC00473	long intergenic non-protein coding RNA 473	-3.60	6.00E-05	-1.51	0.06267
STK32C	serine/threonine kinase 32C	-3.60	0.00125	-1.6	0.13821
MCM10	minichromosome maintenance complex component 10	-3.59	8.00E-05	-1.67	0.02965
BG054960	---	-3.59	0.00026	-1.39	0.19663
LYPD6B	LY6/PLAUR domain containing 6B	-3.58	1.00E-05	1.23	0.19594
MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	-3.57	7.00E-05	-1.07	0.74611
DNASE1L3	deoxyribonuclease I-like 3	-3.56	0.00101	-1.37	0.29023
AI806183	---	-3.55	0.00021	1.05	0.8325
CCNYL1	cyclin Y-like 1	-3.54	0.00777	-1.03	0.93456
SLC7A11	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	-3.54	0.00907	1.06	0.88323
KIAA1644	KIAA1644	-3.53	1.00E-05	-1.33	0.08499
SH3PXD2B	SH3 and PX domains 2B	-3.52	0.00383	1.43	0.31562
UBE2C	ubiquitin-conjugating enzyme E2C	-3.51	0.00696	-1.63	0.22187
S100A9	S100 calcium binding protein A9	-3.51	0.00015	-1.11	0.63018
BF590850	---	-3.50	0.00171	-1.23	0.50862
FAS	Fas (TNF receptor superfamily, member 6)	-3.50	0.00021	-1.17	0.51164
NEIL3	nei endonuclease VIII-like 3 (E. coli)	-3.50	4.00E-04	-1.69	0.05716
SAA2	serum amyloid A2	-3.49	8.00E-05	-1.76	0.01761
LEPROTL1	leptin receptor overlapping transcript-like 1	-3.49	0	-1.14	0.36824
SMC2	structural maintenance of chromosomes 2	-3.49	0.0155	1.09	0.85304
MGC20647	uncharacterized protein MGC20647	-3.48	7.00E-05	-1.18	0.41407
AKAP12	A kinase (PRKA) anchor protein 12	-3.48	0	1.41	0.03918
NCAM1	neural cell adhesion molecule 1	-3.48	0.00082	1.06	0.823
AURKB	aurora kinase B	-3.47	0.02316	-1.42	0.47211
SSH1	slingshot homolog 1 (Drosophila)	-3.47	0.00743	1.13	0.74807
NCAPH	non-SMC condensin I complex, subunit H	-3.47	0.03792	-1.47	0.47798
SPDL1	spindle apparatus coiled-coil protein 1	-3.45	0.00167	-1.41	0.27314
BG112263	---	-3.45	1.00E-04	-1.52	0.06324
RAB3B	RAB3B, member RAS oncogene family	-3.43	0.00945	1	0.99046
IL24	interleukin 24	-3.43	0.04046	1.31	0.6167
ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	-3.42	0.00018	-1.19	0.44815
CXCL2	chemokine (C-X-C motif) ligand 2	-3.41	0.0041	-1.58	0.2029
SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-3.41	0.00082	-1.42	0.21554
CLDN23	claudin 23	-3.41	0.00133	-1.69	0.09183
BC020911	---	-3.41	0.00068	-1.19	0.50858
CA2	carbonic anhydrase II	-3.40	0.01952	1.13	0.78525
TOX2	TOX high mobility group box family member 2	-3.40	0.0143	1.15	0.73783
C1orf112	chromosome 1 open reading frame 112	-3.39	0.00114	-1.1	0.72907

CENPV	centromere protein V	-3.39	0.00011	1.1	0.63599
GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	-3.39	0.00014	1.14	0.54046
FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	-3.39	0.00021	1.04	0.86559
ADD2	adducin 2 (beta)	-3.39	0.00129	-1.68	0.09371
CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	-3.38	1.00E-04	-1.15	0.49464
FAM83A	family with sequence similarity 83, member A	-3.38	0.00279	-1.29	0.43941
HK2	hexokinase 2	-3.37	0	-1.18	0.16748
PGM2	phosphoglucomutase 2	-3.37	0.00069	-1.56	0.11362
CEP128	centrosomal protein 128kDa	-3.37	0.00173	-1.52	0.17622
FAM46C	family with sequence similarity 46, member C	-3.36	0.00079	-1.74	0.05686
SMAD3	SMAD family member 3	-3.36	0.00017	-1.42	0.12612
CNTNAP2	contactin associated protein-like 2	-3.36	0.00154	1.05	0.87244
INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	-3.36	0	-1.37	0.01381
CDC25C	cell division cycle 25 homolog C (S. pombe)	-3.35	0.00603	-1.72	0.15227
SLC17A9	solute carrier family 17, member 9	-3.35	9.00E-05	-1.23	0.31178
PRSS12	protease, serine, 12 (neurotrypsin, motopsin)	-3.35	0.03186	1.32	0.58368
CCNA2	cyclin A2	-3.35	0.03142	-1.25	0.66059
PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	-3.35	0.00146	1.48	0.19682
NUP210	nucleoporin 210kDa	-3.33	6.00E-05	-1.24	0.2806
HJURP	Holliday junction recognition protein	-3.33	0.01518	-1.71	0.22348
RUNX1	runt-related transcription factor 1	-3.32	0.00111	-1.15	0.61944
AI435073	---	-3.32	9.00E-04	-1.26	0.39973
LOC100506860	uncharacterized LOC100506860	-3.31	0	-1.46	0.01351
ERVMER34-1	endogenous retrovirus group MER34, member 1	-3.30	0.00084	-1.09	0.75541
CEP55	centrosomal protein 55kDa	-3.30	0.00328	-1.38	0.33236
CA9	carbonic anhydrase IX	-3.29	0.03444	-1.85	0.23587
THBD	thrombomodulin	-3.29	0.00486	1.05	0.88989
TPBG	trophoblast glycoprotein	-3.29	8.00E-05	-1.15	0.4715
CCNB1	cyclin B1	-3.29	0.00812	-1.39	0.39181
SCLY	selenocysteine lyase	-3.28	0.015	1.31	0.52706
TK1	thymidine kinase 1, soluble	-3.28	0.01742	-1.25	0.61055
ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	-3.28	0.00195	-1.08	0.79403
SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	-3.28	1.00E-05	-1.65	0.00514
NDRG4	NDRG family member 4	-3.28	0.00201	-1.19	0.56409
TMEM51	transmembrane protein 51	-3.28	1.00E-05	-1.32	0.08556
ATAD2	ATPase family, AAA domain containing 2	-3.28	0.03566	1.28	0.62544
NPHP1	nephronophthisis 1 (juvenile)	-3.27	3.00E-05	-1.47	0.0444
HCAR3	hydroxycarboxylic acid receptor 3	-3.27	7.00E-05	-1.06	0.76753
HIP1	huntingtin interacting protein 1	-3.27	0.00596	1.04	0.90959
AW009630	---	-3.27	0.00148	1.16	0.6038
ARHGAP29	Rho GTPase activating protein 29	-3.26	2.00E-05	-1.01	0.94795
FUT11	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)	-3.26	0.01646	-1.66	0.2487
LINC00622	long intergenic non-protein coding RNA 622	-3.26	0.00199	-1.14	0.65081
HPSE	heparanase	-3.26	0.00119	1.89	0.03772
BF056892	---	-3.26	0.00166	-1.31	0.36374

GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	-3.26	0.0029	1.15	0.65494
RAET1E	retinoic acid early transcript 1E	-3.26	3.00E-05	-1.04	0.8185
BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	-3.26	0.00624	-1.1	0.78182
STAC	SH3 and cysteine rich domain	-3.26	0.00029	-1.2	0.43036
RASGEF1A	RasGEF domain family, member 1A	-3.26	0.00165	1.93	0.04032
CDKN3	cyclin-dependent kinase inhibitor 3	-3.25	0.00112	-1.51	0.15075
KIF5C	kinesin family member 5C	-3.25	0.00202	1.08	0.79614
SRPX	sushi-repeat containing protein, X-linked	-3.25	0.00184	1.19	0.54965
AK022474	---	-3.25	0.00018	1.01	0.95255
MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	-3.25	4.00E-05	1.2	0.31914
MFI2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	-3.25	0.00137	-1.07	0.79867
H1F0	H1 histone family, member 0	-3.24	7.00E-05	-1.53	0.04592
JKAMP	JNK1/MAPK8-associated membrane protein	-3.22	0.03274	-1.49	0.42179
SPRY4-IT1	SPRY4 intronic transcript 1 (non-protein coding)	-3.22	0.03184	1.18	0.73759
CDC6	cell division cycle 6 homolog (S. cerevisiae)	-3.22	4.00E-05	-1.01	0.96389
CDCP1	CUB domain containing protein 1	-3.21	0.00111	-1.52	0.14136
RGCC	regulator of cell cycle	-3.21	0.02073	1.1	0.82487
ANGPTL4	angiopoietin-like 4	-3.21	0.00597	-1.22	0.5731
AI640482	---	-3.20	0.00033	1	0.99189
S100A3	S100 calcium binding protein A3	-3.20	0.00835	1.29	0.49349
ENO3	enolase 3 (beta, muscle)	-3.19	8.00E-05	1.41	0.09206
SRGN	serglycin	-3.18	3.00E-04	-1.02	0.93817
AK022350	---	-3.18	0.02706	1.14	0.78143
N69098	---	-3.18	0.00039	-1.03	0.89821
IL4R	interleukin 4 receptor	-3.18	1.00E-04	-1.21	0.33246
GJB2	gap junction protein, beta 2, 26kDa	-3.18	0.00253	1.35	0.32958
EGR2	early growth response 2	-3.17	6.00E-05	-1.27	0.20255
PDP1	pyruvate dehyrogenase phosphatase catalytic subunit 1	-3.17	0.0225	1.14	0.76302
SIX1	SIX homeobox 1	-3.17	0.00489	1.49	0.24833
SPRED1	sprouty-related, EVH1 domain containing 1	-3.16	0.00092	-1.21	0.47189
AI088104	---	-3.16	0.00791	-1.07	0.85801
RASL11B	RAS-like, family 11, member B	-3.16	0.00068	-1.06	0.82468
PRPS1	phosphoribosyl pyrophosphate synthetase 1	-3.16	0.00463	1.03	0.91909
RBM24	RNA binding motif protein 24	-3.16	0.00474	-1.3	0.43812
TIAM1	T-cell lymphoma invasion and metastasis 1	-3.16	0.00886	1.03	0.93353
TEX30	testis expressed 30	-3.15	0.00311	1.28	0.42589
DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	-3.15	0.02276	-2.19	0.09709
PRIMA1	proline rich membrane anchor 1	-3.15	0.00259	-1.13	0.69479
GPRC5B	G protein-coupled receptor, family C, group 5, member B	-3.15	0.00234	-1.9	0.04762
IL36G	interleukin 36, gamma	-3.14	0.00053	-1.11	0.64851
FZD5	frizzled family receptor 5	-3.14	0.00251	-1.25	0.46484
AI761207	---	-3.14	0.00697	1.45	0.29651
LYPD6	LY6/PLAUR domain containing 6	-3.14	0.00333	1.04	0.9077
CHRNA5	cholinergic receptor, nicotinic, alpha 5 (neuronal)	-3.13	0.00119	1.53	0.12825
PCSK9	proprotein convertase subtilisin/kexin type 9	-3.13	0.00098	-1.23	0.4326
PAQR4	progestin and adipoQ receptor family member IV	-3.13	0.00377	1.09	0.78133
KIF23	kinesin family member 23	-3.12	0.02753	-1.37	0.49418
GCH1	GTP cyclohydrolase 1	-3.12	0.00027	-1.07	0.74815

ODF2	outer dense fiber of sperm tails 2	-3.12	0.02259	1.05	0.90229
AW293316	---	-3.12	0.02818	-1.54	0.35271
DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	-3.11	0.0014	1.38	0.2484
C18orf54	chromosome 18 open reading frame 54	-3.11	0.00456	-1.27	0.46304
AI809536	---	-3.10	8.00E-05	-1.64	0.01949
PFAS	phosphoribosylformylglycinamidine synthase	-3.09	0.00084	-1.12	0.64607
SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	-3.09	0.00581	-1.07	0.83558
WDHD1	WD repeat and HMG-box DNA binding protein 1	-3.08	0.00629	1.26	0.50069
CBS	cystathionine-beta-synthase	-3.08	0.01815	1.31	0.51184
TSLP	thymic stromal lymphopoietin	-3.08	0.00553	-1.27	0.46889
CDCA3	cell division cycle associated 3	-3.08	0.01976	-2.16	0.087
TRMU	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	-3.08	0.04821	-1.11	0.83775
AIF1L	allograft inflammatory factor 1-like	-3.08	0.00021	1.81	0.01437
S1PR3	sphingosine-1-phosphate receptor 3	-3.08	0.00619	-1.15	0.67266
DBF4B	DBF4 homolog B (S. cerevisiae)	-3.08	0.02536	-1.31	0.54092
E2F7	E2F transcription factor 7	-3.07	0.0013	1.32	0.30531
WWTR1	WW domain containing transcription regulator 1	-3.07	0.00011	-1.38	0.1171
SCNN1A	sodium channel, non-voltage-gated 1 alpha subunit	-3.07	0.00038	1.56	0.06739
TDRKH	tudor and KH domain containing	-3.07	0.01686	1.03	0.94669
DPH3	DPH3, KTI11 homolog (S. cerevisiae)	-3.07	0.03076	-2.1	0.12742
CENPF	centromere protein F, 350/400kDa (mitosin)	-3.06	0.00437	-1.23	0.51816
ARHGAP19	Rho GTPase activating protein 19	-3.06	0.00498	-1.73	0.11234
C21orf58	chromosome 21 open reading frame 58	-3.06	0.0065	-1.01	0.98383
FAM27E3	family with sequence similarity 27, member E3	-3.06	0.00093	-1.54	0.10883
AI701591	---	-3.06	0.0229	-1.66	0.25507
TTK	TTK protein kinase	-3.05	0.03161	-1.4	0.47166
GDF11	growth differentiation factor 11	-3.05	0.00546	-1.95	0.06114
AI476341	---	-3.04	5.00E-05	1.03	0.85934
HSPA12A	heat shock 70kDa protein 12A	-3.04	0.00543	1.48	0.24674
CYR61	cysteine-rich, angiogenic inducer, 61	-3.04	0.03887	1.09	0.85417
LCN2	lipocalin 2	-3.04	0.01076	-1.37	0.40369
HAUS7	HAUS augmin-like complex, subunit 7	-3.03	0.00015	-1.04	0.8597
ICAM3	intercellular adhesion molecule 3	-3.03	0.00453	-1.16	0.63775
TFPI2	tissue factor pathway inhibitor 2	-3.03	0.00042	-1.31	0.23977
SLC44A3	solute carrier family 44, member 3	-3.03	0.00066	-1.65	0.05393
NELL2	NEL-like 2 (chicken)	-3.02	0.00575	1	0.99726
WRB	tryptophan rich basic protein	-3.02	3.00E-04	-1.64	0.03706
ARPP19	cAMP-regulated phosphoprotein, 19kDa	-3.02	0.03013	-1.66	0.27516
AI085377	---	-3.02	0.00137	1.08	0.78136
MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	-3.01	0.00323	1.17	0.59388
FXYD6	FXYD domain containing ion transport regulator 6	-3.01	0.00057	1.19	0.46711
FAM89A	family with sequence similarity 89, member A	-3.01	0.00233	1.04	0.87931
BMP6	bone morphogenetic protein 6	-3.00	4.00E-05	1.05	0.77486
XDH	xanthine dehydrogenase	-3.00	0.00331	-1.08	0.80158
KIAA1549	KIAA1549	-3.00	0	-1.89	0.00042
QSOX2	quiescin Q6 sulfhydryl oxidase 2	-3.00	1.00E-05	-1.63	0.0033
VSIG1	V-set and immunoglobulin domain containing 1	-3.00	0.00036	-1.08	0.73456
GLIS3	GLIS family zinc finger 3	-3.00	0.00035	-1.25	0.31486

KIF14	kinesin family member 14	-3.00	0.01018	-1.25	0.53575
AMIGO2	adhesion molecule with Ig-like domain 2	-2.99	0.00507	1.25	0.48514
C15orf23	chromosome 15 open reading frame 23	-2.99	0.00277	-1.28	0.4019
HEATR5A	HEAT repeat containing 5A	-2.99	0.01051	-2.03	0.07101
ERLIN1	ER lipid raft associated 1	-2.98	0.01059	-1.25	0.53596
PI3	peptidase inhibitor 3, skin-derived	-2.98	0.00364	-1.99	0.0399
UGGT2	UDP-glucose glycoprotein glucosyltransferase 2	-2.98	0.02363	-2	0.12313
RGS20	regulator of G-protein signaling 20	-2.98	0.00078	1.08	0.73511
WDR76	WD repeat domain 76	-2.98	0.00247	1.52	0.15917
ETV5	Ets variant 5	-2.97	5.00E-05	-1.18	0.34541
CCNE1	cyclin E1	-2.96	6.00E-05	1.74	0.00792
TMTC1	transmembrane and tetratricopeptide repeat containing 1	-2.96	0.00058	-1	0.99439
SYT17	synaptotagmin XVII	-2.96	0.00013	1.01	0.9549
AI494113	---	-2.96	2.00E-05	-1.01	0.9727
BF447286	---	-2.96	0.01319	-2.01	0.08345
AW874669	---	-2.96	0.02715	-1.48	0.37096
AW132066	---	-2.96	0.00756	-1.47	0.26977
TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	-2.95	0.01262	-1.25	0.55424
FST *	follistatin	-2.95	0.00143	2.30	0.01951
PPM1E	protein phosphatase, Mg2+/Mn2+ dependent, 1E	-2.95	0.00011	-1.42	0.08189
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	-2.95	0.03059	1.05	0.9123
LRRC8B	leucine rich repeat containing 8 family, member B	-2.95	0.00057	-1.34	0.21599
SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	-2.94	0	-1.43	0.00962
RBMS3	RNA binding motif, single stranded interacting protein 3	-2.94	6.00E-05	1.2	0.28816
OSBP2	oxysterol binding protein 2	-2.94	0.00121	-1.14	0.60473
TMEM107	transmembrane protein 107	-2.93	0.03492	1.06	0.90022
BIRC5	baculoviral IAP repeat containing 5	-2.93	0.01501	-1.48	0.31013
GRB14	growth factor receptor-bound protein 14	-2.93	1.00E-05	1.08	0.54709
AV700891	---	-2.93	2.00E-05	-1.05	0.7346
AA010315	---	-2.93	0.01968	2.03	0.09937
TSC22D1	TSC22 domain family, member 1	-2.93	8.00E-05	-1.18	0.36
CAMK4	calcium/calmodulin-dependent protein kinase IV	-2.93	8.00E-04	-1.21	0.42432
AK026659	---	-2.93	0.0218	1.4	0.41439
C11orf24	chromosome 11 open reading frame 24	-2.93	0.00014	-1.27	0.22457
ATP8B2	ATPase, aminophospholipid transporter, class I, type 8B, member 2	-2.92	0.01421	1.38	0.39641
CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	-2.92	0.03528	1.2	0.68595
DARS2	aspartyl-tRNA synthetase 2, mitochondrial	-2.92	0.00431	-1.22	0.51669
SMOC1	SPARC related modular calcium binding 1	-2.92	0.00125	-1.32	0.28696
HAUS6	HAUS augmin-like complex, subunit 6	-2.92	0.01471	1.25	0.56259
SMAGP	small cell adhesion glycoprotein	-2.92	8.00E-04	-1.3	0.28407
CDK1	cyclin-dependent kinase 1	-2.92	0.00454	-1.23	0.49924
NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	-2.92	0.00996	-1.5	0.26124
FAM213B	family with sequence similarity 213, member B	-2.92	0.00125	-1.33	0.26472
PRMT3	protein arginine methyltransferase 3	-2.91	0.01206	-1.07	0.86065
OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	-2.91	0.00226	-1.04	0.88464

HEYL	hairy/enhancer-of-split related with YRPW motif-like	-2.91	0.00946	-1.76	0.12237
ZNRF3	zinc and ring finger 3	-2.91	0.00602	-1.81	0.08326
TTF2	transcription termination factor, RNA polymerase II	-2.90	0.00899	-1.21	0.57169
PCDHGC3	protocadherin gamma subfamily C, 3	-2.90	0.0178	1.45	0.34611
AI936724	---	-2.90	0.00923	-1.74	0.12796
FAM72A	family with sequence similarity 72, member A	-2.90	0.00093	-1.39	0.18827
CENPO	centromere protein O	-2.89	0.00093	1.49	0.11519
LOC100506844	uncharacterized LOC100506844	-2.89	0	-1.56	0.00279
DGKG	diacylglycerol kinase, gamma 90kDa	-2.89	0.0097	-1.31	0.4338
RSL1D1	ribosomal L1 domain containing 1	-2.88	0.00529	-1.54	0.18137
ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	-2.88	0.03011	-2.3	0.07575
HSPA2	heat shock 70kDa protein 2	-2.88	0.01408	1.09	0.81676
MMD	monocyte to macrophage differentiation-associated	-2.88	0	1.71	0.00105
IFITM1	interferon induced transmembrane protein 1	-2.87	0.00016	-1.15	0.46912
RAB31	RAB31, member RAS oncogene family	-2.87	1.00E-05	-1.4	0.03554
S1PR1	sphingosine-1-phosphate receptor 1	-2.87	0.00223	-1.07	0.81175
RAB38	RAB38, member RAS oncogene family	-2.87	0.00285	-1.31	0.34402
PLAUR	plasminogen activator, urokinase receptor	-2.87	0.00036	1.39	0.13881
CD58	CD58 molecule	-2.86	0.00297	-1.41	0.2358
EDNRB	endothelin receptor type B	-2.86	0.02402	1.23	0.61451
KIAA1549L	KIAA1549-like	-2.86	4.00E-05	1.06	0.70448
C9orf89	chromosome 9 open reading frame 89	-2.86	0.02207	-2.26	0.06227
R41296	---	-2.86	0.00212	-1.22	0.46582
SPAG5	sperm associated antigen 5	-2.85	0.02843	-1.22	0.64436
CALCA	calcitonin-related polypeptide alpha	-2.85	0.0117	-1.01	0.97185
TMEM194A	transmembrane protein 194A	-2.85	5.00E-05	1.01	0.95389
EFHD2	EF-hand domain family, member D2	-2.85	0.00821	-1.19	0.59714
RGS16	regulator of G-protein signaling 16	-2.84	0.00517	-1.54	0.17751
TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	-2.84	0.00748	-1.21	0.55131
CCSAP	centriole, cilia and spindle-associated protein	-2.84	0.00096	1.11	0.6664
CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	-2.83	0.01374	-1.39	0.37589
SKA1	spindle and kinetochore associated complex subunit 1	-2.83	0.01	1.05	0.88772
LEPREL1	leprecan-like 1	-2.83	5.00E-05	-1.97	0.00139
SEMA4A	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	-2.83	0.00365	-1.04	0.88475
NALCN	sodium leak channel, non-selective	-2.83	0.00227	1.2	0.49713
STAT4	signal transducer and activator of transcription 4	-2.83	0.00011	-1.28	0.18452
AIDA	axin interactor, dorsalization associated	-2.83	0.00041	-1.81	0.01487
FOXD2-AS1	FOXD2 antisense RNA 1	-2.83	0.01082	1.06	0.87496
NDC80	NDC80 kinetochore complex component homolog (S. cerevisiae)	-2.82	0.00164	-1.23	0.42704
AW117383	---	-2.82	0.00021	1.08	0.6898
PHLDA2	pleckstrin homology-like domain, family A, member 2	-2.82	0.00951	1.22	0.55792
LRRN1	leucine rich repeat neuronal 1	-2.82	0.03339	1.32	0.53025
STAMBPL1	STAM binding protein-like 1	-2.82	4.00E-05	-1.06	0.70309

SLFN5	schlafen family member 5	-2.82	0.01198	-1.44	0.30695
EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	-2.81	0.03033	-1.48	0.36778
GOLT1B	golgi transport 1B	-2.81	0.00162	-1.67	0.06248
KIF4A	kinesin family member 4A	-2.81	0.03618	-1.31	0.54604
C17orf96	chromosome 17 open reading frame 96	-2.81	0.00092	-1.08	0.75009
MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	-2.81	0.04619	-1.34	0.53341
BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	-2.81	0.00396	-1.55	0.14757
BICD1	bicaudal D homolog 1 (Drosophila)	-2.80	0.0018	1.01	0.96719
CENPA	centromere protein A	-2.80	0.00658	-1.65	0.12915
EIF5A2	eukaryotic translation initiation factor 5A2	-2.80	0.00101	1.26	0.32932
TRIP13	thyroid hormone receptor interactor 13	-2.80	0.00984	1.09	0.79559
LINC00263	long intergenic non-protein coding RNA 263	-2.79	0.00925	-1.05	0.88683
ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	-2.79	0.04139	-1.27	0.59484
N67305	---	-2.79	0.00457	-1.02	0.95905
ULBP2	UL16 binding protein 2	-2.79	0.00095	-1.61	0.05918
ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	-2.79	0.03505	-1.46	0.38809
BMP8B	bone morphogenetic protein 8b	-2.79	7.00E-05	-1.47	0.03652
BID	BH3 interacting domain death agonist	-2.79	0.03148	1.21	0.65728
TTC39B	Tetratricopeptide repeat domain 39B	-2.78	0.00037	-1.27	0.24713
WFDC2	WAP four-disulfide core domain 2	-2.78	0.00024	-1.27	0.23415
RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae)	-2.78	0.02116	-1.43	0.35958
PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	-2.78	0.00181	1.2	0.4645
CYP4F11	cytochrome P450, family 4, subfamily F, polypeptide 11	-2.77	0.00178	1.01	0.95431
SHCBP1	SHC SH2-domain binding protein 1	-2.77	0.03592	-1.44	0.40584
FADS1	fatty acid desaturase 1	-2.77	0.00127	1.09	0.72362
VEGFA	vascular endothelial growth factor A	-2.77	0.00165	-1.12	0.64269
C9orf72	chromosome 9 open reading frame 72	-2.77	0.00165	-1.01	0.96459
NUSAP1	nucleolar and spindle associated protein 1	-2.77	0.00225	-1.47	0.15907
LOC440288	uncharacterized LOC440288	-2.76	0.02952	-1.31	0.52302
CORO2B	coronin, actin binding protein, 2B	-2.76	0.00062	1.95	0.00943
SPOPL	speckle-type POZ protein-like	-2.76	0.0025	-1.46	0.17139
TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	-2.76	0.01735	1.1	0.79891
TMEM231	transmembrane protein 231	-2.76	0.00393	1.67	0.09057
PRKD1	protein kinase D1	-2.75	0.00064	1.15	0.51782
UPP1	uridine phosphorylase 1	-2.75	0.0041	-1.1	0.74882
PPARG	peroxisome proliferator-activated receptor gamma	-2.75	9.00E-04	-1.46	0.11478
UBTD2	ubiquitin domain containing 2	-2.75	1.00E-05	-1.56	0.00367
FHOD1	formin homology 2 domain containing 1	-2.75	8.00E-04	-1.09	0.69104
IL20RB	interleukin 20 receptor beta	-2.75	0.03429	-1.32	0.52005
FGFR4	fibroblast growth factor receptor 4	-2.74	0.0211	-1.38	0.40818
SUB1	SUB1 homolog (S. cerevisiae)	-2.74	4.00E-05	-1.78	0.00313
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	-2.74	1.00E-05	-1.23	0.11935
RCAN1	regulator of calcineurin 1	-2.74	5.00E-05	-1.52	0.01944
FBXO5	F-box protein 5	-2.74	0.03521	1.06	0.89174

SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	-2.73	0.00472	-1.08	0.78259
GRK5	G protein-coupled receptor kinase 5	-2.73	0.00112	-1.04	0.85224
EGLN3	egl nine homolog 3 (C. elegans)	-2.73	0.01171	-1.53	0.22465
PADI3	peptidyl arginine deiminase, type III	-2.73	2.00E-05	-1.01	0.92524
FANCI	Fanconi anemia, complementation group I	-2.72	0.00417	1.17	0.57839
COL21A1	collagen, type XXI, alpha 1	-2.72	0.00061	1.14	0.52966
RBP4	Retinol binding protein 4, plasma	-2.72	0.00435	-1.61	0.11396
TSPAN18	tetraspanin 18	-2.72	0.00015	1.03	0.86381
BARD1	BRCA1 associated RING domain 1	-2.72	0.00688	1.03	0.91666
CLIP2	CAP-GLY domain containing linker protein 2	-2.72	0.0431	-1.24	0.63537
BE271180	---	-2.72	0.01322	-1.34	0.40306
ADA	adenosine deaminase	-2.72	0.00077	-1.09	0.7056
CXCL16	chemokine (C-X-C motif) ligand 16	-2.71	0.00303	-1.89	0.0338
FAM63B	family with sequence similarity 63, member B	-2.71	0.03303	-2.02	0.11366
LOC100506895	uncharacterized LOC100506895	-2.71	0.00604	-1.12	0.69735
CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	-2.71	0.0394	-2.14	0.10182
B4GALNT1	beta-1,4-N-acetyl-galactosaminyl transferase 1	-2.71	0.03174	-1.17	0.71048
NRN1	neuritin 1	-2.70	0.02391	1.1	0.79767
TMPRSS4	transmembrane protease, serine 4	-2.70	0.00069	1.3	0.24116
KIAA1324	KIAA1324	-2.70	0.00626	-1.18	0.58551
NCR3LG1	natural killer cell cytotoxicity receptor 3 ligand 1	-2.70	0.01343	-1.23	0.54867
SH2D5	SH2 domain containing 5	-2.70	0.00181	1.07	0.78286
CENPK	centromere protein K	-2.70	0.02516	1.42	0.37636
SLC25A43	solute carrier family 25, member 43	-2.69	0.04933	-2.29	0.09123
MCM2	minichromosome maintenance complex component 2	-2.69	0.02566	-1.06	0.87843
DCLRE1B	DNA cross-link repair 1B	-2.69	0.00582	1.04	0.90083
BOP1	block of proliferation 1	-2.69	0.02716	-1.64	0.22988
ZNF114	zinc finger protein 114	-2.69	0.00222	1.15	0.58621
AW961576	---	-2.69	4.00E-05	-1.28	0.11532
LOC100505668	uncharacterized LOC100505668	-2.69	0.00067	1.1	0.6434
RNF144A	ring finger protein 144A	-2.69	0.00058	-1	0.98744
NCAPG	non-SMC condensin I complex, subunit G	-2.69	0.00193	-1.41	0.18312
IL7R	interleukin 7 receptor	-2.69	0.00402	1.38	0.26046
LINC00313	long intergenic non-protein coding RNA 313	-2.69	0.00567	-1.16	0.61782
AI361034	---	-2.69	0.00458	-1.96	0.03328
AURKA	aurora kinase A	-2.68	0.00332	-1.47	0.16832
LARP6	La ribonucleoprotein domain family, member 6	-2.68	0.00864	-1.15	0.66568
ORC6	origin recognition complex, subunit 6	-2.68	0.00107	-1.11	0.65157
MAK16	MAK16 homolog (S. cerevisiae)	-2.67	3.00E-04	-1.26	0.24297
BRI3BP	BRI3 binding protein	-2.67	0.00234	-1.59	0.08937
AI479285	---	-2.67	0.00614	-1.09	0.7642
DSCC1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	-2.67	0.00655	1.43	0.24405
TTC25	tetratricopeptide repeat domain 25	-2.67	0.00066	-1.22	0.35888
PTRH2	peptidyl-tRNA hydrolase 2	-2.67	3.00E-05	-1.88	0.00112
FAM102B	family with sequence similarity 102, member B	-2.67	0.03744	-1.12	0.7825
C12orf52	chromosome 12 open reading frame 52	-2.67	0.01981	-1.98	0.08286
KNTC1	kinetochore associated 1	-2.67	0.0011	1.16	0.51727
AL117546	---	-2.67	0.00285	-1.77	0.04714
KCTD15	potassium channel tetramerisation domain containing 15	-2.67	0.00125	1.1	0.68588

ALAD	aminolevulinate dehydratase	-2.66	0.02093	-1.77	0.14421
POLA2	polymerase (DNA directed), alpha 2, accessory subunit	-2.66	0.02087	-1.18	0.65931
PAPPA	pregnancy-associated plasma protein A, pappalysin 1	-2.66	0.01142	1.15	0.66179
PRKAG2-AS1	PRKAG2 antisense RNA 1 (non-protein coding)	-2.66	0.02381	1.18	0.65786
POLE3	polymerase (DNA directed), epsilon 3, accessory subunit	-2.66	0.046	-1.16	0.73987
CCDC64	coiled-coil domain containing 64	-2.66	0.00017	1.31	0.14993
SERTAD4	SERTA domain containing 4	-2.66	0.00373	1.09	0.75581
GK	glycerol kinase	-2.65	0.00082	-1.15	0.51226
OAF	OAF homolog (Drosophila)	-2.65	0.00922	-1.35	0.34344
AI638195	---	-2.65	0.00427	-1.17	0.56295
ETV4	ets variant 4	-2.65	5.00E-05	-1.07	0.67106
MCTP2	multiple C2 domains, transmembrane 2	-2.65	0.01823	1.46	0.30328
CENPI	centromere protein I	-2.64	0.01343	1.01	0.98709
BLM	Bloom syndrome, RecQ helicase-like	-2.64	0.00072	-1.01	0.95799
TM4SF1	transmembrane 4 L six family member 1	-2.64	0.00084	-1.12	0.59262
ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	-2.64	7.00E-05	-1.07	0.68765
TDP1	tyrosyl-DNA phosphodiesterase 1	-2.64	0.02616	-1.29	0.51841
CNN3	calponin 3, acidic	-2.64	0.01294	-1.01	0.96797
KLHL23	kelch-like 23 (Drosophila)	-2.63	0.00103	-1.3	0.24451
FOXE1	forkhead box E1 (thyroid transcription factor 2)	-2.63	0.00761	-1.25	0.4617
PIGH	phosphatidylinositol glycan anchor biosynthesis, class H	-2.63	0.00153	-1.93	0.01558
GPR126	G protein-coupled receptor 126	-2.63	2.00E-05	1.08	0.56505
DNAL1	dynein, axonemal, light chain 1	-2.63	0.02379	-1.14	0.72023
PLK4	polo-like kinase 4	-2.63	0.02073	1.13	0.73025
BIRC3	baculoviral IAP repeat containing 3	-2.62	0.01083	1.18	0.60078
SLC39A14	solute carrier family 39 (zinc transporter), member 14	-2.62	0.00018	-1.7	0.01055
EPDR1	ependymin related protein 1 (zebrafish)	-2.62	0.00033	-1.06	0.75784
FOXN2	forkhead box N2	-2.62	0	-1.41	0.00385
W91876	---	-2.62	0.00221	1.18	0.50045
LOC100507672	uncharacterized LOC100507672	-2.62	0.00026	-1.17	0.40999
STK17B	serine/threonine kinase 17b	-2.62	0.00872	-1.37	0.3112
EIF3J	eukaryotic translation initiation factor 3, subunit J	-2.62	0.00417	-1.85	0.04021
FEN1	flap structure-specific endonuclease 1	-2.61	0.01326	1.02	0.95445
AI686793	---	-2.61	0.00132	-1.1	0.68277
OVOS2	ovostatin 2	-2.61	0.00123	1.01	0.95877
LONRF3	LON peptidase N-terminal domain and ring finger 3	-2.61	0.00106	-1.3	0.24914
RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	-2.61	0.01114	-1.58	0.17275
PCED1B	PC-esterase domain containing 1B	-2.61	0.00039	-1.18	0.39518
CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	-2.60	0.00744	-1.18	0.57718
KCTD12	potassium channel tetramerisation domain containing 12	-2.60	0.00978	-1.34	0.36295
THAP10	THAP domain containing 10	-2.60	0.00341	1.14	0.6232
MNS1	meiosis-specific nuclear structural 1	-2.60	0.00474	1.24	0.44304
CLSPN	claspin	-2.60	0.02098	1.54	0.24794
AL110176	---	-2.60	0.00086	-1.57	0.05285

TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	-2.60	0.00249	-1.75	0.04176
METTL21A	methyltransferase like 21A	-2.60	0.00919	-1.3	0.39699
GYG2	glycogenin 2	-2.60	0.00267	-1.16	0.56191
UHRF1	ubiquitin-like with PHD and ring finger domains 1	-2.60	0.00694	1.1	0.74569
H59221	---	-2.60	0.00209	-1.12	0.64994
AW274560	---	-2.59	0.00052	1.09	0.67123
C11orf75	chromosome 11 open reading frame 75	-2.59	3.00E-05	-1.06	0.69045
LOC439949	uncharacterized LOC439949	-2.59	0.00097	1.13	0.58207
SYBU	syntabulin (syntaxin-interacting)	-2.59	0.03692	1.08	0.85227
MOXD1	monooxygenase, DBH-like 1	-2.59	3.00E-04	-1.04	0.82282
VMA21	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae)	-2.58	0.00014	-1.71	0.0077
LOC401052	uncharacterized LOC401052	-2.58	0.01759	1.1	0.77821
ETS2	V-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	-2.58	0.00025	-1.02	0.91849
UBL3	ubiquitin-like 3	-2.58	0.01858	-2.09	0.05524
GRB10	growth factor receptor-bound protein 10	-2.58	0.0048	-1.5	0.15747
AA133285	---	-2.58	0.01514	-1.1	0.78522
SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	-2.58	0.00085	-1.97	0.00758
BRCA1	breast cancer 1, early onset	-2.58	0.00862	1	0.98965
LRR1	leucine rich repeat protein 1	-2.58	0.04335	1.07	0.87634
FABP4	fatty acid binding protein 4, adipocyte	-2.57	0.02591	1.05	0.89379
AA404273	---	-2.57	0.02283	-1.6	0.21323
C12orf75	chromosome 12 open reading frame 75	-2.57	0.0174	1.37	0.36353
LOC284561	uncharacterized LOC284561	-2.57	0.01754	-1.15	0.6847
AI475033	---	-2.57	0.00162	-1.08	0.74524
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	-2.57	0.03534	-1.02	0.95535
MYO10	myosin X	-2.57	0.00014	-1.16	0.37092
THBS1	thrombospondin 1	-2.57	0.00079	-1.15	0.49431
EOMES	eomesodermin	-2.57	0.00381	-1.09	0.73514
HEY2	hairy/enhancer-of-split related with YRPW motif 2	-2.56	0.00556	1.13	0.65773
GALNTL4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	-2.56	0.00923	1.06	0.85443
EAF2	ELL associated factor 2	-2.56	0.00149	-1.24	0.35027
HHEX	hematopoietically expressed homeobox	-2.56	0.04495	1.18	0.70322
MLF1IP	MLF1 interacting protein	-2.55	0.00105	1.44	0.10925
ARRB2	arrestin, beta 2	-2.55	0.04086	-1.29	0.54157
ADAM8	ADAM metallopeptidase domain 8	-2.55	0.00074	1.08	0.72133
TACC3	transforming, acidic coiled-coil containing protein 3	-2.55	0.01022	-1.37	0.31784
BE502264	---	-2.55	1.00E-04	-1.1	0.55361
AW151660	---	-2.55	7.00E-05	-1.62	0.00828
ZWINT	ZW10 interactor	-2.55	0.01679	1.04	0.89744
STRBP	spermatid perinuclear RNA binding protein	-2.55	0.01308	-1.36	0.34762
CCDC90A	coiled-coil domain containing 90A	-2.55	0.02223	-1.12	0.75685
SGOL2	shugoshin-like 2 (S. pombe)	-2.55	0.0046	-1.28	0.36083
FNDC3A	fibronectin type III domain containing 3A	-2.55	0.01236	-1.31	0.40733
POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	-2.54	0.01263	1.37	0.32849
TMTC2	transmembrane and tetratricopeptide repeat containing 2	-2.54	0.00252	-1.37	0.20843
GAS2L3	growth arrest-specific 2 like 3	-2.54	0.04244	-1.1	0.81815
SMC4	structural maintenance of chromosomes 4	-2.54	0.00483	-1.4	0.22406

VMP1	vacuole membrane protein 1	-2.54	9.00E-05	-1.39	0.05417
AI300077	---	-2.54	4.00E-05	1.41	0.02884
NNMT	nicotinamide N-methyltransferase	-2.53	0.005	-1.42	0.20975
RAD54L	RAD54-like (S. cerevisiae)	-2.53	0.01111	1.44	0.25023
PCSK5	proprotein convertase subtilisin/kexin type 5	-2.53	0.00853	-1.13	0.67265
ARNTL	aryl hydrocarbon receptor nuclear translocator-like	-2.53	0.00208	-1.1	0.6711
SEMA6D	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	-2.53	0.03247	1.25	0.56394
LOC100505730	uncharacterized LOC100505730	-2.52	0.00012	1.32	0.10401
BF115851	---	-2.52	0.00028	-1.31	0.14364
LZTFL1	leucine zipper transcription factor-like 1	-2.52	0.00664	-1.5	0.17059
SH2D3A	SH2 domain containing 3A	-2.52	0.01852	-1.22	0.56017
PRR3	proline rich 3	-2.52	0.00145	-1.4	0.1508
PTX3	pentraxin 3, long	-2.52	0.02566	1.41	0.35397
RANBP1	RAN binding protein 1	-2.51	0.00084	-1.21	0.3568
E2F2	E2F transcription factor 2	-2.51	0.04144	1.29	0.53078
TMEM209	transmembrane protein 209	-2.51	0.00339	-1.13	0.61827
HS6ST2	heparan sulfate 6-O-sulfotransferase 2	-2.51	7.00E-05	-1.02	0.89493
KIF2C	kinesin family member 2C	-2.51	0.0114	-1.32	0.38124
FKBP11	FK506 binding protein 11, 19 kDa	-2.51	0.00359	1.04	0.88556
SYTL2	synaptotagmin-like 2	-2.51	0.00117	-1.5	0.07694
HTATSF1P2 *	HIV-1 Tat specific factor 1 pseudogene 2	-2.51	0.00041	2.03	0.00266
FOXM1	forkhead box M1	-2.51	0.02301	-1.47	0.28535
LINC00621	long intergenic non-protein coding RNA 621	-2.50	0.00713	-1.56	0.13372
FHDC1	FH2 domain containing 1	-2.50	0.01311	1.48	0.22749
ARL10	ADP-ribosylation factor-like 10	-2.50	0.00162	1.08	0.71664
PNP	purine nucleoside phosphorylase	-2.49	0.00677	-1	0.99832
PANX1	pannexin 1	-2.49	0.00847	1.11	0.7183
ATP2C2	ATPase, Ca++ transporting, type 2C, member 2	-2.49	0.01694	-1.41	0.30556
SREBF1	sterol regulatory element binding transcription factor 1	-2.49	0.00164	-1.49	0.09318
ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	-2.49	0.00624	1.01	0.98354
SMAD2	SMAD family member 2	-2.49	3.00E-05	-1.89	0.00058
HMGA1	high mobility group AT-hook 1	-2.48	0.00011	-1.3	0.10833
DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	-2.48	0.00594	1.24	0.43264
PASK	PAS domain containing serine/threonine kinase	-2.48	0.04558	1.54	0.30582
SPATA13	spermatogenesis associated 13	-2.48	0.03993	-1.17	0.69167
CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	-2.48	0.0024	1.19	0.45233
ELOVL5	ELOVL fatty acid elongase 5	-2.48	0.00051	-1.23	0.2896
PYCR1	pyrroline-5-carboxylate reductase 1	-2.48	0.00853	-1.39	0.26417
COBL	cordon-bleu homolog (mouse)	-2.48	6.00E-05	-1.21	0.19826
CPNE8	copine VIII	-2.48	0.00015	-1.15	0.39584
IQGAP3	IQ motif containing GTPase activating protein 3	-2.48	0.03527	-1.25	0.56398
FAM40B	family with sequence similarity 40, member B	-2.47	0.01704	1.69	0.12949
AA142959	---	-2.47	0.01508	1.7	0.11851
KCTD20	potassium channel tetramerisation domain containing 20	-2.47	0.00021	-1.67	0.00965
TYRP1	tyrosinase-related protein 1	-2.47	0.03317	-1.08	0.83029
GEMIN5	gem (nuclear organelle) associated protein 5	-2.47	0.00879	-1.02	0.94158
LOC283050	uncharacterized LOC283050	-2.47	0.00096	1.29	0.22704

AA933082	---	-2.46	0.01178	1.21	0.53384
RNASEH2A	ribonuclease H2, subunit A	-2.46	0.01731	1.34	0.38308
TYMS	thymidylate synthetase	-2.46	0.00819	1.18	0.56989
MMP28	matrix metallopeptidase 28	-2.46	0.02048	1	0.99977
STK17A	serine/threonine kinase 17a	-2.46	0.00219	-1.21	0.41295
FBLN1	fibulin 1	-2.46	0.00057	-1.2	0.33659
RNASEH1	ribonuclease H1	-2.46	0.00052	-1.81	0.00839
LHX2	LIM homeobox 2	-2.45	0.03229	1.1	0.80041
SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	-2.45	0.00133	-1.02	0.94146
MID1IP1	MID1 interacting protein 1	-2.45	0.00017	1.01	0.94805
ITPR1	inositol 1,4,5-trisphosphate receptor, type 1	-2.45	0.00145	-1.01	0.97876
MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	-2.45	0.00726	1.54	0.14056
UBE2S	ubiquitin-conjugating enzyme E2S	-2.45	0.00311	-1.71	0.04491
MAP3K5	mitogen-activated protein kinase kinase kinase 5	-2.45	0.00771	1.21	0.50078
F2R	coagulation factor II (thrombin) receptor	-2.45	0.00287	1.15	0.57001
NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	-2.45	0.02913	-1.08	0.82628
OIP5	Opa interacting protein 5	-2.45	0.02091	1.06	0.86146
AA416756	---	-2.44	0.00676	-1.18	0.54798
HPRT1	hypoxanthine phosphoribosyltransferase 1	-2.44	0.00084	1.28	0.22244
C19orf48	chromosome 19 open reading frame 48	-2.44	0.00313	-1.33	0.24641
MIR21	microRNA 21	-2.44	0.00043	-1.62	0.02052
AW954199	---	-2.44	0.00038	-1.53	0.03423
CLMN	calmin (calponin-like, transmembrane)	-2.44	3.00E-05	1.49	0.00931
FADS2	fatty acid desaturase 2	-2.44	0.04319	1.21	0.62658
CCDC71L	coiled-coil domain containing 71-like	-2.44	0.00201	1.63	0.04777
KIAA0040	KIAA0040	-2.44	0.00094	1.28	0.23759
MICU1	mitochondrial calcium uptake 1	-2.44	4.00E-04	-1.84	0.00522
BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-2.44	0.00147	1.01	0.97045
TROAP	trophinin associated protein (tastin)	-2.43	0.03039	-1.81	0.12464
AI247368	---	-2.43	0.03106	-1.33	0.44296
PID1	phosphotyrosine interaction domain containing 1	-2.43	0.00313	1.28	0.31848
WRAP53	WD repeat containing, antisense to TP53	-2.43	0.01505	-1.78	0.088
KIF11	kinesin family member 11	-2.43	0.01628	-1.08	0.80488
AI986112	---	-2.43	0.00623	-1.34	0.28044
ATP11A	ATPase, class VI, type 11A	-2.43	0.00037	-1.51	0.0372
KRT80	keratin 80	-2.43	0.0079	1.08	0.79106
AI797678	---	-2.43	0.0016	-1.02	0.91491
PRC1	protein regulator of cytokinesis 1	-2.43	0.02746	1.01	0.97664
NUS1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	-2.43	0.02409	-1.44	0.30188
NMU	neuromedin U	-2.42	0.00326	-1.72	0.0412
PLXNA2	plexin A2	-2.42	0.00274	1.35	0.20934
VWA1	Von Willebrand factor A domain containing 1	-2.42	0.01244	1.04	0.88984
TSPAN4	tetraspanin 4	-2.42	0.02476	-1.5	0.2583
AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	-2.42	0.02888	-1.3	0.46346
CCDC88A	coiled-coil domain containing 88A	-2.42	0.01121	-1.31	0.36406
ARF3	ADP-ribosylation factor 3	-2.42	0.02157	-1.16	0.65946
LRRC49	leucine rich repeat containing 49	-2.42	0.00481	-1.29	0.33232
APOLD1	apolipoprotein L domain containing 1	-2.42	0.01385	-1.03	0.92491

AU144916	---	-2.42	0.0269	1.24	0.53798
C14orf182	chromosome 14 open reading frame 182	-2.42	0.00226	-1.17	0.48849
LANCL2	LanC lantibiotic synthetase component C-like 2 (bacterial)	-2.42	0.00485	-1.85	0.03153
NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	-2.41	0.00187	1.07	0.7651
KIF18A	kinesin family member 18A	-2.41	0.0258	-1.69	0.15318
TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	-2.41	0.01963	1.34	0.37559
AW612461	---	-2.41	1.00E-04	-1.11	0.50334
PLXND1	plexin D1	-2.41	0.00075	1.13	0.52631
AW293012	---	-2.41	0.00121	-1.48	0.07487
RNF24	ring finger protein 24	-2.40	0.00043	-1.09	0.62716
CORO2A	coronin, actin binding protein, 2A	-2.40	0.03249	1.15	0.69604
TMEM154	transmembrane protein 154	-2.40	0.00652	-1.27	0.37194
ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	-2.40	0.00266	-1.29	0.28569
POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	-2.40	0.01732	-1.69	0.12104
CD44	CD44 molecule (Indian blood group)	-2.40	0.00231	-1.73	0.03049
NOLC1	nucleolar and coiled-body phosphoprotein 1	-2.39	0.00096	-1.28	0.22562
UCK2	uridine-cytidine kinase 2	-2.39	0.00064	-1.05	0.77872
TFDP1	transcription factor Dp-1	-2.39	0.04555	-1.36	0.43873
TCOF1	Treacher Collins-Franceschetti syndrome 1	-2.39	4.00E-05	-1.3	0.0639
ADAM28	ADAM metallopeptidase domain 28	-2.39	0.00022	1.1	0.55921
USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	-2.39	0	-1.94	4.00E-05
TNFAIP8	tumor necrosis factor, alpha-induced protein 8	-2.39	0.00443	-1.29	0.31994
TMED4 *	transmembrane emp24 protein transport domain containing 4	-2.39	0.00333	2.73	0
IPO5	importin 5	-2.39	0.00232	-1.43	0.1274
RASIP1	Ras interacting protein 1	-2.39	0.00269	1.12	0.61314
PYCR2	pyrroline-5-carboxylate reductase family, member 2	-2.39	0.02661	-1.04	0.91637
GLT25D1	glycosyltransferase 25 domain containing 1	-2.38	0.02264	-1.52	0.22275
C5orf34	chromosome 5 open reading frame 34	-2.38	0.00023	1.03	0.87192
PDE3B	phosphodiesterase 3B, cGMP-inhibited	-2.38	0.02226	-1.5	0.23952
ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	-2.38	0.02088	-1.45	0.27194
ZAK	sterile alpha motif and leucine zipper containing kinase AZK	-2.38	2.00E-05	-1.6	0.00221
POC1A	POC1 centriolar protein homolog A (Chlamydomonas)	-2.38	0.02784	-1.72	0.13972
MTG1	Mitochondrial GTPase 1 homolog (S. cerevisiae)	-2.38	0.02017	-1.97	0.05623
CBX2	chromobox homolog 2	-2.38	0.01245	1.27	0.4204
AI200546	---	-2.38	0.04207	-1.66	0.20524
CENPH	centromere protein H	-2.38	9.00E-04	1.08	0.7069
XBP1	X-box binding protein 1	-2.38	0.00331	-1.43	0.15053
DKC1	dyskeratosis congenita 1, dyskerin	-2.37	0.00029	1.01	0.96711
ZNF367	zinc finger protein 367	-2.37	0.03245	2.01	0.0731
GNLY	granulysin	-2.37	0.00021	1.06	0.72621
DDX39A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A	-2.37	0.01105	-1.27	0.41319
PER1	period homolog 1 (Drosophila)	-2.37	0.02402	-1.24	0.52737
NASP	nuclear autoantigenic sperm protein (histone-binding)	-2.37	0.00449	1.21	0.43475
BG231709	---	-2.37	0.00197	-1.64	0.03915

POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	-2.37	0.00036	-1.64	0.01309
CACNA1D	calcium channel, voltage-dependent, L type, alpha 1D subunit	-2.37	0.03258	1.52	0.25503
PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	-2.36	0.01839	1.66	0.12838
RAB43	RAB43, member RAS oncogene family	-2.36	0.04006	-1.49	0.29885
LOC728431	uncharacterized LOC728431	-2.36	0.01613	-1	0.99482
TMEM170B	transmembrane protein 170B	-2.36	0.01954	-1.18	0.61547
CDADC1	cytidine and dCMP deaminase domain containing 1	-2.36	0.02164	-1.31	0.41904
PPP3CB	protein phosphatase 3, catalytic subunit, beta isozyme	-2.36	0.00086	-1.69	0.01756
LAMB1	laminin, beta 1	-2.36	6.00E-05	1.2	0.19315
C11orf96	chromosome 11 open reading frame 96	-2.36	0.00313	-1.28	0.29579
LIPG	lipase, endothelial	-2.36	0.02665	-1.53	0.22736
WWTR1-AS1	WWTR1 antisense RNA 1 (non-protein coding)	-2.36	0.03256	-1.14	0.72012
HILPDA	hypoxia inducible lipid droplet-associated	-2.35	0.00459	-1.22	0.42727
MCTP1	multiple C2 domains, transmembrane 1	-2.35	0.00031	1.57	0.01843
PLEKHA6	pleckstrin homology domain containing, family A member 6	-2.34	0.00899	1.23	0.4595
KCNS3	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	-2.34	0.0021	1.19	0.42827
ZFP64	Zinc finger protein 64 homolog (mouse)	-2.34	0.00925	-1.05	0.85819
PDE8B	phosphodiesterase 8B	-2.34	0.02764	-1.31	0.43286
NEK2	NIMA (never in mitosis gene a)-related kinase 2	-2.34	0.00354	-1.21	0.42225
NPNT	nephronectin	-2.34	0.01275	-1.28	0.40209
RECQL	RecQ protein-like (DNA helicase Q1-like)	-2.34	0.01012	-1.33	0.31911
MAGOHB	mago-nashi homolog B (Drosophila)	-2.34	0.03775	1.13	0.73338
KCNC4	potassium voltage-gated channel, Shaw-related subfamily, member 4	-2.34	0.01957	1.04	0.90332
GTSE1	G-2 and S-phase expressed 1	-2.34	0.04456	-1.18	0.66029
TXNDC5	thioredoxin domain containing 5 (endoplasmic reticulum)	-2.34	2.00E-05	-1.23	0.11478
CMTM3	CKLF-like MARVEL transmembrane domain containing 3	-2.33	5.00E-05	-1.11	0.4268
PTGES	prostaglandin E synthase	-2.33	0.00273	1.06	0.80894
TAF1A	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa	-2.33	0.01708	-1.02	0.93794
NRIP1	nuclear receptor interacting protein 1	-2.33	0.00093	-1.62	0.02643
LOC284751	uncharacterized LOC284751	-2.33	0.0069	1.09	0.73639
NCAPH2	non-SMC condensin II complex, subunit H2	-2.33	0.01759	-1.11	0.74224
PPCDC	phosphopantothenoylcysteine decarboxylase	-2.33	0.04319	-1.69	0.18142
CELF2	CUGBP, Elav-like family member 2	-2.33	0.01169	1.34	0.31535
PPP2R2A	protein phosphatase 2, regulatory subunit B, alpha	-2.33	0.00149	-1.82	0.0121
NCALD	neurocalcin delta	-2.33	0.00014	-1.15	0.36343
SIPA1L1	signal-induced proliferation-associated 1 like 1	-2.33	0.00601	1.2	0.46585
RFC4	replication factor C (activator 1) 4, 37kDa	-2.32	0.00145	1.22	0.33972
PRR7-AS1	PRR7 antisense RNA 1 (non-protein coding)	-2.32	0.00051	-1.3	0.15582
MDC1	mediator of DNA-damage checkpoint 1	-2.32	0.00971	-1.69	0.07614
BC000885	---	-2.32	0.03295	-1.3	0.46512
MIR3682	microRNA 3682	-2.32	0.02887	-1.88	0.08475
DISC1	disrupted in schizophrenia 1	-2.32	0.03095	-1.76	0.12541
BFSP1	beaded filament structural protein 1, filensin	-2.32	0.00851	-1.26	0.39768

FAM105A *	family with sequence similarity 105, member A	-2.32	0.01603	2.36	0.01452
NCOA7	nuclear receptor coactivator 7	-2.32	0.00039	-1.37	0.08542
AF052109	---	-2.32	0.04632	1.08	0.83737
RASAL1	RAS protein activator like 1 (GAP1 like)	-2.32	0.00679	1	0.99857
AV702787	---	-2.31	0.00058	-1.1	0.57949
RFC3	replication factor C (activator 1) 3, 38kDa	-2.31	0.02842	1.36	0.36987
IL15RA	interleukin 15 receptor, alpha	-2.31	0.00159	-1.23	0.31591
TUBA1A	tubulin, alpha 1a	-2.31	0.04361	1.23	0.57629
NRTN	neurturin	-2.31	0.03453	1.27	0.5095
ROBO3	roundabout, axon guidance receptor, homolog 3 (Drosophila)	-2.31	0.00022	-1.3	0.11889
CDC42EP1	CDC42 effector protein (Rho GTPase binding) 1	-2.31	0.00354	-1.64	0.04973
TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	-2.31	0.00108	1.24	0.2806
DPYSL2	dihydropyrimidinase-like 2	-2.31	0.0017	1.32	0.1926
PIGA	phosphatidylinositol glycan anchor biosynthesis, class A	-2.31	0.00549	1	0.98415
TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	-2.31	0.02723	-1.33	0.40738
LOC100129104	uncharacterized LOC100129104	-2.31	6.00E-05	-1.26	0.10608
DCTN1	dynactin 1	-2.31	0.0107	1.23	0.4649
BCL10	B-cell CLL/lymphoma 10	-2.31	0.00822	-1.4	0.21756
PAX6	paired box 6	-2.31	0.00485	1.03	0.89084
TRIM27	tripartite motif containing 27	-2.31	0.00749	-1.34	0.27343
PRKCA	protein kinase C, alpha	-2.31	0.00127	-1.71	0.01815
TRAF3IP3	TRAF3 interacting protein 3	-2.31	0.00154	-1.31	0.19567
SGMS2	sphingomyelin synthase 2	-2.31	2.00E-05	1.07	0.59431
VARS	valyl-tRNA synthetase	-2.31	0.00934	-1.23	0.45472
AL050136	---	-2.31	0.02903	-1.34	0.39566
IER5	immediate early response 5	-2.31	0.0228	-1.23	0.52188
CCDC147	coiled-coil domain containing 147	-2.31	0.02621	-1.22	0.5585
MSANTD2	Myb/SANT-like DNA-binding domain containing 2	-2.31	0.02649	-1.14	0.70128
RFESD	Rieske (Fe-S) domain containing	-2.31	0.00189	-1.2	0.38633
SNX10	sorting nexin 10	-2.31	0.0223	1.39	0.31104
PSEN1	presenilin 1	-2.31	0.03516	-1.67	0.16472
MGC39372	serpin peptidase inhibitor, clade B (ovalbumin), member 9 pseudogene	-2.30	0.0039	-1.17	0.50529
LOC100652770	Uncharacterized LOC100652770	-2.30	0.00571	-1.06	0.82361
EIF3E	eukaryotic translation initiation factor 3, subunit E	-2.30	7.00E-05	-1.8	0.00112
GPC4	glypican 4	-2.30	0.00761	-1.29	0.33632
ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3	-2.30	0.00629	-1.14	0.59394
FAM190B	family with sequence similarity 190, member B	-2.30	0.00196	-1.1	0.66213
TMEM92	transmembrane protein 92	-2.30	0.00223	-1.12	0.58951
PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	-2.30	0.00028	-1	0.98934
SEMA3B	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	-2.30	0.00081	-1.51	0.04284
FAM84B	family with sequence similarity 84, member B	-2.30	0.00118	-1.16	0.45548
BF995452	---	-2.30	0.04067	-1.37	0.39493
ADCY3	adenylate cyclase 3	-2.29	0.00472	1.5	0.10951
CHAF1B	chromatin assembly factor 1, subunit B (p60)	-2.29	0.00059	1.25	0.21498

FJX1	four jointed box 1 (Drosophila)	-2.29	0.04942	-1.2	0.64211
RAP2A	RAP2A, member of RAS oncogene family	-2.29	0.00376	-1.83	0.02146
LITAF	lipopolysaccharide-induced TNF factor	-2.29	0.00026	-1.93	0.00147
LONRF1	LON peptidase N-terminal domain and ring finger 1	-2.29	0.00133	-1.36	0.13622
CTSC	cathepsin C	-2.29	4.00E-05	-1.26	0.08709
SLC36A4	solute carrier family 36 (proton/amino acid symporter), member 4	-2.29	0.01173	1.15	0.62712
SRR	Serine racemase	-2.29	0.02903	-1.2	0.58904
EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	-2.28	0.00095	-1.6	0.02672
RCC1	regulator of chromosome condensation 1	-2.28	0.00153	-1.17	0.43042
PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1	-2.28	0.00025	1.06	0.69483
NABP1	nucleic acid binding protein 1	-2.28	0.00709	-1.37	0.22549
CD83	CD83 molecule	-2.28	0.00021	-1.01	0.94113
AV646177	---	-2.28	0.00343	-1.14	0.57543
HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	-2.28	0.01828	-1.09	0.78276
PC	pyruvate carboxylase	-2.28	0.00514	-1.28	0.3139
FAP	fibroblast activation protein, alpha	-2.28	0.03047	-1.12	0.73734
ZBTB38	zinc finger and BTB domain containing 38	-2.28	0.00617	-1.09	0.72987
THRB	thyroid hormone receptor, beta	-2.28	0.00074	1.01	0.96019
ORC1	origin recognition complex, subunit 1	-2.27	0.04202	-1.01	0.97576
GCSH	glycine cleavage system protein H (aminomethyl carrier)	-2.27	0.00012	1.02	0.8895
MOCOS	molybdenum cofactor sulfurase	-2.27	0.01098	-1.13	0.65229
ERGIC1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	-2.27	0.04547	-1.11	0.7814
BC037339	---	-2.27	0.01655	-1.12	0.70323
FKBP5	FK506 binding protein 5	-2.27	5.00E-05	1.04	0.76769
FMNL3	formin-like 3	-2.27	0.02731	1.06	0.85782
DPYD	dihydropyrimidine dehydrogenase	-2.27	0.01544	-1.09	0.77531
AW301241	---	-2.27	0.03729	-1.63	0.18327
OGFR	opioid growth factor receptor	-2.27	0.00811	-1.93	0.02449
AGXT2L2	alanine-glyoxylate aminotransferase 2-like 2	-2.27	0.00335	-1.68	0.03746
NEDD1	neural precursor cell expressed, developmentally down-regulated 1	-2.27	0.00303	-1.02	0.93983
RHEBL1 *	Ras homolog enriched in brain like 1	-2.27	0.00013	2.24	0.00015
PTER	phosphotriesterase related	-2.26	6.00E-05	-1.38	0.02738
ADD3	adducin 3 (gamma)	-2.26	0.01916	1.02	0.9494
A2M	alpha-2-macroglobulin	-2.26	0.01347	-1.18	0.55515
FGFR1	fibroblast growth factor receptor 1	-2.26	0.00545	1.39	0.18379
SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	-2.26	0.02401	-1.63	0.14507
PKP4	plakophilin 4	-2.26	0.00177	-1.38	0.12607
PRIM1	primase, DNA, polypeptide 1 (49kDa)	-2.26	0.01068	-1.23	0.45306
MOSPD1	motile sperm domain containing 1	-2.26	0.04144	-1.28	0.49783
CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1	-2.26	0.00017	1.43	0.02915
FIBIN	fin bud initiation factor homolog (zebrafish)	-2.26	0.04173	1.33	0.43852
E2F1	E2F transcription factor 1	-2.25	0.00247	-1.31	0.21302
RGS10	Regulator of G-protein signaling 10	-2.25	0.00125	-1.14	0.49111
LOC100506021	uncharacterized LOC100506021	-2.25	0.00178	1.06	0.76355

PROCR	protein C receptor, endothelial	-2.25	0.0136	-1.25	0.42589
SH2D4A	SH2 domain containing 4A	-2.25	0.00016	-1.03	0.86157
AL563613	---	-2.25	0.00569	-1.51	0.10853
DNMT1	DNA (cytosine-5-)-methyltransferase 1	-2.25	0.00827	-1.07	0.80552
C8orf33	chromosome 8 open reading frame 33	-2.25	0.00187	-1.91	0.0075
AGFG1	ArfGAP with FG repeats 1	-2.25	0.00335	-1.43	0.1261
AW302848	---	-2.25	0.00219	-1.05	0.79831
SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	-2.25	0.04642	1.73	0.15474
SAMD9	sterile alpha motif domain containing 9	-2.25	0.02845	1.21	0.56532
ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial	-2.25	0.01237	-1.33	0.31499
BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	-2.25	0.00379	-1.26	0.31986
ANKRD29	ankyrin repeat domain 29	-2.25	0.00601	-1.38	0.20437
SPRED2	sprouty-related, EVH1 domain containing 2	-2.24	0.03321	-1.13	0.71683
SLC30A1	solute carrier family 30 (zinc transporter), member 1	-2.24	0.00011	-1.61	0.00516
VKORC1L1	vitamin K epoxide reductase complex, subunit 1-like 1	-2.24	0.0034	-1.55	0.06868
GJC1	gap junction protein, gamma 1, 45kDa	-2.24	0.02626	1.88	0.0706
RFC2	replication factor C (activator 1) 2, 40kDa	-2.24	0.00028	-1.25	0.16756
HPCAL1	hippocalcin-like 1	-2.24	0.00325	-1.43	0.11893
DPYSL3	dihydropyrimidinase-like 3	-2.24	0.00301	-1.15	0.51253
NQO1	NAD(P)H dehydrogenase, quinone 1	-2.24	0.00109	-1.5	0.04684
ZNF227	zinc finger protein 227	-2.24	0.03937	-1.66	0.16846
C12orf60	chromosome 12 open reading frame 60	-2.24	0.00625	1.15	0.5622
RFC5	replication factor C (activator 1) 5, 36.5kDa	-2.24	0.02702	1.24	0.50596
CENPJ	centromere protein J	-2.24	0.01464	-1.19	0.54285
TSNAX	translin-associated factor X	-2.24	0.01814	-1.45	0.22274
SGK494	uncharacterized serine/threonine-protein kinase SgK494	-2.24	0.0028	-1.06	0.78249
BATF3	basic leucine zipper transcription factor, ATF-like 3	-2.24	0.02917	1.09	0.79182
RAB27A	RAB27A, member RAS oncogene family	-2.23	0.00712	-1.1	0.69552
ITM2C	integral membrane protein 2C	-2.23	0.00116	-1.48	0.05686
MYO1B	myosin IB	-2.23	0.00385	-1.14	0.55547
DHRS13	dehydrogenase/reductase (SDR family) member 13	-2.23	0.00021	1.3	0.09816
PPM1J	protein phosphatase, Mg2+/Mn2+ dependent, 1J	-2.23	0.00236	-1.15	0.49572
NLN	neurolysin (metallopeptidase M3 family)	-2.23	0.00424	1.21	0.41328
PPT1	palmitoyl-protein thioesterase 1	-2.23	1.00E-04	-1.77	0.00138
CENPM	centromere protein M	-2.23	0.01289	-1.23	0.45803
PHF19	PHD finger protein 19	-2.23	0.0144	-1.05	0.86182
SNX3	sorting nexin 3	-2.23	0.00377	-1.45	0.11734
NCAPG2	non-SMC condensin II complex, subunit G2	-2.23	0.00446	1.11	0.65583
MFSD12	major facilitator superfamily domain containing 12	-2.23	0.00065	1.28	0.17262
SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	-2.23	0.00075	-1.5	0.03687
BF432941	---	-2.23	0.01014	-1.44	0.18532
AL832803	---	-2.23	0.00444	-1.05	0.82855
KITLG	KIT ligand	-2.23	0.00035	1.18	0.29968

CORO1C	coronin, actin binding protein, 1C	-2.23	0.00317	1.03	0.90464
RTKN2	rhotekin 2	-2.23	0.04338	-1.22	0.58403
TMPO	thymopoietin	-2.22	0.02857	1.07	0.8362
ALKBH2	alkB, alkylation repair homolog 2 (E. coli)	-2.22	0.03059	-1.13	0.71055
KIAA1524	KIAA1524	-2.22	0.0155	-1.25	0.44209
PRPS2	Phosphoribosyl pyrophosphate synthetase 2	-2.22	0.01436	1.26	0.40752
TFR2	transferrin receptor 2	-2.22	0.00478	1.89	0.0165
TOP1MT	topoisomerase (DNA) I, mitochondrial	-2.22	0.00256	-1.85	0.01217
TMC7	transmembrane channel-like 7	-2.22	0.00061	-1.21	0.27778
ARSI	arylsulfatase family, member I	-2.22	0.00063	-1.1	0.57633
IRAK2	interleukin-1 receptor-associated kinase 2	-2.22	0.00285	1.36	0.16075
C3orf80	chromosome 3 open reading frame 80	-2.22	0.02345	1.87	0.06251
SORD	sorbitol dehydrogenase	-2.22	0.00933	-1.1	0.70219
MAPRE2	microtubule-associated protein, RP/EB family, member 2	-2.22	0.03019	-1.09	0.79444
ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	-2.22	0.01145	-1.18	0.54771
TMEM205	transmembrane protein 205	-2.22	0.02995	-1.13	0.70617
KRT6B	keratin 6B	-2.22	0.0132	-1.03	0.90177
CARS	cysteinyl-tRNA synthetase	-2.22	0.01605	1.38	0.27103
TRAM2	translocation associated membrane protein 2	-2.21	0.00268	-1.43	0.10677
DTYMK	deoxythymidylate kinase (thymidylate kinase)	-2.21	0.0375	-1.18	0.63197
CCL20 *	chemokine (C-C motif) ligand 20	-2.21	0.01529	3.63	0.00076
ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-2.21	0.02918	-1.35	0.35864
CHAF1A	chromatin assembly factor 1, subunit A (p150)	-2.21	0.04633	-1.07	0.84735
DBF4	DBF4 homolog (S. cerevisiae)	-2.21	0.02998	1.09	0.79053
GIT2	G protein-coupled receptor kinase interacting ArfGAP 2	-2.21	0.00715	-1.12	0.64614
ADAM19	ADAM metallopeptidase domain 19	-2.21	0.01085	1.89	0.03121
NTRK2	neurotrophic tyrosine kinase, receptor, type 2	-2.21	0.02626	1.14	0.67468
PURA	purine-rich element binding protein A	-2.21	0.00904	-1.76	0.04505
MIS18A	MIS18 kinetochore protein homolog A (S. pombe)	-2.21	0.00038	-1.07	0.66733
UBE4A	ubiquitination factor E4A	-2.21	0.00016	-1.63	0.00495
SLC44A1	solute carrier family 44, member 1	-2.21	0.00111	-1.63	0.02018
RNF157-AS1	RNF157 antisense RNA 1 (non-protein coding)	-2.21	0.03193	-1.24	0.52195
TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	-2.20	0.00939	-1.39	0.2117
SAAL1	serum amyloid A-like 1	-2.20	1.00E-04	1.03	0.84244
FRMD5	FERM domain containing 5	-2.20	0.04546	-1.56	0.22615
AI807197	---	-2.20	0.01074	-1.14	0.62055
KRT86	keratin 86	-2.20	0.00972	-1.19	0.51024
PPP4R4	protein phosphatase 4, regulatory subunit 4	-2.20	0.01076	-1.05	0.8398
CDK17	cyclin-dependent kinase 17	-2.20	0.00038	-2	0.00103
AGMAT	agmatine ureohydrolase (agmatinase)	-2.20	0.03134	1.15	0.66494
TGOLN2	trans-golgi network protein 2	-2.20	0.02572	-1.48	0.22278
ENOX2	ecto-NOX disulfide-thiol exchanger 2	-2.20	0.00178	-1.74	0.01448
SNORA56	small nucleolar RNA, H/ACA box 56	-2.20	2.00E-05	-1.1	0.39192
LRRC8D	leucine rich repeat containing 8 family, member D	-2.20	8.00E-05	-1.44	0.01527
MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	-2.20	0.03525	-1.35	0.37997
CDC20	cell division cycle 20 homolog (S. cerevisiae)	-2.20	0.0152	-1.42	0.22698
POLE2	polymerase (DNA directed), epsilon 2, accessory subunit	-2.19	0.00305	1.38	0.14561

SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	-2.19	0.00064	-1.35	0.09497
ACOT7	acyl-CoA thioesterase 7	-2.19	0.01286	1.49	0.1606
BRCA2	breast cancer 2, early onset	-2.19	0.00337	-1.05	0.82534
CD97	CD97 molecule	-2.19	0.01929	-1.13	0.68602
WBSCR22	Williams Beuren syndrome chromosome region 22	-2.19	0.00539	-1.59	0.06411
GATA6	GATA binding protein 6	-2.19	0.00924	-1.08	0.75527
APOE	Apolipoprotein E	-2.19	0.03356	-1.52	0.21785
TXNDC16	thioredoxin domain containing 16	-2.19	0.01059	1.08	0.76037
LIMCH1	LIM and calponin homology domains 1	-2.19	1.00E-05	-1.03	0.79926
AW362945	---	-2.19	0.00149	1.05	0.78704
BC040884	---	-2.19	0.01115	1.05	0.84784
C11orf9	chromosome 11 open reading frame 9	-2.19	0.008	-1.68	0.05511
PDXP	pyridoxal (pyridoxine, vitamin B6) phosphatase	-2.19	0.01438	-1.19	0.53518
BAG4	BCL2-associated athanogene 4	-2.19	0.00817	-1.33	0.25824
RPL31	ribosomal protein L31	-2.19	0.00079	-1.35	0.10374
HAUS1	HAUS augmin-like complex, subunit 1	-2.18	0.00335	-1	0.99311
IFT81	intraflagellar transport 81 homolog (Chlamydomonas)	-2.18	0.00016	1.32	0.06921
AI638063	---	-2.18	0.03209	-1.29	0.44455
PRIM2	primase, DNA, polypeptide 2 (58kDa)	-2.18	0.02349	1.05	0.87948
WAPAL	wings apart-like homolog (Drosophila)	-2.18	0.01618	-1.36	0.28639
AI672356	---	-2.18	0.00827	-1.18	0.51216
WDR35	WD repeat domain 35	-2.18	0.00308	-1.21	0.3632
GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	-2.18	0.00635	-1.64	0.05574
AK021887	---	-2.18	0.00157	1.06	0.74497
BE551781	---	-2.17	0.00067	-1.15	0.40243
PLK1S1	polo-like kinase 1 substrate 1	-2.17	0.00292	-1.37	0.14501
N34514	---	-2.17	0.04764	-1.18	0.64836
PRDX3	peroxiredoxin 3	-2.17	2.00E-05	-1.15	0.20936
TRIB1	tribbles homolog 1 (Drosophila)	-2.17	0.00769	-1.95	0.01698
LOC100507535	uncharacterized LOC100507535	-2.17	0.0046	-2.47	0.00172
CASP9	caspase 9, apoptosis-related cysteine peptidase	-2.17	4.00E-05	1.24	0.0897
PXK	PX domain containing serine/threonine kinase	-2.17	0.02051	1.02	0.95044
LOC100505634	uncharacterized LOC100505634	-2.17	0.03313	1.05	0.8707
PPIF	peptidylprolyl isomerase F	-2.17	6.00E-05	-1.94	0.00022
ZNF37BP	zinc finger protein 37B, pseudogene	-2.17	0.04363	1.09	0.79847
AA523939	---	-2.17	0.00911	1.64	0.06745
AP2B1	adaptor-related protein complex 2, beta 1 subunit	-2.17	0.00038	-1.44	0.03486
CREB5 *	cAMP responsive element binding protein 5	-2.17	0.02318	2.11	0.02696
POLD3	polymerase (DNA-directed), delta 3, accessory subunit	-2.17	0.00555	-1.01	0.96754
ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	-2.16	0.04856	-1.08	0.83066
LOC728613	programmed cell death 6 pseudogene	-2.16	0.00034	-1.23	0.19204
LEPREL4	leprecan-like 4	-2.16	0.00053	-1.55	0.01858
EXOSC2	exosome component 2	-2.16	8.00E-05	-1.32	0.04517
TBL2	transducin (beta)-like 2	-2.16	0.00899	-1.56	0.0937
SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	-2.16	0.01212	1.11	0.68504
CUL4A	cullin 4A	-2.16	0.01549	-1.48	0.17069

GNAS-AS1	GNAS antisense RNA 1 (non-protein coding)	-2.16	0.02563	-1.19	0.56398
EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	-2.16	0.02229	-1.35	0.32407
RASSF10	Ras association (RalGDS/AF-6) domain family (N-terminal) member 10	-2.16	0.01003	1.16	0.55756
SOCS2 *	suppressor of cytokine signaling 2	-2.16	0.01048	2.3	0.00678
PER2	period homolog 2 (Drosophila)	-2.16	0.03433	-1.46	0.25977
MTMR2	myotubularin related protein 2	-2.16	0.01277	-1.21	0.46671
ADPRM	ADP-ribose/CDP-alcohol diphosphatase, manganes	-2.16	0.03609	-1.61	0.16578
PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	-2.16	0.002	-1.03	0.87025
XK	X-linked Kx blood group (McLeod syndrome)	-2.16	1.00E-04	1.07	0.62658
RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	-2.16	0.01001	-1.77	0.04175
HIST1H1A	histone cluster 1, H1a	-2.16	0.00339	-1.35	0.16533
MCM4	minichromosome maintenance complex component 4	-2.16	0.02153	-1.24	0.46879
AV700165	---	-2.16	0.00874	1.14	0.6041
NOP16	NOP16 nucleolar protein homolog (yeast)	-2.16	0.02944	-1.33	0.37344
RPL13P5	ribosomal protein L13 pseudogene 5	-2.16	0.00609	-1.3	0.26351
HOXA2	homeobox A2	-2.16	0.00518	1.18	0.47046
ANKRD27	ankyrin repeat domain 27 (VPS9 domain)	-2.16	2.00E-05	-1.85	0.00012
HYAL1	hyaluronoglucosaminidase 1	-2.15	0.01291	-1.32	0.3061
CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	-2.15	0.00644	-1.2	0.44065
PCP4L1	Purkinje cell protein 4 like 1	-2.15	0.00098	-1.05	0.76425
DUSP1	Dual specificity phosphatase 1	-2.15	0.03823	-1.1	0.77805
STEAP1B	STEAP family member 1B	-2.15	0.00217	-1.09	0.65694
ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	-2.15	0.01575	1.11	0.70745
SLC37A3	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	-2.15	0.00781	-1.56	0.08471
HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	-2.14	0.00923	1.03	0.90883
GOSR2	golgi SNAP receptor complex member 2	-2.14	0.03711	-1.43	0.2883
THSD4	thrombospondin, type I, domain containing 4	-2.14	0.01684	1.1	0.73467
UBA2	ubiquitin-like modifier activating enzyme 2	-2.14	0.01256	-1.35	0.2591
SAMD8	sterile alpha motif domain containing 8	-2.14	0.04886	1.05	0.89641
FZD4	frizzled family receptor 4	-2.14	0.00046	-1.15	0.37176
BZW1	basic leucine zipper and W2 domains 1	-2.14	0.00568	-1.19	0.43636
C1orf198	chromosome 1 open reading frame 198	-2.14	0.01711	-1.02	0.93921
DCAF13	DDB1 and CUL4 associated factor 13	-2.14	0.00442	-1.36	0.17158
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	-2.14	0.04806	1.08	0.83268
NAMPT	nicotinamide phosphoribosyltransferase	-2.14	0.00475	1.05	0.80757
TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	-2.14	0.02505	1.26	0.44406
TRIB2	tribbles homolog 2 (Drosophila)	-2.13	0.04787	-1.04	0.91538
MMP1	matrix metallopeptidase 1 (interstitial collagenase)	-2.13	0.00423	-1.02	0.91305
UBE2T	ubiquitin-conjugating enzyme E2T (putative)	-2.13	0.00971	1.1	0.70586
BF445387	---	-2.13	0.00411	-1.09	0.68739
APLP1	amyloid beta (A4) precursor-like protein 1	-2.13	0.00032	1.16	0.33678
ZNF473	zinc finger protein 473	-2.13	0.04825	-1.61	0.1864
FLJ11871	hypothetical protein FLJ11871	-2.13	0.04852	-1.96	0.07438

SLC2A14	solute carrier family 2 (facilitated glucose transporter), member 14	-2.13	0.00724	1.45	0.13219
IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2	-2.13	0.00054	-1.28	0.14498
USP54	ubiquitin specific peptidase 54	-2.13	0.01173	-1.3	0.31978
AW611560	---	-2.13	0.00268	1.08	0.71556
TMF1	TATA element modulatory factor 1	-2.13	0.00277	-1.36	0.14701
BCL2	B-cell CLL/lymphoma 2	-2.13	0.03334	-1.1	0.77085
DST	dystonin	-2.13	0.01481	-1.17	0.55258
BACE1	beta-site APP-cleaving enzyme 1	-2.13	0.02133	-1.41	0.24932
AA825721	---	-2.13	0.01918	1.04	0.88351
ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	-2.13	0.00489	-1.33	0.21263
PARPBP	PARP1 binding protein	-2.13	0.02254	-1.29	0.3817
CSNK1E	casein kinase 1, epsilon	-2.13	0.00075	-1.26	0.17844
PVR	poliovirus receptor	-2.12	0.00169	-1.3	0.17956
AK094711	---	-2.12	0.01695	1.23	0.44773
TOP2A	topoisomerase (DNA) II alpha 170kDa	-2.12	0.00545	-1.28	0.27155
S100A13	S100 calcium binding protein A13	-2.12	0.0352	-1.26	0.46861
AA861608	---	-2.12	0.00044	-1.21	0.23625
RBM11	RNA binding motif protein 11	-2.12	0.03091	-1.29	0.42476
MTSS1	metastasis suppressor 1	-2.12	0.02179	-1.14	0.65932
ACER3	alkaline ceramidase 3	-2.12	0.00174	-1.35	0.12654
EFEMP2	EGF containing fibulin-like extracellular matrix protein 2	-2.12	0.0274	1	0.99424
CC2D2A	coiled-coil and C2 domain containing 2A	-2.12	0.04185	-1.91	0.07349
JDP2	Jun dimerization protein 2	-2.12	0.01512	-1.22	0.46319
SLC35F2	solute carrier family 35, member F2	-2.12	6.00E-04	1.31	0.11413
PEX13	peroxisomal biogenesis factor 13	-2.12	0.02168	-1.08	0.79611
AA532745	---	-2.12	0.00979	-1.81	0.0313
ADRB2	adrenoceptor beta 2, surface	-2.12	0.03602	-1.35	0.35892
NUP155	nucleoporin 155kDa	-2.12	0.00081	1.1	0.57927
NM_024853	---	-2.12	0.03494	-1.03	0.9377
C4orf46	chromosome 4 open reading frame 46	-2.12	0.00087	-1.3	0.13945
CBLB	Cbl proto-oncogene, E3 ubiquitin protein ligase B	-2.11	0.00998	-1.08	0.76557
AI356405	---	-2.11	0.03733	-1.28	0.44278
LOC283278	uncharacterized LOC283278	-2.11	0.0027	-1.13	0.5417
TJP2	tight junction protein 2 (zona occludens 2)	-2.11	0.01622	1.23	0.43917
UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	-2.11	0.00398	-1.32	0.19649
AI300571	---	-2.11	0.04021	-1.95	0.06234
TTC39C	tetratricopeptide repeat domain 39C	-2.11	0.04239	-1.48	0.24892
ATP2A1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	-2.11	0.04682	1.08	0.81904
EPHA5	EPH receptor A5	-2.11	0.01668	-1.04	0.8906
TRAF3IP2-AS1	TRAF3IP2 antisense RNA 1 (non-protein coding)	-2.11	0.00039	-1.44	0.02909
WARS	tryptophanyl-tRNA synthetase	-2.11	0.03212	1.23	0.5037
NRIP3	nuclear receptor interacting protein 3	-2.11	0.01216	-1.09	0.72272
MFAP3	microfibrillar-associated protein 3	-2.11	0.04492	-1.3	0.43557
LOC100130357	uncharacterized LOC100130357	-2.11	0.00492	1.07	0.76912
RGS2	regulator of G-protein signaling 2, 24kDa	-2.11	0.02556	1.22	0.50575
GPN3	GPN-loop GTPase 3	-2.11	0.04951	1.48	0.26851
IKBIP	IKBKB interacting protein	-2.11	0.01915	-1.17	0.57842
ADCY1	adenylate cyclase 1 (brain)	-2.10	0.02722	1.07	0.81966

TMEM5	transmembrane protein 5	-2.10	0.03205	-1.52	0.19151
AK4	adenylate kinase 4	-2.10	0.00485	1.11	0.63144
ALG14	asparagine-linked glycosylation 14 homolog (S. cerevisiae)	-2.10	0.02983	-1.57	0.15398
WDR5	WD repeat domain 5	-2.10	0.03197	-1.11	0.73922
LOC100505880	uncharacterized LOC100505880	-2.10	0.00269	1.1	0.62417
METTL1	methyltransferase like 1	-2.10	0.00493	-1.05	0.80711
HELLS	helicase, lymphoid-specific	-2.10	0.00621	1.12	0.61808
FANCD2	Fanconi anemia, complementation group D2	-2.10	0.01249	-1.09	0.72181
FZD7	frizzled family receptor 7	-2.10	0.02181	-1.17	0.5862
CNKSR2	connector enhancer of kinase suppressor of Ras 2	-2.10	0.04231	1.38	0.33922
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	-2.10	0.00407	-1.34	0.17698
AI286239	---	-2.10	0.0135	-1.45	0.16327
TRIL	TLR4 interactor with leucine-rich repeats	-2.09	0.00287	1.19	0.38747
AW779917	---	-2.09	0.00244	-1.55	0.0382
LOC100128653	uncharacterized LOC100128653	-2.09	0.00161	-1.23	0.26237
SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	-2.09	0.00426	-1.08	0.72202
ENOSF1	enolase superfamily member 1	-2.09	0.00308	1.1	0.61494
NEURL1B	neuralized homolog 1B (Drosophila)	-2.09	0.02728	1.24	0.46796
FAM131B	family with sequence similarity 131, member B	-2.09	0.00325	-1.07	0.71885
DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	-2.09	1.00E-04	-1.87	0.00038
SIX4	SIX homeobox 4	-2.09	0.00031	-1.17	0.27764
NMNAT1	nicotinamide nucleotide adenylyltransferase 1	-2.09	0.04481	-1.39	0.3366
ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	-2.09	0.0024	-1.17	0.40876
PRR11	proline rich 11	-2.09	0.00017	-1.56	0.00618
ARHGEF39	Rho guanine nucleotide exchange factor (GEF) 39	-2.09	0.03228	-1.14	0.67624
TOR3A	torsin family 3, member A	-2.09	0.01209	-1.16	0.54897
CSPG5	chondroitin sulfate proteoglycan 5 (neuroglycan C)	-2.09	0.04667	1.7	0.13319
NCAPD2	non-SMC condensin I complex, subunit D2	-2.09	0.02831	-1.31	0.3657
OGT	O-linked N-acetylglucosamine (GlcNAc) transferase	-2.09	0.01695	-1.49	0.15551
ITPRIP	inositol 1,4,5-trisphosphate receptor interacting protein	-2.09	0.00459	-1.07	0.73413
ZSCAN12P1	zinc finger and SCAN domain containing 12 pseudogene 1	-2.09	0.01342	1.03	0.9222
ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2	-2.08	0.01164	1.05	0.82975
TBCE	tubulin folding cofactor E	-2.08	9.00E-04	-1.55	0.01994
WWC2	WW and C2 domain containing 2	-2.08	0.02987	-1.91	0.04991
NCEH1	neutral cholesterol ester hydrolase 1	-2.08	0.00352	-1.83	0.01074
MCOLN2	mucolipin 2	-2.08	0.00296	-1.07	0.72433
NR4A1	nuclear receptor subfamily 4, group A, member 1	-2.08	7.00E-05	1.06	0.63157
APOC1	apolipoprotein C-I	-2.08	0.0031	-1.11	0.58266
MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	-2.08	0.00045	-1.34	0.07265
RECQL4	RecQ protein-like 4	-2.08	0.04024	1.01	0.98139
AUNIP	aurora kinase A and ninein interacting protein	-2.08	0.02833	-1.19	0.55395
GLT8D1	Glycosyltransferase 8 domain containing 1	-2.08	0.03698	-1.03	0.93728
LOC100289092	uncharacterized LOC100289092	-2.08	0.02825	1.1	0.75448

STRN	striatin, calmodulin binding protein	-2.08	0.00099	-1.47	0.03665
G3BP2	GTPase activating protein (SH3 domain) binding protein 2	-2.08	0.02488	-1.26	0.42408
ERGIC2	ERGIC and golgi 2	-2.08	0.01276	-1.91	0.02396
OSBPL6	oxysterol binding protein-like 6	-2.08	0.00057	1.09	0.57641
ETFA	electron-transfer-flavoprotein, alpha polypeptide	-2.08	0.00011	-1.95	0.00023
BF515158	---	-2.08	0.00054	-1.3	0.10931
EIF1AX	eukaryotic translation initiation factor 1A, X-linked	-2.08	0.03204	1.05	0.85947
CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	-2.08	0.0052	1.1	0.66153
BICC1	bicaudal C homolog 1 (Drosophila)	-2.08	0.02366	1.12	0.68087
LINC00669	long intergenic non-protein coding RNA 669	-2.08	0.00229	-1.04	0.81659
TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	-2.07	0.00388	-1.04	0.83987
NFE2L3	nuclear factor (erythroid-derived 2)-like 3	-2.07	0.00518	1.05	0.83404
GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	-2.07	1.00E-04	-1.01	0.91354
TRIM14	tripartite motif containing 14	-2.07	0.0415	1.26	0.47306
SDC2	syndecan 2	-2.07	0.00019	1.09	0.51334
WDR67	WD repeat domain 67	-2.07	0.00094	-1.03	0.84153
PPIH	peptidylprolyl isomerase H (cyclophilin H)	-2.07	0.02623	-1.04	0.88104
CHN1	chimerin (chimaerin) 1	-2.07	0.00667	1.26	0.3083
SLC25A45	solute carrier family 25, member 45	-2.07	0.01745	1.71	0.06179
ERP29	endoplasmic reticulum protein 29	-2.07	6.00E-05	-1.87	0.00021
SRPX2	sushi-repeat containing protein, X-linked 2	-2.07	0.00409	-1.65	0.0292
FEM1B	fem-1 homolog b (C. elegans)	-2.07	0.02164	-1.32	0.32656
EML4	echinoderm microtubule associated protein like 4	-2.07	0.0045	-1.19	0.41811
RASSF8	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	-2.07	0.02099	-1.06	0.83329
EPHA2	EPH receptor A2	-2.07	0.00177	1.06	0.72688
ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	-2.07	0.00797	-1.69	0.03836
SF3B3	splicing factor 3b, subunit 3, 130kDa	-2.06	0.02853	-1.1	0.73432
ZNF263	zinc finger protein 263	-2.06	0.04543	-1.47	0.25046
TBC1D16	TBC1 domain family, member 16	-2.06	0.00465	-1.9	0.00963
ZBTB9	zinc finger and BTB domain containing 9	-2.06	0.03688	-1.2	0.56096
MCM3	minichromosome maintenance complex component 3	-2.06	0.0169	1.06	0.81579
AA088388	---	-2.06	0.01107	1.11	0.66161
ZNF385C	zinc finger protein 385C	-2.06	0.02141	-1.1	0.73741
PEX10	peroxisomal biogenesis factor 10	-2.06	0.03359	-1.33	0.35871
DIAPH3	diaphanous homolog 3 (Drosophila)	-2.06	0.02926	-1.02	0.93635
DHX8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	-2.06	0.01829	-1.74	0.05665
SH3BP5	SH3-domain binding protein 5 (BTK-associated)	-2.06	0.00039	-1.04	0.78127
ELMO1	engulfment and cell motility 1	-2.06	0.00336	-1.05	0.81557
ARTN	artemin	-2.06	0.00453	-1.27	0.25824
FAM198B	family with sequence similarity 198, member B	-2.06	0.00012	1.12	0.37748
RPE	ribulose-5-phosphate-3-epimerase	-2.06	0.00109	-1.33	0.11126
CPD	carboxypeptidase D	-2.06	0.00087	-1.11	0.51506
SMYD5	SMYD family member 5	-2.06	0.04089	-1.9	0.06403
ARL5A	ADP-ribosylation factor-like 5A	-2.06	0.0119	-1.3	0.29514
EIF1	eukaryotic translation initiation factor 1	-2.06	0.00275	-1.14	0.50123
ZEB1-AS1	ZEB1 antisense RNA 1 (non-protein coding)	-2.06	0.04228	-1.2	0.56652

TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	-2.06	0.02594	1.26	0.42857
THNSL2	threonine synthase-like 2 (S. cerevisiae)	-2.06	0.00108	-1.04	0.7973
ACLY	ATP citrate lyase	-2.05	0.00024	-1.02	0.90364
LOC389641	uncharacterized LOC389641	-2.05	0.01517	1.05	0.84144
HSF2BP	heat shock transcription factor 2 binding protein	-2.05	0.01388	-1.04	0.88789
CENPN	centromere protein N	-2.05	0.00782	-1.14	0.57236
ITPRIPL2	inositol 1,4,5-trisphosphate receptor interacting protein-like 2	-2.05	0.0014	1.07	0.68963
AA026390	---	-2.05	0.00039	-1.06	0.70233
NCBP2	nuclear cap binding protein subunit 2, 20kDa	-2.05	0.02411	-1.43	0.21531
SNRPB	small nuclear ribonucleoprotein polypeptides B and B1	-2.05	0.0381	-1.33	0.36939
DSN1	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	-2.05	0.02104	-1.05	0.87008
SSFA2	sperm specific antigen 2	-2.05	0.03658	-1.42	0.27024
FAM3C	family with sequence similarity 3, member C	-2.05	0.01	-1.25	0.34797
AA213799	---	-2.05	0.01688	1.01	0.95778
GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	-2.05	0.00053	-1.19	0.26906
BBIP1	BBSome interacting protein 1	-2.05	0.04477	-1.02	0.96111
EGR3	early growth response 3	-2.05	0.00916	-1.01	0.95385
WHSC1	Wolf-Hirschhorn syndrome candidate 1	-2.05	0.04454	-1.13	0.69595
ZDHHC23	zinc finger, DHHC-type containing 23	-2.05	0.00567	1.07	0.7429
PSD3	pleckstrin and Sec7 domain containing 3	-2.05	0.0173	1.15	0.59378
CDRT1	CMT1A duplicated region transcript 1	-2.04	0.00933	1.01	0.97279
RHOA	ras homolog family member A	-2.04	0.03555	-1.25	0.46985
LINC00184	long intergenic non-protein coding RNA 184	-2.04	0.04128	-1.23	0.52202
ASIC1	acid-sensing (proton-gated) ion channel 1	-2.04	0.00991	1.19	0.46583
DDX11L2	DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11 like 2	-2.04	0.04299	-1.13	0.7063
EML6	echinoderm microtubule associated protein like 6	-2.04	0.01769	1.49	0.14757
F3	coagulation factor III (thromboplastin, tissue factor)	-2.04	0.00206	1.09	0.62391
SP110	SP110 nuclear body protein	-2.04	0.03737	1.04	0.89555
CLPB	ClpB caseinolytic peptidase B homolog (E. coli)	-2.04	0.02817	-1.22	0.49816
COMMD10	COMM domain containing 10	-2.04	0.00911	-1.59	0.06484
FAM49A	family with sequence similarity 49, member A	-2.04	0.00519	-1.05	0.82492
PARP1	poly (ADP-ribose) polymerase 1	-2.04	0.00028	-1.27	0.09999
SERINC2	serine incorporator 2	-2.04	0.0145	1.1	0.71506
MTBP	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) binding protein, 104kDa	-2.04	0.00798	-1.23	0.35576
AA601997	---	-2.04	0.02956	1.06	0.85235
SRP72	signal recognition particle 72kDa	-2.04	0.00062	-1.48	0.02407
AF070618	---	-2.04	0.04162	-1.57	0.17052
HIST1H4F	histone cluster 1, H4f	-2.03	0.00567	-1.49	0.0779
GFI1	growth factor independent 1 transcription repressor	-2.03	0.00676	1.84	0.01521
KLF4	Kruppel-like factor 4 (gut)	-2.03	0.03448	1.36	0.3129
GPR125	G protein-coupled receptor 125	-2.03	0.03642	1.3	0.39706
SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	-2.03	0.0199	-1.47	0.16585
HAUS8	HAUS augmin-like complex, subunit 8	-2.03	0.03245	-1.03	0.9241

KIAA1958	KIAA1958	-2.03	0.02018	-1.18	0.53279
TPM3	tropomyosin 3	-2.03	0.02308	-1.1	0.73508
GALC	galactosylceramidase	-2.03	0.00849	-1.09	0.7058
STIL	SCL/TAL1 interrupting locus	-2.03	0.01191	-1.04	0.86449
HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	-2.03	0.01363	1.09	0.73021
ELP5	elongator acetyltransferase complex subunit 5	-2.03	0.01955	-1.35	0.26387
SYS1	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	-2.03	0.00314	-1.33	0.15102
URI1	URI1, prefoldin-like chaperone	-2.03	0.01291	-1.57	0.0854
NOL7	nucleolar protein 7, 27kDa	-2.03	0.03974	-1.63	0.13478
ITGA1	integrin, alpha 1	-2.03	0.01548	1.08	0.75614
WDR25	WD repeat domain 25	-2.03	0.04827	1.04	0.89944
AI382026	---	-2.03	0.00126	-1.01	0.93655
STAMBP	STAM binding protein	-2.03	0.04001	-1.59	0.15265
MFAP5 *	microfibrillar associated protein 5	-2.03	0.01464	2.41	0.00118
C19orf24	chromosome 19 open reading frame 24	-2.03	0.0084	-1.86	0.01687
MPP1	membrane protein, palmitoylated 1, 55kDa	-2.02	0.00204	1.05	0.77192
PCSK6	proprotein convertase subtilisin/kexin type 6	-2.02	0.02436	-1.55	0.1328
PPAN	peter pan homolog (Drosophila)	-2.02	0.03712	-1.17	0.60591
IL21R	interleukin 21 receptor	-2.02	0.00279	-1.02	0.92278
C20orf112	chromosome 20 open reading frame 112	-2.02	0.04396	-1.41	0.28462
EMC1	ER membrane protein complex subunit 1	-2.02	0.00019	-1.65	0.00226
ERLIN2	ER lipid raft associated 2	-2.02	0.02035	-1.66	0.07512
UCA1	urothelial cancer associated 1 (non-protein coding)	-2.02	0.00278	1.68	0.01566
FAM167A	family with sequence similarity 167, member A	-2.02	0.0128	1.7	0.04469
MBTPS2	membrane-bound transcription factor peptidase, site 2	-2.02	0.00384	-1.47	0.06765
TLN2	talin 2	-2.01	0.04812	-1.12	0.72476
DLGAP1-AS1	DLGAP1 antisense RNA 1	-2.01	0.00014	-1.3	0.05454
CDC25A	cell division cycle 25 homolog A (S. pombe)	-2.01	0.03937	1.97	0.04454
G2E3	G2/M-phase specific E3 ubiquitin protein ligase	-2.01	0.02372	-1.74	0.06243
B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	-2.01	0.00479	1.07	0.75068
ITGB5	integrin, beta 5	-2.01	0.03345	1.54	0.15914
DERL1	derlin 1	-2.01	0.00076	-1.63	0.00775
FAM100B	family with sequence similarity 100, member B	-2.01	0.00195	-1.3	0.15831
LZIC	leucine zipper and CTNNBIP1 domain containing	-2.01	0.00122	-1.27	0.16251
PAQR8	progestin and adipoQ receptor family member VIII	-2.01	0.03285	1.23	0.48066
NPM3	nucleophosmin/nucleoplasmin 3	-2.01	0.00211	-1.1	0.59068
MAOA	monoamine oxidase A	-2.01	0.01365	1.01	0.95531
GPATCH2L	G patch domain containing 2-like	-2.01	0.01497	-1.18	0.50247
BE742377	---	-2.01	0.00467	-1.5	0.06284
TBC1D9B	TBC1 domain family, member 9B (with GRAM domain)	-2.01	0.01225	-1.66	0.05114
CCDC68	coiled-coil domain containing 68	-2.01	0.00297	-1.02	0.92354
ASPHD2	aspartate beta-hydroxylase domain containing 2	-2.01	0.00241	1.1	0.58007
BC016787	---	-2.01	0.00466	-1.76	0.01475
NEDD9	neural precursor cell expressed, developmentally down-regulated 9	-2.01	0.02511	-1.09	0.74749
CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	-2.01	0.03377	1.32	0.35605

PLCL2	phospholipase C-like 2	-2.01	0.00163	-1.21	0.27202
SNAI1	snail homolog 1 (Drosophila)	-2.01	0.00233	-1.24	0.24799
TMEM64	transmembrane protein 64	-2.01	0.01925	-1.5	0.13482
PPP2R2C	protein phosphatase 2, regulatory subunit B, gamma	-2.01	0.00452	1.81	0.01133
GLA	galactosidase, alpha	-2.00	0.007	-1.17	0.4602
BIN1	bridging integrator 1	-2.00	0.04147	-1.5	0.20228
AI679555	---	-2.00	5.00E-04	1.01	0.93089
RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	-2.00	0.00888	-1.61	0.05157
MSH5	mutS homolog 5 (E. coli)	-2.00	0.01466	-1.31	0.28384
BF003032	---	-2.00	0.00325	1.19	0.36197
LPCAT4	lysophosphatidylcholine acyltransferase 4	-2.00	0.00768	1.3	0.24687
TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	-2.00	0.0172	1.07	0.79329
UST	uronyl-2-sulfotransferase	-2.00	0.01024	1.14	0.55528
PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	-2.00	0.03961	-1.66	0.11467
FGF13-AS1	FGF13 antisense RNA 1	2.00	0.01298	1.1	0.68338
N4BP2L1	NEDD4 binding protein 2-like 1	2.00	0.00501	1.29	0.22239
SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	2.00	0.01735	1.75	0.04514
ABLIM2	actin binding LIM protein family, member 2	2.00	0.00122	-1.22	0.24204
AI003508	---	2.00	0.02093	-1.02	0.93765
ANKRD65	ankyrin repeat domain 65	2.00	0.00034	1.08	0.5582
VPS13D	Vacuolar protein sorting 13 homolog D (S. cerevisiae)	2.00	0.00037	1.03	0.83058
AU144961	---	2.00	0.00069	1.21	0.21481
C10orf116	chromosome 10 open reading frame 116	2.01	0.00478	-1.01	0.95032
MKRN1	makorin ring finger protein 1	2.01	0.00893	1.36	0.19071
AA195276	---	2.01	0.0154	-1.02	0.92461
AI832594	---	2.01	0.02789	1.29	0.36881
CCDC102B	coiled-coil domain containing 102B	2.01	0.01925	-1.04	0.89214
ACP5	acid phosphatase 5, tartrate resistant	2.01	0.02793	-1.1	0.74457
AU147291	---	2.01	0.03791	-1.09	0.77455
WDR77	WD repeat domain 77	2.01	0.00308	1.11	0.57488
HIST1H2AG	histone cluster 1, H2ag	2.01	0.00181	1.88	0.00359
AI761498	---	2.01	0.00618	1.09	0.69168
LOC158960	uncharacterized protein BC009467	2.02	0.00023	-1.04	0.76944
PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	2.02	0.04169	1.08	0.81566
NUDT14	nudix (nucleoside diphosphate linked moiety X)-type motif 14	2.02	0.00882	-1.27	0.29956
AK096998	---	2.03	0.00068	-1.01	0.95586
PCDHB9	protocadherin beta 9	2.03	0.00476	1.28	0.23385
CD24	CD24 molecule	2.03	0.00102	1.04	0.82659
ABHD12	abhydrolase domain containing 12	2.03	0.00054	-1.38	0.04816
FAM168A	family with sequence similarity 168, member A	2.03	0.00078	1.5	0.02156
CREG2	cellular repressor of E1A-stimulated genes 2	2.03	0.02738	1.17	0.57582
LOC100996455	uncharacterized LOC100996455	2.03	0.01343	-1.03	0.91661
COBLL1	COBL-like 1	2.03	0.00461	1.21	0.3618
AL138240	---	2.03	0.00219	-1.2	0.31961
HOXA10	homeobox A10	2.04	0.00012	1.38	0.02153

FKBP3	FK506 binding protein 3, 25kDa	2.04	0.00427	1.35	0.15381
AK000792	---	2.04	0.03573	1.25	0.46118
AI733194	---	2.04	0.00067	-1.14	0.39928
GPR39	G protein-coupled receptor 39	2.04	0.01846	-1.1	0.71956
LOC283788	FSHD region gene 1 pseudogene	2.04	0.00034	-1.24	0.14181
NAIP	NLR family, apoptosis inhibitory protein	2.04	0.00169	1.14	0.46342
ALS2CR8	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 8	2.04	0.00411	1.23	0.31791
C1orf101	chromosome 1 open reading frame 101	2.04	0.00143	1.14	0.46068
ADAM17	ADAM metallopeptidase domain 17	2.05	0.00086	1.05	0.74106
MIR4448	microRNA 4448	2.05	0.00859	1.13	0.58873
LOC254057	uncharacterized LOC254057	2.05	0.00033	-1.03	0.80994
ASMTL-AS1	ASMTL antisense RNA 1 (non-protein coding)	2.05	0.00094	1.13	0.46551
SIAE	sialic acid acetylesterase	2.05	0.01643	1.75	0.04921
FBXL14	F-box and leucine-rich repeat protein 14	2.05	0.00563	1.33	0.19441
C16orf53	Chromosome 16 open reading frame 53	2.06	0.01534	-1.16	0.55377
LOC550643	uncharacterized LOC550643	2.06	2.00E-04	1.11	0.44152
ACOX1	acyl-CoA oxidase 1, palmitoyl	2.06	0.00013	1.33	0.04352
BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1	2.06	0.00118	1.05	0.77688
LOC283713	uncharacterized LOC283713	2.06	0.01445	-1.01	0.98122
AL137616	---	2.06	0.01173	1.03	0.8916
GGTLC2	gamma-glutamyltransferase light chain 2	2.07	0.00272	-1.02	0.9107
STAP2	signal transducing adaptor family member 2	2.07	0.0029	1.05	0.79627
HEG1	HEG homolog 1 (zebrafish)	2.07	0.00062	1.76	0.00362
AK026824	---	2.07	0.00021	-1.1	0.47321
GSN	gelsolin	2.07	0.03916	1.4	0.30593
C1orf85	chromosome 1 open reading frame 85	2.08	0.01274	-1.62	0.07457
PCDHB13	protocadherin beta 13	2.08	0.01211	1.05	0.83425
AK025218	---	2.08	0.003	1.34	0.15435
BF511336	---	2.08	0.00188	1.01	0.96832
PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	2.08	0.00444	1.23	0.32848
TNS3	tensin 3	2.08	0.00144	-1.5	0.03891
LAGE3	L antigen family, member 3	2.08	0.00098	1.42	0.05291
PHYH	phytanoyl-CoA 2-hydroxylase	2.09	0.00094	1.6	0.0146
TRIM29	tripartite motif containing 29	2.09	0.00459	1.38	0.14362
PPP1R3F	Protein phosphatase 1, regulatory subunit 3F	2.09	0.03058	-1.09	0.77736
RASA4	RAS p21 protein activator 4	2.09	0.00965	1.95	0.0161
COL5A1	collagen, type V, alpha 1	2.09	0.00254	1.17	0.42331
RNFT1	ring finger protein, transmembrane 1	2.09	0.01525	1.2	0.48369
LOC92249	uncharacterized LOC92249	2.09	0.0414	1.27	0.46341
BU929456	---	2.10	0.02389	1.49	0.18274
LRRC70	leucine rich repeat containing 70	2.10	0.00524	-1.26	0.29618
ESYT1	Extended synaptotagmin-like protein 1	2.10	0.00228	1	0.98191
TYMP	thymidine phosphorylase	2.10	0.00195	1.23	0.2731
POU3F1	POU class 3 homeobox 1	2.10	0.03782	-1.21	0.55021
ZNF264	zinc finger protein 264	2.11	0.00722	1.04	0.86
SNRNP27	small nuclear ribonucleoprotein 27kDa (U4/U6.U5)	2.11	0.00042	1.63	0.00705
HEATR7A	HEAT repeat containing 7A	2.11	0.00545	1.22	0.37226
TRPM7	transient receptor potential cation channel, subfamily M, member 7	2.12	0.01021	1.21	0.44209
FCHSD2	FCH and double SH3 domains 2	2.12	0.00012	1.82	0.00073

PARD3B	par-3 partitioning defective 3 homolog B (C. elegans)	2.13	0.00148	1.36	0.10947
KLHL24	kelch-like 24 (Drosophila)	2.13	0.00038	1	0.98012
MORC2-AS1	MORC2 antisense RNA 1 (non-protein coding)	2.13	6.00E-05	-1.12	0.37322
LOC90246	uncharacterized LOC90246	2.13	0.00525	1.08	0.73091
SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	2.13	0.03689	1.16	0.65377
BG232090	---	2.13	0.01274	1.02	0.92906
KRI1	KRI1 homolog (S. cerevisiae)	2.14	0.00339	1.14	0.53505
ECHDC2	enoyl CoA hydratase domain containing 2	2.14	0.00084	1.31	0.13304
PATL2	protein associated with topoisomerase II homolog 2 (yeast)	2.14	0.00148	1.5	0.04419
TPM1	tropomyosin 1 (alpha)	2.14	0.00161	-1.03	0.87218
AU157675	---	2.14	0.00064	-1.06	0.71295
BF724733	---	2.14	0.00131	-1.06	0.74114
C1QTNF3	C1q and tumor necrosis factor related protein 3	2.14	0.04033	1.38	0.34722
CXCR7	Chemokine (C-X-C motif) receptor 7	2.14	0.0034	1.05	0.80132
TSHZ1	teashirt zinc finger homeobox 1	2.15	0.00687	1.02	0.94378
AI223854	---	2.15	0.00628	1.08	0.73394
FLJ13197	uncharacterized FLJ13197	2.15	0.04223	1.19	0.60376
PCDHB5	protocadherin beta 5	2.15	0.02824	1	0.98756
WWOX	WW domain containing oxidoreductase	2.15	0.00046	1.54	0.01682
C17orf108	chromosome 17 open reading frame 108	2.15	0.00208	1.03	0.86556
PARM1	prostate androgen-regulated mucin-like protein 1	2.16	0.00136	1	0.97831
ZBTB20	zinc finger and BTB domain containing 20	2.16	0.00686	1.15	0.56129
PLCD3	phospholipase C, delta 3	2.16	0.00288	1.05	0.79755
UNC13D	unc-13 homolog D (C. elegans)	2.16	8.00E-05	1.35	0.03391
ATG4D	autophagy related 4D, cysteine peptidase	2.16	0.00176	1.07	0.71567
NBPF1	neuroblastoma breakpoint family, member 1	2.17	0.02157	1.27	0.42214
GATA3	GATA binding protein 3	2.17	0.00095	-1.41	0.07244
RASSF6	Ras association (RalGDS/AF-6) domain family member 6	2.17	0.02682	-1.36	0.33041
AA262084	---	2.17	0.03946	-1.08	0.81551
LOC728978	uncharacterized LOC728978	2.18	0.02444	-1.15	0.64854
ZMYM6	zinc finger, MYM-type 6	2.18	0.00019	1.15	0.32879
BDH2	3-hydroxybutyrate dehydrogenase, type 2	2.18	1.00E-05	1.2	0.09172
TTC18	tetratricopeptide repeat domain 18	2.18	0.00182	1.28	0.21352
AI298089	---	2.18	0.0468	1.08	0.83562
HSPB1	heat shock 27kDa protein 1	2.18	0.02484	1.04	0.88568
NKIRAS2	NFKB inhibitor interacting Ras-like 2	2.19	0.00053	1.39	0.06596
LRRC37A4P	leucine rich repeat containing 37, member A4, pseu	2.19	0.00033	1.17	0.31018
AU144676	---	2.19	0.02347	1.3	0.3977
AL049975	---	2.19	0.0336	1.14	0.68317
FLJ40852	uncharacterized LOC285962	2.19	0.00078	1.13	0.47245
SORCS2	sortilin-related VPS10 domain containing receptor 2	2.19	0.00024	1.45	0.02582
TNNT2	troponin T type 2 (cardiac)	2.19	0.02191	-1.18	0.5735
LIMK2	LIM domain kinase 2	2.19	0.00035	1.46	0.03027
PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	2.19	0.01695	1.23	0.47672
AK025797	---	2.19	0.00536	1.23	0.38601
RIT1	Ras-like without CAAX 1	2.19	0.00065	1.98	0.00174
BF830560	---	2.19	0.001	-1.22	0.28443

USP15	ubiquitin specific peptidase 15	2.20	0.00027	1.43	0.03219
FOXP4	forkhead box P4	2.20	0.00347	-1.03	0.90793
TNNI2	troponin I type 2 (skeletal, fast)	2.20	0.00176	1.02	0.93594
CCDC171	coiled-coil domain containing 171	2.21	0.04585	1.44	0.32171
TMEM19	transmembrane protein 19	2.21	0.00031	1.04	0.79873
CYFIP2	cytoplasmic FMR1 interacting protein 2	2.21	0.00134	-1.35	0.12695
AA826176	---	2.21	0.01913	1.27	0.42891
C14orf164	chromosome 14 open reading frame 164	2.21	0.00123	1.14	0.47351
NTF4	neurotrophin 4	2.21	0.0318	1.09	0.7921
W60691	---	2.21	0.00071	1.3	0.15038
MSX2	msh homeobox 2	2.22	0.02264	1.15	0.64938
SLC31A2	solute carrier family 31 (copper transporters), member 2	2.22	0.0313	1.46	0.26686
BC038589	---	2.23	0.01091	1.07	0.78592
AW518747	---	2.23	3.00E-05	-1.25	0.07916
SCARF1	scavenger receptor class F, member 1	2.23	0.0238	-1.08	0.8043
EHD2	EH-domain containing 2	2.24	0.00413	1.29	0.27936
ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5	2.24	2.00E-05	1.21	0.11617
SPECC1	sperm antigen with calponin homology and coiled-coil domains 1	2.24	0.03375	1.27	0.4909
TPTE2P5	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2 pseudogene 5	2.24	0.02917	-1.01	0.98163
AGAP11	ankyrin repeat and GTPase domain Arf GTPase activating protein 11	2.24	0.0014	1.08	0.67841
KANK1	KN motif and ankyrin repeat domains 1	2.24	0.01039	1.07	0.78857
GTF2IRD2	GTF2I repeat domain containing 2	2.25	0.04855	1.07	0.85271
JAG2	jagged 2	2.25	0.00069	1.2	0.30957
CLCN4	chloride channel, voltage-sensitive 4	2.25	0.00045	-1.06	0.7175
RPL10	ribosomal protein L10	2.25	0.00086	1.23	0.26847
BF055351	---	2.25	0.00457	1.12	0.61965
TOLLIP	toll interacting protein	2.26	0.00363	1.25	0.32907
MTCH2	mitochondrial carrier 2	2.26	3.00E-05	1.23	0.10178
CAB39L	calcium binding protein 39-like	2.26	0.02214	1	0.98838
NUDT19	nudix (nucleoside diphosphate linked moiety X)-type motif 19	2.26	8.00E-05	1.8	0.00103
R37728	---	2.26	0.03292	1.08	0.83026
PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (beta)	2.26	0.00135	1.01	0.94671
ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	2.27	0.00677	1.5	0.12531
AMT	aminomethyltransferase	2.27	7.00E-05	1.03	0.82082
PPIEL	peptidylprolyl isomerase E-like pseudogene	2.28	0.01001	1.02	0.93498
C5orf46	chromosome 5 open reading frame 46	2.28	0.00056	-1.15	0.42013
MARVELD1	MARVEL domain containing 1	2.29	0.00019	1.24	0.17822
DQX1	DEAQ box RNA-dependent ATPase 1	2.29	0.0023	1.48	0.08801
TJP3	tight junction protein 3 (zona occludens 3)	2.29	6.00E-05	-1.06	0.66876
COL18A1	collagen, type XVIII, alpha 1	2.29	0.01342	1.23	0.46997
DECR1	2,4-dienoyl CoA reductase 1, mitochondrial	2.30	8.00E-05	1.21	0.17307
ABCC10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	2.30	0.00895	1.39	0.23724
MACROD2	MACRO domain containing 2	2.30	0.01558	1.19	0.56634
NODAL	nodal homolog (mouse)	2.30	0.00052	-1.07	0.70918
AW576443	---	2.30	0.00097	1.36	0.12558

AI990613	---	2.31	0.033	1.04	0.91665
IFITM10	interferon induced transmembrane protein 10	2.31	0.02374	-1.43	0.28573
NRF1	nuclear respiratory factor 1	2.31	9.00E-05	1.01	0.96325
PER3	period homolog 3 (Drosophila)	2.31	0.00025	1.18	0.31749
KRTAP19-1	keratin associated protein 19-1	2.32	0.00791	1.16	0.56431
TP53INP1	tumor protein p53 inducible nuclear protein 1	2.32	0.00257	1.44	0.11363
TMCC1	transmembrane and coiled-coil domain family 1	2.32	2.00E-04	1.56	0.01398
AK021983	---	2.32	0.00403	1.12	0.62022
AI797043	---	2.32	0.00903	1.43	0.20276
LRTOMT	leucine rich transmembrane and 0-methyltransferase domain containing	2.33	0.00486	1.02	0.93902
AU146764	---	2.33	0.00319	-1.07	0.75727
ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	2.34	0.00046	-1.02	0.89421
KRTAP19-3	keratin associated protein 19-3	2.34	0.03429	1.01	0.96693
TAGLN	transgelin	2.34	0.03019	-1.39	0.34995
ALS2CL	ALS2 C-terminal like	2.34	0.00318	1.31	0.25332
ZNF652	zinc finger protein 652	2.35	0.01964	-1	0.99832
DUSP5P	dual specificity phosphatase 5 pseudogene	2.35	0.00587	1.29	0.32585
SYT8	synaptotagmin VIII	2.35	0.00062	1.03	0.88476
AI369187	---	2.35	0.01507	1.32	0.3678
AW419344	---	2.35	0.00697	-1.1	0.72472
TPTE2P6	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2 pseudogene 6	2.35	0.00653	1.11	0.69569
MKNK2	MAP kinase interacting serine/threonine kinase 2	2.37	0.0013	1.64	0.03092
TRIM73	tripartite motif containing 73	2.37	0.00371	-1.17	0.51377
HYI	hydroxypyruvate isomerase (putative)	2.37	3.00E-05	1.24	0.10149
BF507518	---	2.37	0.00321	1.33	0.24153
TAPBP	TAP binding protein (tapasin)	2.37	0.00028	1.33	0.10536
R76828	---	2.37	0.0014	1.31	0.20241
KCNIP3	Kv channel interacting protein 3, calsenilin	2.37	0.00315	1.13	0.59461
AU146493	---	2.38	0.00349	1.3	0.28289
R62588	---	2.38	0.03948	-1.41	0.37184
SLC7A8	solute carrier family 7 (amino acid transporter light chain, L system), member 8	2.38	0.00423	1.22	0.41428
BC014318	---	2.39	0.00048	1.25	0.2264
MAP3K12	mitogen-activated protein kinase kinase kinase 12	2.40	0.00276	1.34	0.21773
ARNT	aryl hydrocarbon receptor nuclear translocator	2.40	0.03055	1.19	0.62804
N25555	---	2.40	0.01166	1.74	0.08128
LOC158696	uncharacterized LOC158696	2.40	0.01369	1.12	0.71499
ADHFE1	alcohol dehydrogenase, iron containing, 1	2.41	0.00011	1.46	0.02704
TP53AIP1	tumor protein p53 regulated apoptosis inducing protein 1	2.42	0.0429	-1.17	0.68548
AI002328	---	2.42	0.00014	1.08	0.61826
QKI	QKI, KH domain containing, RNA binding	2.42	8.00E-05	-1.17	0.29872
TMLHE-AS1	TMLHE antisense RNA 1	2.42	0.00013	1.15	0.37539
PPM1L	protein phosphatase, Mg2+/Mn2+ dependent, 1L	2.42	5.00E-04	1.33	0.13923
DNASE1L1	deoxyribonuclease I-like 1	2.42	4.00E-05	1.17	0.24881
ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative)	2.42	4.00E-05	-1.04	0.7721
CHADL	chondroadherin-like	2.43	0.00027	1.12	0.52001
SEC31B	SEC31 homolog B (S. cerevisiae)	2.43	0.01562	1.09	0.785
C5orf56	chromosome 5 open reading frame 56	2.43	0.00029	1.47	0.04385
FBXO32	F-box protein 32	2.44	0.02761	1.18	0.63639
SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A	2.45	0.00035	1.64	0.01603

RNA45S5	RNA, 45S pre-ribosomal 5	2.45	0.0064	1.23	0.44628
AI097501	---	2.46	0.00085	-1.03	0.87228
AW976035	---	2.46	0.03597	1.02	0.95553
BMF	Bcl2 modifying factor	2.46	0.0078	1.08	0.78909
AW189097	---	2.46	0.03749	1.02	0.95771
ARMCX1	armadillo repeat containing, X-linked 1	2.47	0.00665	1.09	0.75567
CRYL1	crystallin, lambda 1	2.47	0.0071	1.64	0.09685
ADAMTS5 *	ADAM metallopeptidase with thrombospondin type 1 motif, 5	2.47	0.00743	-2.26	0.01801
PRICKLE1	prickle homolog 1 (Drosophila)	2.48	0.0021	1.34	0.21789
UHRF1BP1L	UHRF1 binding protein 1-like	2.48	3.00E-05	1.38	0.03248
LOC100129890	similar to hCG1750329	2.48	0.00643	1.05	0.85927
AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	2.49	0.00012	-1.09	0.58062
CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	2.49	0.00047	1.72	0.01311
ERC1	ELKS/RAB6-interacting/CAST family member 1	2.50	0.00103	-1.11	0.60298
ARHGAP24	Rho GTPase activating protein 24	2.50	0.001	-1.12	0.59272
TMEM178A	transmembrane protein 178A	2.52	0.02309	1.27	0.50566
MARCKS	myristoylated alanine-rich protein kinase C substrate	2.52	0.0027	1.07	0.78962
EPHA4	EPH receptor A4	2.53	0.02907	1.06	0.87192
MACC1	metastasis associated in colon cancer 1	2.53	0.0175	-1.03	0.93825
ZNF277	zinc finger protein 277	2.53	0.02947	1.24	0.56981
RCAN2	regulator of calcineurin 2	2.54	0.00063	1.04	0.82534
ARID5B	AT rich interactive domain 5B (MRF1-like)	2.54	0.01386	-1	0.9977
LOC284837	uncharacterized LOC284837	2.55	0.01852	1.06	0.86776
AK022004	---	2.55	0.00027	1.21	0.29197
HOXD9	homeobox D9	2.56	0.00068	-1.32	0.18692
SLCO6A1	solute carrier organic anion transporter family, member 6A1	2.56	0.00157	1.24	0.35535
HOXD10	homeobox D10	2.56	6.00E-05	1.69	0.00434
GRAMD2	GRAM domain containing 2	2.56	1.00E-05	1.23	0.08914
BMP7	bone morphogenetic protein 7	2.57	0.00327	1.14	0.60026
EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	2.57	1.00E-05	1.04	0.74187
AI287817	---	2.57	0.01101	1.21	0.5544
LRRN4CL	LRRN4 C-terminal like	2.58	0.00483	1.18	0.54147
HSPB3	heat shock 27kDa protein 3	2.58	0.01175	1.09	0.78095
MYLK	myosin light chain kinase	2.58	0.00098	-1.13	0.57064
N35099	---	2.58	0.00375	1.18	0.5246
SNRPN	small nuclear ribonucleoprotein polypeptide N	2.59	0.00037	1.21	0.32605
LOC338651	uncharacterized LOC338651	2.60	0.02727	1.26	0.55128
AL110133	---	2.61	0.00103	-1.15	0.53153
ARHGAP22	Rho GTPase activating protein 22	2.61	0.00308	-1.05	0.84621
COX7B	cytochrome c oxidase subunit VIIb	2.61	3.00E-05	1.51	0.01156
ZNF503-AS1	ZNF503 antisense RNA 1 (non-protein coding)	2.62	0.00131	1.06	0.78335
AL833462	---	2.62	0.00017	1.39	0.07922
HSPB2	heat shock 27kDa protein 2	2.62	0.00016	-1.04	0.81823
IGHG3	immunoglobulin heavy constant gamma 3 (G3m ma	2.63	0.00409	-1.07	0.81139
SNHG7	small nucleolar RNA host gene 7 (non-protein coding)	2.64	0.00013	-1.3	0.13732
PRODH	proline dehydrogenase (oxidase) 1	2.66	0.01094	1.65	0.14232
APCDD1	adenomatosis polyposis coli down-regulated 1	2.67	0.00134	1.06	0.80664
PLA2R1 *	phospholipase A2 receptor 1, 180kDa	2.68	0.00043	-2.03	0.00428

BAG1	BCL2-associated athanogene	2.68	0.00699	-1.33	0.35244
ZMYM3	zinc finger, MYM-type 3	2.69	0.00149	1.38	0.19142
PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	2.70	2.00E-05	1.9	8.00E-04
LOC100859930	uncharacterized LOC100859930	2.70	0.00485	-1.09	0.76229
AI421234	---	2.71	0.00033	-1.08	0.69165
AI612775	---	2.72	0.00671	1.09	0.77381
CDHR1	cadherin-related family member 1	2.72	0.00197	-1.05	0.85695
HMCN1	hemicentin 1	2.72	0.00695	1.17	0.61087
NRBP2	nuclear receptor binding protein 2	2.73	4.00E-05	1.7	0.00505
PLCD4	phospholipase C, delta 4	2.74	0.02692	1.02	0.95945
CXorf56	chromosome X open reading frame 56	2.74	0.00029	-1.24	0.2819
AI686664	---	2.75	1.00E-04	-1.37	0.08707
SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	2.76	0.0021	-1.06	0.83247
ANXA4	annexin A4	2.76	0.00047	1.71	0.02361
LOC100507117	uncharacterized LOC100507117	2.77	0.01431	-1.01	0.98515
OVGP1	oviductal glycoprotein 1, 120kDa	2.78	8.00E-05	-1.1	0.57301
DLX5	distal-less homeobox 5	2.78	0.00562	-1.15	0.64782
DGCR11	DiGeorge syndrome critical region gene 11 (non-protein coding)	2.79	3.00E-05	1.29	0.11696
NREP	neuronal regeneration related protein homolog (rat)	2.79	9.00E-05	1.55	0.02402
W96062	---	2.82	0.01089	1.69	0.14607
ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1	2.84	0.00023	1.5	0.05582
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	2.84	0.00295	1.31	0.34664
KAL1	Kallmann syndrome 1 sequence	2.86	0.00116	-1.21	0.44599
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	2.86	0.00103	1.06	0.81366
ATOH8	atonal homolog 8 (Drosophila)	2.87	0.00687	-1.38	0.32394
FLJ33630	uncharacterized LOC644873	2.87	0.00018	1.38	0.11262
U46120	---	2.87	0.00822	1.19	0.60449
NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	2.89	0.01287	1.3	0.47444
EGFL6	EGF-like-domain, multiple 6	2.90	0.02041	1.18	0.68475
MCCC2	methylcrotonoyl-CoA carboxylase 2 (beta)	2.91	0.00769	1.05	0.87969
KRT16	keratin 16	2.92	0.00046	1.39	0.15277
AA031832	---	2.96	0.00914	1.07	0.84765
B3GALT4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	2.98	0.00203	1.67	0.08386
ZNF703	zinc finger protein 703	2.99	0.00035	-1.37	0.16491
FRY	furry homolog (Drosophila)	3.00	0.00094	1.5	0.12302
ZMYND12	zinc finger, MYND-type containing 12	3.01	0.00254	1.9	0.04282
CKMT1A	creatine kinase, mitochondrial 1A	3.01	9.00E-05	1.37	0.10844
SOX6	SRY (sex determining region Y)-box 6	3.03	0.02047	1.12	0.78705
BF844863	---	3.04	6.00E-05	1.61	0.01858
LGR6	leucine-rich repeat containing G protein-coupled receptor 6	3.10	0.00011	1.3	0.18888
KIAA1456	KIAA1456	3.14	0.02984	1.71	0.26633
C1orf54	chromosome 1 open reading frame 54	3.15	0.00012	1.78	0.01332
KRT13	keratin 13	3.17	0.00511	1.35	0.38327
ZMAT1	zinc finger, matrin-type 1	3.19	0.00225	1.48	0.20645

VIPR1	vasoactive intestinal peptide receptor 1	3.29	0.00018	-1.1	0.65495
IQCH-AS1	IQCH antisense RNA 1 (non-protein coding)	3.34	0.00017	1.55	0.0642
BF435593	---	3.36	1.00E-04	-1.05	0.81941
WNT10A	Wingless-type MMTV integration site family, member 10A	3.38	0.00059	1.03	0.92006
AA001390	---	3.38	0.0182	1.21	0.67273
WNT4	wingless-type MMTV integration site family, member 4	3.39	0.00012	-1.12	0.57986
GPNMB	glycoprotein (transmembrane) nmb	3.47	0.01109	-1.55	0.30571
GPR133	G protein-coupled receptor 133	3.55	0.00646	1.21	0.62202
AL357212	---	3.57	0.00051	1.12	0.6731
SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal	3.59	1.00E-04	1.19	0.42387
DYNLRB1	dynein, light chain, roadblock-type 1	3.64	0	1.93	0.00083
GGT6	gamma-glutamyltransferase 6	3.68	4.00E-05	-1.07	0.72291
OLR1	oxidized low density lipoprotein (lectin-like) receptor 1	3.73	2.00E-05	1.22	0.2916
LOC100292680	uncharacterized LOC100292680	3.76	0.0032	-1.2	0.61063
PLEKHB1	pleckstrin homology domain containing, family B (evectins) member 1	3.77	0	-1.28	0.12964
LGR5	leucine-rich repeat containing G protein-coupled receptor 5	3.79	0.00017	-1.05	0.84761
TPCN2	two pore segment channel 2	3.81	3.00E-05	1.63	0.02946
HIST3H2A	histone cluster 3, H2a	3.82	1.00E-05	1.06	0.73512
HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10	3.84	0	1.69	0.00572
SLC47A2	solute carrier family 47, member 2	3.86	2.00E-05	1.74	0.01412
STX19	syntaxin 19	3.89	7.00E-05	1.07	0.76025
EDN2	endothelin 2	4.04	0.00168	1.3	0.44591
EDN1	endothelin 1	4.04	0.00056	1.32	0.35072
AK021431	---	4.18	0.00837	1.13	0.78478
AHNAK	AHNAK nucleoprotein	4.47	3.00E-04	1.73	0.07986
MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	4.50	3.00E-05	1.57	0.05957
UGT1A1	UDP glucuronosyltransferase 1 family, polypeptide A1 /// UDP glucuronosyltransferase 1 family, polypeptide A10 /// UDP glucuronosyltransferase 1 family, polypeptide A3 /// UDP glucuronosyltransferase 1 family, polypeptide A4 /// UDP glucuronosyltransferase 1 family, polypeptide A5 /// UDP glucuronosyltransferase 1 family, polypeptide A6 /// UDP glucuronosyltransferase 1 family, polypeptide A7 /// UDP glucuronosyltransferase 1 family, polypeptide A8 /// UDP glucuronosyltransferase 1 family, polypeptide A9	4.64	4.00E-05	1.35	0.21751
AK096324	---	5.05	0.00021	1.1	0.75854
MEGF6	multiple EGF-like-domains 6	5.18	0	1.17	0.26274
AHNAK2	AHNAK nucleoprotein 2	5.50	2.00E-04	1.66	0.1261
C18orf1	chromosome 18 open reading frame 1	5.86	0.00027	-1.04	0.90742
AXIN2	axin 2	5.87	4.00E-05	1.21	0.4851
RYR3	ryanodine receptor 3	5.91	3.00E-05	1.15	0.59195
KRT15	keratin 15	5.94	2.00E-05	1.44	0.15179
CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	5.96	0.00111	-1.53	0.3133

CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	6.35	4.00E-05	1.5	0.17043
WFDC5	WAP four-disulfide core domain 5	6.72	0.00018	-1.03	0.92517

Table S3. A list of common differentially expressed genes affected by CRTC1-MAML2- or CREB-depletion in human MEC H3118 cells. This gene list represents candidate genes regulated by fusion/CREB interaction. The "positive" and "negative" signs denote up-regulated or down-regulated genes in KD compared to control groups, respectively. The asterisk indicates the common gene in different regulatory direction between fusion and CREB.

Gene Symbol	Gene Title	Fusion Fold Change	Fusion p.value	CREB Fold Change	CREB p.value
LINC00473	chromosome 6 open reading frame 176	-37.12	0	-3.6	6.00E-05
DMBT1	deleted in malignant brain tumors 1	-35.73	0	-8.39	5.00E-05
STC1	stanniocalcin 1	-21.74	0	-26.98	2.00E-05
LOC100288985	Hypothetical protein LOC100288985	-17.73	0	-41.04	8.00E-05
NR4A3	nuclear receptor subfamily 4, group A, member 3	-16.29	1.00E-05	-6.19	3.00E-05
AW302848	---	-12.93	0.00013	-2.25	0.00219
OSBP2	oxysterol binding protein 2	-9.52	1.00E-05	-2.94	0.00121
SORBS2	sorbin and SH3 domain containing 2	-8.42	6.00E-04	-4.23	0.00779
LUM	lumican	-6.98	0.00061	-4.16	0.03358
HAL	histidine ammonia-lyase	-6.79	2.00E-05	-9.33	0
SMOC1	SPARC related modular calcium binding 1	-6.47	0	-2.92	0.00125
BC027448	---	-6.45	0.00045	-10.18	0
BC020911	---	-6.44	0.00377	-3.41	0.00068
NR4A1	nuclear receptor subfamily 4, group A, member 1	-6.14	4.00E-05	-2.08	7.00E-05
NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	-6	0.00019	-2.45	0.02913
AA523939	---	-6	1.00E-05	-2.17	0.00911
CREG2	cellular repressor of E1A-stimulated genes 2	-5.91	2.00E-05	2.03	0.02738
CHL1-AS2	CHL1 antisense RNA 2	-5.54	0.00083	-5.91	2.00E-05
LGSN	lengsin, lens protein with glutamine synthetase domain	-5.27	2.00E-05	-3.65	0.02779
MFSD2A	major facilitator superfamily domain containing 2A	-4.96	5.00E-05	-10.08	0
AI476341	---	-4.87	0.00659	-3.04	5.00E-05
DUSP1	dual specificity phosphatase 1	-4.81	0.00017	-2.15	0.03823
A2M	alpha-2-macroglobulin	-4.62	0.00102	-2.26	0.01347
AK022474	---	-4.51	0.01964	-3.25	0.00018
CHL1	Cell adhesion molecule with homology to L1CAM	-4.47	0.00163	-2.92	0.03528
ZNF331	zinc finger protein 331	-4.24	8.00E-05	-3.73	1.00E-05
IL20	interleukin 20	-4.23	0.00345	-4.53	0.0017
ENO3	enolase 3 (beta, muscle)	-4.14	0.00033	-3.19	8.00E-05
AI806183	---	-4.1	0.00016	-3.55	0.00021
EOMES	eomesodermin	-4.1	1.00E-05	-2.57	0.00381
SRGN	serglycin	-3.95	0.00518	-3.18	3.00E-04
DUSP4	dual specificity phosphatase 4	-3.93	0.00155	-5.23	0
NM_024853	---	-3.92	0.00013	-2.12	0.03494
PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	-3.89	0	-7.16	9.00E-05
AV702787	---	-3.81	0.00075	-2.31	0.00058
BG112263	---	-3.55	3.00E-05	-3.45	1.00E-04
CALCA	calcitonin-related polypeptide alpha	-3.49	0.00643	-2.85	0.0117
SLCO4A1	solute carrier organic anion transporter family, member 4A1	-3.46	0	-7.92	6.00E-05
CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	-3.38	0.00044	-10.27	0
NCALD	neurocalcin delta	-3.34	5.00E-05	-2.33	0.00014
LOC100506870	hypothetical LOC100506870	-3.24	0.00071	-10.04	0.00016
GRAMD1B	GRAM domain containing 1B	-3.24	0.00167	-4.47	5.00E-05

SLC2A14	solute carrier family 2 (facilitated glucose transporter), member 14	-3.2	0.00037	-2.13	0.00724
LOC283713	hypothetical protein LOC283713	-3.19	0.01709	2.06	0.01445
FAM83A	family with sequence similarity 83, member A	-3.18	0.00238	-3.38	0.00279
AA416756	---	-3.16	0.00578	-2.44	0.00676
SFRP1	secreted frizzled-related protein 1	-3.12	0.00018	-4.85	4.00E-05
F2RL2	coagulation factor II (thrombin) receptor-like 2	-3.11	0.00039	-5.63	0.00428
MGC39372	serpin peptidase inhibitor, clade B (ovalbumin), member 9 pseudogene	-3.09	0.00106	-2.3	0.0039
TPRG1	tumor protein p63 regulated 1	-3.06	3.00E-05	-4.22	0.00033
RASD1	RAS, dexamethasone-induced 1	-3.05	1.00E-04	-4.96	2.00E-05
STEAP4	STEAP family member 4	-3.03	0.00022	-4.27	0.00091
E2F2	E2F transcription factor 2	-3.03	0.0024	-2.51	0.04144
SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	-2.98	0.00472	-6.82	0
SYT12	synaptotagmin XII	-2.97	0.00015	-4.85	1.00E-05
SMOX	spermine oxidase	-2.95	0.01324	-21.45	0
ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit a4	-2.9	0.00544	-13.97	0
TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	-2.89	0.00018	-2.31	0.02723
XDH	xanthine dehydrogenase	-2.87	0.02018	-3	0.00331
BC037339	---	-2.86	0.00021	-2.27	0.01655
LOC338651	hypothetical LOC338651	-2.82	0.04575	2.6	0.02727
PTGES	prostaglandin E synthase	-2.81	0.0132	-2.33	0.00273
SEMA3B	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	-2.78	0.00031	-2.3	0.00081
XPR1	xenotropic and polytropic retrovirus receptor 1	-2.77	0.00322	-4.14	0.00657
CA9	carbonic anhydrase IX	-2.77	0.00402	-3.29	0.03444
RAET1E	retinoic acid early transcript 1E	-2.72	0.02536	-3.26	3.00E-05
SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	-2.7	0.01542	-2.73	0.00472
ULBP2	UL16 binding protein 2	-2.67	0.00021	-2.79	0.00095
SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-2.65	0.00144	-4.22	0.00034
KYNU	kynureninase (L-kynurenine hydrolase)	-2.63	0.00098	-6.23	0
BF590850	---	-2.6	4.00E-05	-3.5	0.00171
GPR133	G protein-coupled receptor 133	-2.52	0.00279	3.55	0.00646
ANO3	anoctamin 3	-2.5	0.00317	-5.59	0
PIGH	phosphatidylinositol glycan anchor biosynthesis, class H	-2.5	0.00017	-2.63	0.00153
NID2	nidogen 2 (osteonidogen)	-2.49	0.00011	-3.68	0.00591
TGFB2	transforming growth factor, beta 2	-2.48	0.00244	-4.76	0.00034
PSD3	pleckstrin and Sec7 domain containing 3	-2.47	0.03327	-2.05	0.0173
RASSF10	Ras association (RalGDS/AF-6) domain family (N-terminal) member 10	-2.45	0.00684	-2.16	0.01003
LOC100128653	hypothetical LOC100128653	-2.44	0.00019	-2.09	0.00161
SSH1	slingshot homolog 1 (Drosophila)	-2.42	0.00079	-3.47	0.00743
FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	-2.42	9.00E-05	-3.39	0.00021
KLF9	Kruppel-like factor 9	-2.4	0.00169	-6.3	0.00242
CENPV	centromere protein V	-2.4	0.00211	-3.39	0.00011
RNF157-AS1	RNF157 antisense RNA 1	-2.4	0.01288	-2.21	0.03193
AI761207	---	-2.39	0.00236	-3.14	0.00697
BMP8B	bone morphogenetic protein 8b	-2.38	0.00438	-2.79	7.00E-05
WDR76	WD repeat domain 76	-2.35	0.00499	-2.98	0.00247

BE271180	---	-2.34	0.00459	-2.72	0.01322
CASP9	caspase 9, apoptosis-related cysteine peptidase	-2.33	0.00016	-2.17	4.00E-05
C11orf86	chromosome 11 open reading frame 86	-2.31	0.00125	-4.34	0.00013
ZNF367	zinc finger protein 367	-2.31	0.00111	-2.37	0.03245
LOC728431	hypothetical LOC728431	-2.3	0.00174	-2.36	0.01613
SLC25A45	solute carrier family 25, member 45	-2.3	0.01443	-2.07	0.01745
PER1	period homolog 1 (Drosophila)	-2.28	0.00018	-2.37	0.02402
IL24	interleukin 24	-2.27	0.04771	-3.43	0.04046
AW611560	---	-2.26	0.00519	-2.13	0.00268
AI686793	---	-2.25	0.00066	-2.61	0.00132
AREG	amphiregulin	-2.23	0.04495	-18.34	0
EDNRB	endothelin receptor type B	-2.23	0.00037	-2.86	0.02402
GYG2	glycogenin 2	-2.23	0.00261	-2.6	0.00267
BF445387	---	-2.23	0.0027	-2.13	0.00411
KIAA1549	flavin containing monooxygenase 4	-2.22	0.00013	-3	0
STAMBPL1	STAM binding protein-like 1	-2.2	0.0049	-2.82	4.00E-05
MCM10	minichromosome maintenance complex component 10	-2.19	0.04848	-3.59	8.00E-05
ZBTB38	zinc finger and BTB domain containing 38	-2.19	0.04405	-2.28	0.00617
DNASE1L3	deoxyribonuclease I-like 3	-2.18	0.00419	-3.56	0.00101
ARID5B	AT rich interactive domain 5B (MRF1-like)	-2.18	0.00052	2.54	0.01386
PC	pyruvate carboxylase	-2.17	0.00064	-2.28	0.00514
FAM216A	family with sequence similarity 216, member A	-2.16	0.00016	-5.08	0.00011
PRKCH	protein kinase C, eta	-2.16	0.00061	-3.73	0.00024
BRI3BP	BRI3 binding protein	-2.15	0.0253	-2.67	0.00234
AI300077	---	-2.15	0.00412	-2.54	4.00E-05
LOC100506021	hypothetical LOC100506021	-2.15	0.01054	-2.25	0.00178
ITPR1	inositol 1,4,5-triphosphate receptor, type 1	-2.14	0.00162	-2.45	0.00145
DLGAP1-AS1	DLGAP1 antisense RNA 1	-2.14	0.04809	-2.01	0.00014
DST	dystonin	-2.11	0.03694	-2.13	0.01481
LOC158696	hypothetical LOC158696	-2.11	0.00213	2.4	0.01369
TYMS	thymidylate synthetase	-2.1	0.02143	-2.46	0.00819
MSX2	msh homeobox 2	-2.1	0.01319	2.22	0.02264
MCTP2	multiple C2 domains, transmembrane 2	-2.09	0.00189	-2.65	0.01823
FNDC3A	Fibronectin type III domain containing 3A	-2.09	0.04589	-2.55	0.01236
AW293012	---	-2.09	0.00093	-2.41	0.00121
AA088388	---	-2.08	0.04262	-2.06	0.01107
CYFIP2	cytoplasmic FMR1 interacting protein 2	-2.07	0.0021	2.21	0.00134
AL049245	---	-2.06	0.00369	-5.75	0
SSFA2	sperm specific antigen 2	-2.05	0.00073	-2.05	0.03658
NCAM1	Neural cell adhesion molecule 1	-2.04	0.00845	-3.48	0.00082
SMAD2	SMAD family member 2	-2.04	0.00215	-2.49	3.00E-05
RGCC	regulator of cell cycle	-2.03	0.03419	-3.21	0.02073
TMEM231	transmembrane protein 231	-2.03	0.02144	-2.76	0.00393
C11orf96	chromosome 11 open reading frame 96	-2.03	0.01409	-2.36	0.00313
ATOH8	Atonal homolog 8 (Drosophila)	-2.02	0.03864	2.87	0.00687
PRKAG2-AS1	PRKAG2 antisense RNA 1	-2.01	0.01612	-2.66	0.02381
TRAF3IP3	TRAF3 interacting protein 3	-2.01	0.00273	-2.31	0.00154
ERGIC1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	-2.01	0.00621	-2.27	0.04547
LINC00313	long intergenic non-protein coding RNA 313	-2	0.01814	-2.69	0.00567
HOXA10	homeobox A10	2.01	0.00161	2.04	0.00012
NREP	neuronal regeneration related protein homolog (rat)	2.01	0.04319	2.79	9.00E-05

PADI3	peptidyl arginine deiminase, type III	2.03	0.00887	-2.73	2.00E-05
HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	2.03	0.02889	-2.03	0.01363
PRKCA	protein kinase C, alpha	2.04	0.00066	-2.31	0.00127
GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	2.05	0.02429	-2.05	0.00053
RASL11B	RAS-like, family 11, member B	2.08	0.00127	-3.16	0.00068
PI3	peptidase inhibitor 3, skin-derived	2.08	0.03815	-2.98	0.00364
IRAK2	interleukin-1 receptor-associated kinase 2	2.1	0.00105	-2.22	0.00285
WFDC2	WAP four-disulfide core domain 2	2.14	0.00652	-2.78	0.00024
CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	2.14	0.00679	2.49	0.00047
SERTAD4	SERTA domain containing 4	2.17	0.00122	-2.66	0.00373
ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	2.17	0.00029	-2.09	0.0024
WNT10A	Wingless-type MMTV integration site family, member 10A	2.17	0.00265	3.38	0.00059
LOC728978	uncharacterized LOC728978	2.18	0.00056	2.18	0.02444
MARCKS	myristoylated alanine-rich protein kinase C substrate	2.18	0.00228	2.52	0.0027
LOC100292680	hypothetical LOC100292680	2.19	0.00376	3.76	0.0032
SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	2.27	0.00614	-4.65	0.00044
AI936724	---	2.27	0.00302	-2.9	0.00923
CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	2.29	0.0261	5.96	0.00111
RUNX1	runt-related transcription factor 1	2.3	0.00957	-3.32	0.00111
AW189097	---	2.3	0.01593	2.46	0.03749
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	2.31	0.01038	2.84	0.00295
AI223854	---	2.34	0.00425	2.15	0.00628
IFITM10	interferon induced transmembrane protein 10	2.38	0.04561	2.31	0.02374
UPP1	uridine phosphorylase 1	2.39	0.02813	-2.75	0.0041
COL5A1	collagen, type V, alpha 1	2.41	0.00067	2.09	0.00254
CD44	CD44 molecule (Indian blood group)	2.62	0.00099	-2.4	0.00231
CORO2B	coronin, actin binding protein, 2B	2.72	0.0018	-2.76	0.00062
LRRN1	leucine rich repeat neuronal 1	2.79	8.00E-05	-2.82	0.03339
KRT6B	keratin 6B	2.84	0.00038	-2.22	0.0132
FAM49A	family with sequence similarity 49, member A	2.84	9.00E-05	-2.04	0.00519
DUSP5P	dual specificity phosphatase 5 pseudogene	2.89	5.00E-04	2.35	0.00587
ALDH1A3	aldehyde dehydrogenase 1 family, member A3	2.92	0.00026	-4.04	0.00105
TUBA1A	tubulin, alpha 1a	2.94	0.00044	-2.31	0.04361
THBD	thrombomodulin	2.96	0.00033	-3.29	0.00486
RASSF6	Ras association (RalGDS/AF-6) domain family member 6	3.01	0.00019	2.17	0.02682
KRT16	keratin 16	3.04	0.00032	2.92	0.00046
UGT1A1	UDP glucuronosyltransferase 1 family, polypeptide A1	3.06	0.00336	4.64	4.00E-05
MYLK	myosin light chain kinase	3.09	0.00691	2.58	0.00098
TAGLN	transgelin	3.1	0.04019	2.34	0.03019
MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	3.2	0.01557	4.5	3.00E-05
TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	3.34	0.00567	-2.84	0.00748

PLAU	plasminogen activator, urokinase	3.55	0.00081	-6.56	0
AHNAK2	AHNAK nucleoprotein 2	3.58	0.00281	5.5	2.00E-04
SLC47A2	solute carrier family 47, member 2	3.61	0.00311	3.86	2.00E-05
ERC1	ELKS/RAB6-interacting/CAST family member 1	4.15	9.00E-05	2.5	0.00103
MMP28	matrix metallopeptidase 28	4.23	0.00033	-2.46	0.02048
EPHA4	EPH receptor A4	4.3	0.00042	2.53	0.02907
FABP4	fatty acid binding protein 4, adipocyte	4.45	0.01837	-2.57	0.02591
C18orf1	chromosome 18 open reading frame 1	4.58	0.0013	5.86	0.00027
GPR39	G protein-coupled receptor 39	4.64	0.00029	2.04	0.01846
MTSS1	metastasis suppressor 1	4.83	0.00047	-2.12	0.02179
FBXO32	F-box protein 32	5.68	0.00022	2.44	0.02761
SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	5.78	0.00155	-4.85	8.00E-04
KRT15	keratin 15	6.65	0.00113	5.94	2.00E-05
MMP1	matrix metallopeptidase 1 (interstitial collagenase)	11.48	7.00E-05	-2.13	0.00423
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	15.77	0	-2.95	0.03059
GPNMB	glycoprotein (transmembrane) nmb	16	2.00E-05	3.47	0.01109