Table S1. mpkCCD Cell Transcriptomes.

Gene Symbol	Gene Title	GeneID	Clone 11	Ori. Clone	Clone 2	Ratio (11/2)	Correlation Coefficient
Copg	coatomer protein complex, subunit gamma	54161	1.99	1.81	2.48	0.80	-0.49 ns
Atp6v0d1	ATPase, H+ transporting, lysosomal V0 subunit D1	11972	3.37	2.87	3.00	1.12	0.74 ns
Golga7	golgi autoantigen, golgin subfamily a, 7	57437	3.03	3.40	3.58	0.84	-0.34 ns
Psph	phosphoserine phosphatase	100678	0.38	0.66	0.64	0.59	-0.61 ns
Trappc4	trafficking protein particle complex 4	60409	1.17	1.12	1.08	1.08	0.64 ns
Dpm2	dolichol-phosphate (beta-D) mannosyltransferase 2	13481	0.74	0.87	0.81	0.91	-0.31 ns
Psmb5	proteasome (prosome, macropain) subunit, beta type 5	19173	2.92	3.00	2.92	0.99	0.32 ns
Dhrs1	dehydrogenase/reductase (SDR family) member 1	52585	0.74	0.68	0.88	0.83	-0.18 ns
Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	19042	2.43	2.60	2.96	0.82	-0.53 ns
Psenen	presenilin enhancer 2 homolog (C. elegans)	66340	2.52	2.88	3.80	0.66	-0.77 ns
Anapc1	anaphase promoting complex subunit 1	17222	1.16	1.33	1.61	0.72	-0.33 ns
Mrpl43	mitochondrial ribosomal protein L43	94067	2.15	2.15	1.84	1.16	0.91 *
Nmt1	N-myristoyltransferase 1	18107	3.21	2.71	3.36	0.95	0.31 ns
Atg5	autophagy-related 5 (yeast)	11793	0.70	0.73	0.66	1.05	-0.23 ns
Mtif2	mitochondrial translational initiation factor 2	76784	1.16	1.29	1.19	0.97	-0.36 ns
Psap	prosaposin	19156	8.07	7.25	8.37	0.96	0.02 ns
Ube2g1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	67128	4.02	3.60	3.88	1.03	-0.22 ns
Zkscan3	zinc finger with KRAB and SCAN domains 3	72739	0.88	0.86	0.92	0.96	0.22 ns
Mrpl27	mitochondrial ribosomal protein L27	94064	1.88	1.59	2.05	0.91	-0.22 ns
Dlg1	discs, large homolog 1 (Drosophila)	13383	4.74	4.06	3.63	1.30	0.52 ns
Canx	calnexin	12330	8.75	8.46	8.92	0.98	-0.63 ns
Psma1	proteasome (prosome, macropain) subunit, alpha type 1	26440	3.18	3.02	4.04	0.78	-0.67 ns
Sar1a	SAR1 gene homolog A (S. cerevisiae)	20224	2.69	2.17	1.88	1.43	0.88 *
Gps1	G protein pathway suppressor 1	209318	3.26	2.83	3.10	1.05	0.47 ns
Ctbp1	C-terminal binding protein 1	13016	3.99	4.83	5.02	0.79	-0.69 ns
Huwe1	HECT, UBA and WWE domain containing 1	59026	2.05	2.28	3.13	0.65	-0.18 ns
Cdv3	carnitine deficiency-associated gene expressed in ventricle 3	321022	4.01	3.89	3.12	1.28	0.84 *
Copa	coatomer protein complex subunit alpha	12847	3.95	3.57	3.27	1.20	0.80 ns
Anapc2	anaphase promoting complex subunit 2	99152	2.20	2.00	1.61	1.36	0.77 ns
Cox18	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	231430	0.76	0.82	1.07	0.71	-0.82 *
Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	211673	6.19	5.53	4.52	1.36	0.15 ns
Zranb1	zinc finger, RAN-binding domain containing 1	360216	0.62	0.59	0.66	0.94	-0.28 ns
Ddx24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	27225	1.06	0.89	0.98	1.07	0.48 ns
Tmem129	transmembrane protein 129	68366	0.38	0.53	0.61	0.61	-0.94 **
Rps27	ribosomal protein S27	57294	21.87	20.97	15.03	1.45	0.71 ns
Sap30l	SAP30-like	50724	1.13	1.20	1.77	0.64	-0.54 ns
Mad2l1bp	MAD2L1 binding protein	66591	0.76	0.75	0.52	1.46	0.92 **
Vta1	Vps20-associated 1 homolog (S. cerevisiae)	66201	1.72	1.50	1.69	1.01	-0.30 ns
Eif5	eukaryotic translation initiation factor 5	217869	7.61	7.15	7.25	1.04	0.19 ns
Rrn3	RRN3 RNA polymerase I transcription factor homolog (yeast)	106298	0.69	0.72	0.94	0.73	-0.92 *
Apoa1bp	apolipoprotein A-I binding protein	246703	3.97	4.27	3.45	1.14	0.40 ns
Pdpk1	3-phosphoinositide dependent protein kinase-1	18607	2.48	2.14	1.53	1.62	0.92 **
5730453I16Rik	RIKEN cDNA 5730453I16 gene	269061	2.48	2.62	2.08	1.19	0.78 ns
Bat5	HLA-B associated transcript 5	193742	1.01	0.75	0.54	1.86	0.92 **
Rab7	RAB7, member RAS oncogene family	19349	4.25	4.78	4.91	0.86	-0.46 ns
Ddb1	damage specific DNA binding protein 1	13194	5.39	5.93	4.75	1.13	0.72 ns
Txndc12	thioredoxin domain containing 12 (endoplasmic reticulum)	66073	1.53	1.59	1.93	0.79	-0.41 ns
Psmc5	protease (prosome, macropain) 26S subunit, ATPase 5	19184	2.80	2.42	2.30	1.21	0.70 ns
Tmem165	transmembrane protein 165	21982	3.13	3.10	3.66	0.85	-0.84 *
Aup1	ancient ubiquitous protein	11993	1.06	1.07	1.00	1.05	-0.08 ns
Hdac5	histone deacetylase 5	15184	0.62	0.56	0.95	0.65	-0.24 ns
H2-Ke2	H2-K region expressed gene 2	14976	2.51	2.55	1.94	1.28	0.87 *
Dscr3	Down syndrome critical region gene 3	13185	1.27	1.12	1.46	0.87	-0.37 ns
Cic	capicua homolog (Drosophila)	71722	0.70	0.82	1.00	0.69	-0.71 ns
Riok3	RIO kinase 3 (yeast)	66878	1.35	1.33	1.45	0.93	0.29 ns
Dctn5	dynactin 5	59288	0.91	0.86	1.13	0.80	-0.71 ns
Rragc	Ras-related GTP binding C	54170	1.56	1.52	1.48	1.05	-0.22 ns
Tbl3	transducin (beta)-like 3	213773	0.62	0.70	0.51	1.21	0.72 ns
Hp1bp3	heterochromatin protein 1, binding protein 3	15441	2.20	2.25	2.56	0.86	-0.29 ns
BC031181	cDNA sequence BC031181	407819	1.49	1.70	1.66	0.89	-0.02 ns
Polr2f	polymerase (RNA) II (DNA directed) polypeptide F	69833	2.21	2.45	2.86	0.77	-0.48 ns
Gbf1	golgi-specific brefeldin A-resistance factor 1	107338	0.89	0.90	0.76	1.17	0.18 ns
Fryl	furry homolog-like (Drosophila)	72313	1.28	1.07	1.19	1.07	-0.04 ns
Atox1	ATX1 (antioxidant protein 1) homolog 1 (yeast)	11927	1.44	1.66	2.33	0.61	-0.62 ns
2510006D16Rik	RIKEN cDNA 2510006D16 gene	76799	1.55	1.57	1.58	0.97	0.25 ns
Zc3h11a	zinc finger CCCH type containing 11A	70579	6.72	6.04	6.02	1.11	0.83 *
Ube2r2	ubiquitin-conjugating enzyme E2R 2	67615	1.62	1.50	1.57	1.03	0.02 ns
Itch	itchy, E3 ubiquitin protein ligase	16396	1.93	1.89	2.32	0.83	-0.39 ns
Ncl	nucleolin	17975	9.80	11.07	7.21	1.35	0.63 ns
Aldh3a2	aldehyde dehydrogenase family 3, subfamily A2	11671	0.41	0.36	0.47	0.87	-0.26 ns
Actg1	actin, gamma, cytoplasmic 1	11465	25.73	24.15	21.65	1.18	0.72 ns
LOC672381		672381	21.93	20.28	18.54	1.18	0.96 **
LOC675440		675440	21.93	20.28	18.54	1.18	0.96 **
Sumo2		170930	21.93	20.28	18.54	1.18	0.96 **
Vps35	vacuolar protein sorting 35	65114	6.87	6.05	6.64	1.03	0.45 ns
Cct8	chaperonin subunit 8 (theta)	12469	4.12	3.97	4.91	0.84	-0.77 ns
Ganab	alpha glucosidase 2 alpha neutral subunit	14376	1.97	2.24	2.10	0.93	-0.67 ns
Ublcp1	ubiquitin-like domain containing CTD phosphatase 1	79560	1.00	1.11	1.19	0.84	-0.40 ns
Rnf34	ring finger protein 34	80751	0.79	0.87	0.72	1.10	0.01 ns
Rbck1	RanBP-type and C3HC4-type zinc finger containing 1	24105	1.11	1.10	1.24	0.90	-0.50 ns

Pnpo	pyridoxine 5'-phosphate oxidase	103711	0.39	0.40	0.41	0.93	-0.44	ns
Dazap2	DAZ associated protein 2	23994	7.50	7.47	8.84	0.84	-0.76	ns
Wbp11	WW domain binding protein 11	60321	1.67	1.73	2.04	0.81	-0.85	*
Slc16a1	solute carrier family 16 (monocarboxylic acid transporters), member 1	20501	6.17	6.01	4.84	1.27	0.26	ns
Cx3cl1	chemokine (C-X3-C motif) ligand 1	20312	0.57	0.52	0.63	0.91	-0.58	ns
Plat	plasminogen activator, tissue	18791	0.08	0.15	0.52	0.16	-0.89	*
Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	18140	5.40	5.35	4.14	1.30	0.88	*
Atp6v1b2	ATPase, H+ transporting, lysosomal V1 subunit B2	11966	1.52	1.47	1.43	1.06	0.39	ns
Cct7	chaperonin subunit 7 (eta)	12468	5.26	6.19	6.55	0.80	-0.15	ns
Anxa6	annexin A6	11749	1.37	1.29	1.51	0.91	0.30	ns
Nptn	neuroplastin	20320	4.51	3.53	3.51	1.28	0.83	*
Scd2	stearoyl-Coenzyme A desaturase 2	20250	20.29	18.95	15.63	1.29	0.39	ns
Atp6v1h	ATPase, H+ transporting, lysosomal V1 subunit H	108664	1.30	1.41	1.28	1.01	-0.42	ns
Lbr	lamin B receptor	98386	3.08	3.89	3.39	0.91	0.30	ns
Orc5l	origin recognition complex, subunit 5-like (S. cerevisiae)	26429	0.73	0.72	0.96	0.75	-0.90	*
Psmd2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	21762	6.17	5.86	6.79	0.90	-0.02	ns
Dusp6	dual specificity phosphatase 6	67603	0.94	1.27	2.32	0.40	-0.88	*
Npm1	nucleophosmin 1	18148	14.18	14.21	13.99	1.01	-0.01	ns
Elovl5	ELOVL family member 5, elongation of long chain fatty acids (yeast)	68801	2.11	2.34	2.02	1.04	0.59	ns
Dync1i2	dynein cytoplasmic 1 intermediate chain 2	13427	2.79	2.50	2.48	1.12	-0.03	ns
Gbl	G protein beta subunit-like	56716	0.40	0.35	0.29	1.37	0.65	ns
Stmn1	stathmin 1	16765	15.57	15.96	15.02	1.03	0.68	ns
Impdh2	inosine 5'-phosphate dehydrogenase 2	23918	4.34	4.78	3.65	1.19	0.72	ns
Kpna2		16647	6.88	7.59	8.26	0.83	0.08	ns
Bpgm	2,3-bisphosphoglycerate mutase	12183	0.22	0.30	0.43	0.51	-0.60	ns
Calu	calumenin	12321	3.84	3.68	4.11	0.93	0.10	ns
Actr1a	ARP1 actin-related protein 1 homolog A (yeast)	54130	2.18	2.49	2.18	0.99	0.45	ns
Spry1	sprouty homolog 1 (Drosophila)	24063	1.54	1.62	1.05	1.46	0.01	ns
Rps26	ribosomal protein S26	27370	18.02	17.21	13.20	1.36	0.74	ns
Rrm1	ribonucleotide reductase M1	20133	2.78	3.20	3.64	0.76	-0.80	ns
Rplp2	ribosomal protein, large P2	67186	26.72	22.69	21.33	1.25	0.68	ns
Lamp1	lysosomal-associated membrane protein 1	16783	7.95	8.58	8.59	0.92	0.27	ns
Ghitm	growth hormone inducible transmembrane protein	66092	4.30	3.98	4.22	1.01	-0.44	ns
Tfg	Trk-fused gene	21787	4.27	3.62	4.32	0.98	-0.13	ns
Hdgf	hepatoma-derived growth factor	15191	5.85	6.19	5.01	1.16	0.50	ns
Hsp90b1	heat shock protein 90kDa beta (Grp94), member 1	22027	6.62	7.73	6.75	0.98	-0.31	ns
Papss1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	23971	3.92	3.81	3.18	1.23	0.15	ns
Suclg1	succinate-CoA ligase, GDP-forming, alpha subunit	56451	1.76	1.75	2.16	0.81	-0.73	ns
Sgpl1	sphingosine phosphate lyase 1	20397	1.02	1.05	0.69	1.46	0.33	ns
Mgst1	microsomal glutathione S-transferase 1	56615	0.39	1.64	3.15	0.12	-0.95	**
Junb	Jun-B oncogene	16477	1.22	1.25	0.86	1.42	0.90	*
Plod3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	26433	0.92	0.89	0.99	0.93	-0.13	ns
Tmsb4x	thymosin, beta 4, X chromosome	19241	9.58	11.12	14.10	0.68	-0.22	ns
Ccnd3	cyclin D3	12445	1.01	0.88	0.72	1.39	0.86	*
Tspyl1	testis-specific protein, Y-encoded-like 1	22110	1.47	1.33	1.42	1.03	-0.31	ns
Stip1	stress-induced phosphoprotein 1	20867	2.91	2.65	2.64	1.10	0.69	ns
Ciapin1	cytokine induced apoptosis inhibitor 1	109006	0.96	0.80	1.06	0.90	0.12	ns
Ddx1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	104721	4.83	4.94	5.57	0.86	-0.07	ns
Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthase	108156	2.51	2.22	2.11	1.18	0.24	ns
Tpi1	triosephosphate isomerase 1	21991	19.52	18.83	21.93	0.89	-0.10	ns
Npdc1	neural proliferation, differentiation and control gene 1	18146	1.01	1.07	0.85	1.18	-0.09	ns
Cstf2t	cleavage stimulation factor, 3' pre-RNA subunit 2, tau	83410	5.52	5.92	3.30	1.66	0.51	ns
Map1lc3b	microtubule-associated protein 1 light chain 3 beta	67443	4.56	4.31	2.88	1.58	0.75	ns
Cox5a	cytochrome c oxidase, subunit Va	12858	7.91	6.81	7.45	1.06	0.38	ns
Cops8	COP9 (constitutive photomorphogenic) homolog, subunit 8 (Arabidopsis thaliana)	108679	1.06	1.14	0.78	1.35	0.80	ns
Bcar3	breast cancer anti-estrogen resistance 3	29815	0.94	1.22	0.98	0.95	-0.36	ns
Zfand2a	zinc finger, AN1-type domain 2A	100494	0.82	0.92	1.44	0.57	-0.57	ns
EG234703		234703	16.62	14.95	15.24	1.08	0.66	ns
LOC638133		638133	16.62	14.95	15.24	1.08	0.66	ns
Cpe	carboxypeptidase E	12876	4.65	4.69	1.91	2.42	-0.02	ns
Mark2	MAP/microtubule affinity-regulating kinase 2	13728	2.84	2.56	1.75	1.61	0.88	*
Itm2c	integral membrane protein 2C	64294	2.19	2.12	1.63	1.34	0.03	ns
Scd1	stearoyl-Coenzyme A desaturase 1	20249	3.17	1.90	0.82	3.84	0.93	**
Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	17995	5.72	4.89	3.89	1.46	0.97	**
Cox6c	cytochrome c oxidase, subunit VIc	12864	9.88	8.92	10.65	0.92	-0.19	ns
Marcks	myristoylated alanine rich protein kinase C substrate	17118	1.69	1.50	0.80	2.08	0.15	ns
Map2k2	mitogen activated protein kinase kinase 2	26396	1.35	1.45	1.39	0.97	-0.53	ns
Carhsp1	calcium regulated heat stable protein 1	52502	1.84	1.70	1.97	0.93	-0.65	ns
Isyna1	myo-inositol 1-phosphate synthase A1	71780	1.45	1.27	1.01	1.43	0.28	ns
Rpl7	ribosomal protein L7	19989	21.71	20.59	15.57	1.39	0.73	ns
Atp5g2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	67942	9.92	9.02	9.01	1.10	0.03	ns
Herpud2	HERPUD family member 2	80517	1.00	0.79	0.75	1.34	0.83	*
Acadm	acyl-Coenzyme A dehydrogenase, medium chain	11364	2.78	2.51	1.48	1.87	0.29	ns
Sf3b3	splicing factor 3b, subunit 3	101943	3.02	3.21	2.61	1.15	0.50	ns
Clcn4-2	chloride channel 4-2	12727	0.72	0.80	0.89	0.81	-0.70	ns
Vdac2	voltage-dependent anion channel 2	22334	7.38	6.67	5.61	1.31	0.49	ns
Klhdc3	kelch domain containing 3	71765	3.58	3.03	2.96	1.20	0.82	*
Sqle	squalene epoxidase	20775	2.82	2.11	2.78	1.01	0.05	ns
Casp6	caspase 6	12368	0.65	0.56	0.64	1.02	-0.47	ns
Txnip	thioredoxin interacting protein	56338	10.34	8.11	9.45	1.09	0.11	ns
Ywhah	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	22629	5.48	5.48	6.15	0.89	0.13	ns
Psmc1	protease (prosome, macropain) 26S subunit, ATPase 1	19179	2.37	2.87	3.28	0.72	-0.80	ns
Tspan3	tetraspanin 3	56434	2.03	1.71	1.72	1.18	0.77	ns

Ehd1	EH-domain containing 1	13660	1.05	1.12	1.00	1.04	0.58	ns
Pld3	phospholipase D family, member 3	18807	0.73	0.78	0.72	1.00	0.18	ns
Abce1	ATP-binding cassette, sub-family E (OABP), member 1	24015	1.84	1.90	1.94	0.94	0.34	ns
Dr1	down-regulator of transcription 1	13486	0.87	0.91	1.20	0.72	-0.88	*
Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	11951	2.58	2.18	2.11	1.22	0.02	ns
Cct3	chaperonin subunit 3 (gamma)	12462	7.96	8.65	6.77	1.17	0.13	ns
Pdcd6	programmed cell death 6	18570	2.08	2.93	3.69	0.56	-0.89	*
Klf10	Kruppel-like factor 10	21847	0.97	1.08	1.38	0.70	-0.29	ns
Snd1	staphylococcal nuclease and tudor domain containing 1	56463	1.83	1.51	1.49	1.22	0.71	ns
Cyr61	cysteine rich protein 61	16007	3.76	5.37	4.08	0.92	-0.38	ns
Nasp	nuclear autoantigenic sperm protein (histone-binding)	50927	1.71	1.70	1.99	0.86	-0.63	ns
Flii	flightless I homolog (Drosophila)	14248	1.83	1.89	2.27	0.80	-0.46	ns
Smarcb1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	20587	1.64	1.56	1.22	1.33	0.51	ns
Fuca2	fucosidase, alpha-L- 2, plasma	66848	1.34	1.38	1.25	1.07	-0.48	ns
Scarb1	scavenger receptor class B, member 1	20778	0.73	0.78	1.00	0.73	-0.83	*
Rps5	ribosomal protein S5	20103	17.38	15.13	13.56	1.28	0.38	ns
Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	104130	4.13	4.22	6.08	0.68	-0.50	ns
Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	11949	9.88	7.95	6.28	1.57	0.94	**
Sec23b	SEC23B (S. cerevisiae)	27054	2.48	2.61	2.31	1.07	0.00	ns
Tbc1d15	TBC1 domain family, member 15	66687	3.10	2.74	2.47	1.25	0.42	ns
Hspa5	heat shock 70kD protein 5 (glucose-regulated protein)	14828	10.31	9.99	6.80	1.51	0.91	*
Ankrd10	ankyrin repeat domain 10	102334	1.76	2.01	2.26	0.77	-0.59	ns
Cd9	CD9 antigen	12527	5.43	5.03	8.01	0.68	-0.48	ns
Ifrd1	interferon-related developmental regulator 1	15982	2.07	2.79	3.63	0.57	-0.52	ns
Kars		85305	2.44	2.32	1.83	1.33	0.68	ns
LOC631033		631033	2.44	2.32	1.83	1.33	0.68	ns
Pfkp	phosphofructokinase, platelet	56421	4.46	4.43	7.08	0.63	-0.22	ns
Ddx18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	66942	1.11	1.05	0.79	1.41	0.28	ns
Nup85	nucleoporin 85	445007	1.83	1.86	1.85	0.98	0.52	ns
Rpl28	ribosomal protein L28	19943	22.90	21.40	18.34	1.24	0.20	ns
EG434175		434175	1.18	1.54	2.09	0.56	-0.61	ns
Arpc1a	actin related protein 2/3 complex, subunit 1A	56443	1.45	1.11	1.61	0.89	-0.34	ns
Rab1	RAB1, member RAS oncogene family	19324	7.83	7.22	10.20	0.76	-0.82	*
Zfand5	zinc finger, AN1-type domain 5	22682	5.47	6.10	4.56	1.19	0.53	ns
Tpst2	protein-tyrosine sulfotransferase 2	22022	0.57	0.65	0.58	0.98	-0.34	ns
Ap1s1	adaptor protein complex AP-1, sigma 1	11769	1.24	1.31	1.45	0.85	-0.39	ns
Rps15	ribosomal protein S15	20054	21.98	19.42	15.03	1.46	0.84	*
Pdhb	pyruvate dehydrogenase (lipoamide) beta	68263	3.00	2.65	2.48	1.20	0.49	ns
Mtap4	microtubule-associated protein 4	17758	0.51	0.58	0.76	0.66	0.00	ns
Mrpl20	mitochondrial ribosomal protein L20	66448	0.72	0.78	1.00	0.72	-0.37	ns
Adam9	a disintegrin and metallopeptidase domain 9 (meltrin gamma)	11502	2.28	2.42	2.39	0.95	-0.16	ns
1110005A23Rik	RIKEN cDNA 1110005A23 gene	66118	3.10	3.10	2.84	1.09	0.47	ns
EG621100		621100	17.59	16.09	14.78	1.18	0.89	*
Rpl27		19942	17.59	16.09	14.78	1.18	0.89	*
Hist1h1c	histone cluster 1, H1c	50708	2.88	1.75	1.53	1.87	0.73	ns
Mpdu1	mannose-P-dolichol utilization defect 1	24070	0.46	0.59	0.91	0.50	-0.83	*
Nnt	nicotinamide nucleotide transhydrogenase	18115	0.94	1.03	1.07	0.87	-0.87	*
Kti12	KTI12 homolog, chromatin associated (S. cerevisiae)	100087	0.51	0.46	0.49	1.04	0.21	ns
Tmed3	transmembrane emp24 domain containing 3	66111	0.83	0.95	1.21	0.68	-0.44	ns
Fuca1	fucosidase, alpha-L- 1, tissue	71665	0.93	1.17	1.56	0.60	-0.79	ns
Slc35a4	solute carrier family 35, member A4	67843	0.68	0.80	0.81	0.84	-0.08	ns
Cox8a	cytochrome c oxidase, subunit VIIIa	12868	6.15	5.13	4.09	1.50	0.57	ns
Fkbp8	FK506 binding protein 8	14232	1.64	1.34	2.06	0.79	0.12	ns
Orc3l	origin recognition complex, subunit 3-like (S. cerevisiae)	50793	0.32	0.28	0.50	0.64	-0.51	ns
LOC630539	similar to mouse RING finger 1	630539	4.05	3.92	3.72	1.08	-0.17	ns
Txn1	thioredoxin 1	22166	9.80	9.36	10.56	0.92	-0.30	ns
Fkbp5	FK506 binding protein 5	14229	1.15	1.32	1.03	1.11	0.54	ns
Dnpep	aspartyl aminopeptidase	13437	2.31	2.24	1.61	1.43	0.23	ns
Errfi1	ERBB receptor feedback inhibitor 1	74155	1.88	1.72	2.09	0.90	-0.58	ns
Anxa7	annexin A7	11750	2.98	2.86	2.95	1.00	0.54	ns
Dhx30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	72831	1.35	1.26	1.28	1.05	0.62	ns
EG666577		666577	25.77	23.82	20.47	1.25	0.95	**
LOC667739		667739	25.77	23.82	20.47	1.25	0.95	**
Rps6		20104	25.77	23.82	20.47	1.25	0.95	**
Atp5j	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	11957	5.80	5.53	6.81	0.85	-0.51	ns
Dhx15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	13204	5.91	5.58	6.62	0.89	-0.52	ns
Hspa4	heat shock protein 4	15525	2.78	3.05	3.43	0.81	-0.61	ns
Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)	20383	7.57	8.18	6.65	1.13	0.46	ns
Hmgb3	high mobility group box 3	15354	2.69	2.92	5.06	0.53	-0.75	ns
Vcl	vinculin	22330	7.85	7.63	6.07	1.29	0.70	ns
Nr2f2	nuclear receptor subfamily 2, group F, member 2	11819	0.44	0.53	0.38	1.16	-0.08	ns
Rad21	RAD21 homolog (S. pombe)	19357	8.69	8.49	12.01	0.72	-0.83	*
Cops4	COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)	26891	1.37	1.43	1.59	0.85	-0.70	ns
Rab31	RAB31, member RAS oncogene family	106572	0.74	0.66	0.56	1.32	0.80	ns
Prdx4	peroxiredoxin 4	53381	2.78	3.11	3.89	0.71	0.20	ns
Trap1	TNF receptor-associated protein 1	68015	1.68	1.42	1.88	0.89	-0.08	ns
2310037I24Rik	RIKEN cDNA 2310037I24 gene	69612	1.85	1.61	1.94	0.95	-0.16	ns
Pes1	pescadillo homolog 1, containing BRCT domain (zebrafish)	64934	0.99	1.21	1.22	0.80	-0.18	ns
Rbbp9	retinoblastoma binding protein 9	26450	0.75	0.63	0.99	0.75	-0.72	ns
Vdac3	voltage-dependent anion channel 3	22335	5.71	6.08	5.95	0.95	0.38	ns
Rbmxrt	RNA binding motif protein, X chromosome retrogene	19656	3.18	3.43	3.92	0.81	-0.31	ns
Mesdc2	mesoderm development candiate 2	67943	1.57	1.64	1.77	0.88	-0.49	ns
Apba3	amyloid beta (A4) precursor protein-binding, family A, member 3	57267	0.74	0.74	0.75	0.98	0.26	ns

Hmga1	high mobility group AT-hook 1	15361	2.71	2.72	2.55	1.06	0.63	ns
Adh5	alcohol dehydrogenase 5 (class III), chi polypeptide	11532	4.65	4.89	3.70	1.25	-0.01	ns
Pnrc2	proline-rich nuclear receptor coactivator 2	52830	1.48	1.70	2.11	0.70	-0.84	*
Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	53421	3.14	3.57	3.89	0.80	-0.68	ns
Snrpc	U1 small nuclear ribonucleoprotein C	20630	3.47	3.05	2.41	1.43	0.94	**
Th1l	TH1-like homolog (Drosophila)	57314	1.11	1.22	1.40	0.79	-0.64	ns
Kifc3	kinesin family member C3	16582	1.07	1.05	0.93	1.14	0.45	ns
Glb1	galactosidase, beta 1	12091	0.41	0.41	0.36	1.13	0.72	ns
Sipa1	signal-induced proliferation associated gene 1	20469	0.48	0.46	0.39	1.23	0.72	ns
Taz	tafazzin	66826	0.73	0.78	1.09	0.67	-0.67	ns
Usp14	ubiquitin specific peptidase 14	59025	1.07	1.29	1.72	0.62	-0.26	ns
Imp3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	102462	1.82	1.34	1.30	1.40	0.86	*
Magoh	mago-nashi homolog, proliferation-associated (Drosophila)	17149	3.89	3.82	4.04	0.96	0.01	ns
Mcm4	minichromosome maintenance deficient 4 homolog (S. cerevisiae)	17217	8.40	7.69	7.88	1.06	-0.15	ns
Gosr1	golgi SNAP receptor complex member 1	53334	0.84	0.66	0.58	1.45	0.37	ns
LOC629949		629949	0.63	0.72	0.36	1.74	0.32	ns
LOC640991		640991	0.63	0.72	0.36	1.74	0.32	ns
Rpl19	ribosomal protein L19	19921	20.92	19.03	17.98	1.16	0.74	ns
Nsdhl	NAD(P) dependent steroid dehydrogenase-like	18194	1.22	1.00	1.99	0.61	-0.61	ns
Sh3bp5l	SH3 binding domain protein 5 like	79566	0.47	0.44	0.38	1.23	0.94	**
Arpc1b	actin related protein 2/3 complex, subunit 1B	11867	3.77	3.79	4.17	0.90	-0.12	ns
Pin1	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	23988	1.68	1.25	1.35	1.24	0.66	ns
Rfk	riboflavin kinase	54391	1.97	1.86	1.80	1.09	0.48	ns
Vac14	Vac14 homolog (S. cerevisiae)	234729	0.36	0.40	0.28	1.28	0.68	ns
Lrrc59	leucine rich repeat containing 59	98238	2.22	1.98	3.15	0.70	-0.76	ns
Ass1	argininosuccinate synthetase 1	11898	0.34	0.55	0.47	0.73	-0.33	ns
Psmb7	proteasome (prosome, macropain) subunit, beta type 7	19177	8.89	7.91	6.86	1.29	0.93	**
Sec13	SEC13 homolog (S. cerevisiae)	110379	1.20	1.15	1.53	0.78	-0.38	ns
Cnbp	cellular nucleic acid binding protein	12785	9.04	8.89	7.70	1.17	0.58	ns
Aurkaip1	aurora kinase A interacting protein 1	66077	1.82	1.84	2.12	0.85	-0.25	ns
Dctn3	dynactin 3	53598	1.15	1.09	1.25	0.92	-0.03	ns
Nadk	NAD kinase	192185	0.62	0.56	0.71	0.87	-0.56	ns
Btg2	B-cell translocation gene 2, anti-proliferative	12227	1.34	1.51	1.46	0.91	-0.59	ns
Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	17219	9.33	8.40	7.09	1.31	0.81	ns
Stk38	serine/threonine kinase 38	106504	2.85	2.62	2.16	1.31	0.64	ns
Cdkn2d	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	12581	0.83	0.86	1.00	0.83	0.31	ns
Vps16	vacuolar protein sorting 16 (yeast)	80743	0.70	0.58	0.84	0.83	-0.21	ns
Tubb5	tubulin, beta 5	22154	14.74	13.55	12.19	1.20	0.73	ns
Capn2	calpain 2	12334	2.59	2.50	1.90	1.36	0.26	ns
Tk1	thymidine kinase 1	21877	1.51	1.35	1.46	1.03	0.46	ns
Pex12	peroxisomal biogenesis factor 12	103737	0.33	0.33	0.44	0.76	-0.51	ns
Snx1	sorting nexin 1	56440	1.10	0.94	0.93	1.17	0.75	ns
Tmem19	transmembrane protein 19	67226	0.66	0.57	0.49	1.34	0.27	ns
Scoc	short coiled-coil protein	56367	0.38	0.44	0.47	0.79	-0.31	ns
Ets2	E26 avian leukemia oncogene 2, 3' domain	23872	2.30	2.77	2.27	1.01	-0.12	ns
Polr2g	polymerase (RNA) II (DNA directed) polypeptide G	67710	3.70	4.05	3.75	0.98	-0.02	ns
Perp	PERP, TP53 apoptosis effector	64058	1.72	1.79	2.20	0.78	-0.70	ns
Rps4x	ribosomal protein S4, X-linked	20102	22.35	21.95	20.67	1.08	0.70	ns
Rplp1	ribosomal protein, large, P1	56040	24.19	20.69	16.55	1.45	0.96	**
Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	28080	9.69	8.79	8.64	1.12	0.76	ns
Ap1b1	adaptor protein complex AP-1, beta 1 subunit	11764	0.68	0.60	0.71	0.95	-0.40	ns
Wdr45l	Wdr45 like	66840	2.57	2.16	2.13	1.20	0.84	*
Psmc3	proteasome (prosome, macropain) 26S subunit, ATPase 3	19182	4.31	4.52	3.10	1.38	0.69	ns
Gart	phosphoribosylglycinamide formyltransferase	14450	1.09	1.09	1.05	1.03	0.03	ns
Mrpl28	mitochondrial ribosomal protein L28	68611	1.67	1.79	1.37	1.21	0.78	ns
Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	15502	3.76	3.85	4.16	0.90	-0.86	*
Psmc4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	23996	1.78	3.35	3.80	0.47	-0.65	ns
Prdx3	peroxiredoxin 3	11757	1.91	2.32	1.57	1.21	0.05	ns
Scamp3	secretory carrier membrane protein 3	24045	1.00	0.99	0.92	1.08	-0.07	ns
Shcbp1	Shc SH2-domain binding protein 1	20419	1.95	1.90	2.94	0.66	-0.12	ns
Slc25a3	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	18674	15.18	13.02	10.31	1.46	0.64	ns
Litaf	LPS-induced TN factor	56722	6.01	4.86	6.53	0.92	-0.21	ns
Sh3bp4	SH3-domain binding protein 4	98402	0.47	0.52	0.28	1.66	0.53	ns
Ugdh	UDP-glucose dehydrogenase	22235	2.13	2.57	2.85	0.74	-0.94	**
Nusap1	nucleolar and spindle associated protein 1	108907	3.02	2.33	2.16	1.39	0.79	ns
Tuba3a		22144	0.47	0.53	0.54	0.87	-0.27	ns
Tuba3b		22147	0.47	0.53	0.54	0.87	-0.27	ns
Rars	arginyl-tRNA synthetase	104458	2.63	2.68	2.54	1.03	0.32	ns
Sec22a	SEC22 vesicle trafficking protein-like A (S. cerevisiae)	317717	0.84	0.77	0.78	1.07	0.74	ns
Crip1	cysteine-rich protein 1 (intestinal)	12925	3.30	5.39	4.05	0.81	0.07	ns
Ufc1	ubiquitin-fold modifier conjugating enzyme 1	66155	1.62	1.58	1.22	1.32	0.67	ns
Atp6v0e	ATPase, H+ transporting, lysosomal V0 subunit E	11974	3.93	3.41	3.13	1.25	0.65	ns
Cyfip1	cytoplasmic FMR1 interacting protein 1	20430	2.70	2.45	3.05	0.88	-0.64	ns
Cd81	CD 81 antigen	12520	5.01	4.71	5.36	0.93	0.29	ns
Nfe2l1	nuclear factor, erythroid derived 2,-like 1	18023	1.54	1.36	1.28	1.19	0.42	ns
Cirbp	cold inducible RNA binding protein	12696	1.11	0.85	0.76	1.45	0.37	ns
Mif	macrophage migration inhibitory factor	17319	17.64	16.69	16.01	1.10	0.57	ns
Snrpd1	small nuclear ribonucleoprotein D1	20641	1.19	1.60	1.79	0.66	-0.31	ns
Sh3gl1	SH3-domain GRB2-like 1	20405	1.21	1.15	0.76	1.59	0.89	*
Prkcsh	protein kinase C substrate 80K-H	19089	1.57	1.82	1.70	0.92	0.17	ns
Man2b1	mannosidase 2, alpha B1	17159	0.84	0.89	0.82	1.02	0.56	ns
Polr2c	polymerase (RNA) II (DNA directed) polypeptide C	20021	1.77	1.86	2.14	0.82	0.14	ns
Timm8a1	translocase of inner mitochondrial membrane 8 homolog a1 (yeast)	30058	1.13	1.64	1.71	0.66	0.10	ns
Men1	multiple endocrine neoplasia 1	17283	1.51	1.51	1.32	1.14	0.81	*
Mrpl34	mitochondrial ribosomal protein L34	94065	0.90	0.96	1.05	0.85	-0.08	ns

Klf16	Kruppel-like factor 16	118445	0.63	0.65	0.67	0.94	-0.71	ns
Map2k1	mitogen activated protein kinase kinase 1	26395	1.50	1.35	1.92	0.78	0.10	ns
Nr1h2	nuclear receptor subfamily 1, group H, member 2	22260	0.72	0.73	1.10	0.65	-0.83	*
Rbmx	RNA binding motif protein, X chromosome	19655	0.51	0.41	0.23	2.23	0.01	ns
Gmpr2	guanosine monophosphate reductase 2	105446	0.65	0.73	0.83	0.78	-0.63	ns
Fkbp4	FK506 binding protein 4	14228	2.34	2.72	3.22	0.72	-0.92	**
Hsp90ab1	heat shock protein 90kDa alpha (cytosolic), class B member 1	15516	14.41	14.33	10.43	1.38	0.68	ns
Gsta4	glutathione S-transferase, alpha 4	14860	0.34	0.49	0.43	0.79	-0.68	ns
Hiatl1	hippocampus abundant transcript-like 1	66631	1.40	1.87	2.57	0.54	-0.91	*
Ptdss1	phosphatidylserine synthase 1	19210	1.03	1.47	1.51	0.68	-0.51	ns
Nfs1	nitrogen fixation gene 1 (S. cerevisiae)	18041	1.16	1.00	1.29	0.90	-0.36	ns
Tmem97	transmembrane protein 97	69071	0.35	0.35	0.37	0.95	-0.33	ns
Pnkp	polynucleotide kinase 3'- phosphatase	59047	0.26	0.32	0.38	0.69	-0.95	**
Prdx5	peroxiredoxin 5	54683	6.21	4.84	3.37	1.83	0.80	ns
Ctsc	cathepsin C	13032	1.51	1.62	3.34	0.45	-0.61	ns
Pcx	pyruvate carboxylase	18563	0.45	0.43	0.29	1.57	0.92	**
Cope	coatomer protein complex, subunit epsilon	59042	2.68	2.88	3.68	0.73	-0.38	ns
M6pr	mannose-6-phosphate receptor, cation dependent	17113	3.88	3.90	4.51	0.85	-0.26	ns
Rcbtb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	105670	0.44	0.51	0.50	0.87	-0.45	ns
Emg1	EMG1 nucleolar protein homolog (S. cerevisiae)	14791	3.43	3.21	3.73	0.92	0.00	ns
Bag1	Bcl2-associated athanogene 1	12017	2.05	2.23	2.46	0.83	-0.68	ns
Guk1	guanylate kinase 1	14923	0.48	0.71	0.81	0.60	-0.70	ns
Hmox2	heme oxygenase (decycling) 2	15369	2.04	2.01	2.39	0.85	-0.71	ns
Pycrl	pyrroline-5-carboxylate reductase-like	66194	0.53	0.58	0.52	1.01	0.53	ns
Cd82	CD82 antigen	12521	2.85	2.51	2.90	0.98	-0.47	ns
Abcb10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	56199	0.56	0.43	0.35	1.58	0.82	*
Pea15a	phosphoprotein enriched in astrocytes 15A	18611	3.11	3.06	3.75	0.83	-0.82	*
Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	11430	1.43	1.30	1.32	1.08	0.20	ns
Pafah1b3	platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit	18476	1.64	1.64	2.04	0.80	-0.70	ns
Gstm2	glutathione S-transferase, mu 2	14863	3.57	6.38	3.65	0.97	0.21	ns
EG666634		666634	22.58	22.46	18.48	1.22	0.70	ns
H2afz		51788	22.58	22.46	18.48	1.22	0.70	ns
Gstm1	glutathione S-transferase, mu 1	14862	6.71	8.18	3.63	1.84	0.25	ns
Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	66916	4.47	4.58	4.38	1.02	0.48	ns
Gabarapl1	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	57436	3.27	2.06	2.43	1.34	0.27	ns
EG637379		637379	22.02	20.62	18.04	1.21	0.87	*
Rpl9		20005	22.02	20.62	18.04	1.21	0.87	*
M6prbp1	mannose-6-phosphate receptor binding protein 1	66905	2.17	2.05	1.56	1.38	0.95	**
Pex19	peroxisome biogenesis factor 19	19298	0.68	0.51	0.50	1.36	0.31	ns
Rab5a	RAB5A, member RAS oncogene family	271457	3.37	3.63	3.06	1.10	0.44	ns
Ccni	cyclin I	12453	13.48	11.34	12.55	1.07	0.35	ns
Thap11	THAP domain containing 11	59016	0.86	0.92	0.80	1.06	0.64	ns
Cat	catalase	12359	0.91	0.68	0.42	2.13	0.24	ns
Tubb6	tubulin, beta 6	67951	0.89	1.28	1.52	0.58	0.08	ns
Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	170768	0.36	0.40	0.35	1.01	0.09	ns
Rpa2	replication protein A2	19891	1.06	1.15	1.17	0.90	0.17	ns
Ltbr	lymphotoxin B receptor	17000	0.83	0.79	0.81	1.02	-0.43	ns
2410015N17Rik	RIKEN cDNA 2410015N17 gene	66422	1.24	1.47	1.41	0.88	0.12	ns
Cd164	CD164 antigen	53599	7.59	6.88	7.37	1.03	-0.49	ns
Ier2	immediate early response 2	15936	2.83	3.57	2.66	1.06	0.45	ns
Sae1	SUMO1 activating enzyme subunit 1	56459	2.52	2.42	2.86	0.87	-0.16	ns
2810405J04Rik	RIKEN cDNA 2810405J04 gene	72722	1.22	1.20	0.93	1.32	0.83	*
Itpa	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	16434	0.76	0.85	0.84	0.90	-0.13	ns
EG432865		432865	22.35	20.22	15.20	1.46	0.74	ns
LOC670832		670832	22.35	20.22	15.20	1.46	0.74	ns
LOC671641		671641	22.35	20.22	15.20	1.46	0.74	ns
Ddah2	dimethylarginine dimethylaminohydrolase 2	51793	2.36	1.99	1.06	2.22	0.91	*
Arf2	ADP-ribosylation factor 2	11841	0.59	0.57	0.53	1.12	0.50	ns
Vapa	vesicle-associated membrane protein, associated protein A	30960	7.06	5.93	4.95	1.42	0.98	***
Luzp1	leucine zipper protein 1	269593	1.14	0.80	1.17	0.97	-0.37	ns
Cept1	choline/ethanolaminephosphotransferase 1	99712	1.78	1.82	1.16	1.52	0.79	ns
Syap1	synapse associated protein 1	67043	1.40	1.51	2.57	0.54	-0.42	ns
Ube2d2	ubiquitin-conjugating enzyme E2D 2	56550	2.17	3.25	3.65	0.59	-0.75	ns
Tmem14c	transmembrane protein 14C	66154	1.30	1.28	1.81	0.71	-0.56	ns
Higd1a	HIG1 domain family, member 1A	56295	2.69	3.30	4.36	0.61	-0.32	ns
Timm23	translocase of inner mitochondrial membrane 23 homolog (yeast)	53600	3.31	3.15	3.21	1.03	0.35	ns
Scye1	small inducible cytokine subfamily E, member 1	13722	3.09	3.28	2.40	1.28	0.52	ns
Ccng2	cyclin G2	12452	2.70	2.30	4.10	0.66	-0.60	ns
Pi4k2b	phosphatidylinositol 4-kinase type 2 beta	67073	1.31	1.31	1.42	0.92	-0.55	ns
Ddost	dolichyl-di-phosphooligosaccharide-protein glycotransferase	13200	2.69	2.59	2.90	0.92	0.17	ns
Ndufs5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	595136	1.66	1.79	2.36	0.70	-0.65	ns
Mrfap1	Morf4 family associated protein 1	67568	7.47	7.99	8.64	0.86	-0.33	ns
Pdia4	protein disulfide isomerase associated 4	12304	0.80	0.87	1.02	0.79	-0.52	ns
Ppic	peptidylprolyl isomerase C	19038	0.16	0.57	0.19	0.81	0.15	ns
Dctn6	dynactin 6	22428	1.44	1.51	2.28	0.63	-0.59	ns
Sacm1l	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)	83493	1.42	1.48	1.72	0.82	-0.02	ns
Lxn	latexin	17035	3.12	2.76	1.62	1.92	0.74	ns
Nr4a1	nuclear receptor subfamily 4, group A, member 1	15370	0.98	1.12	0.96	1.02	-0.18	ns
Med28	mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)	66999	3.16	3.48	3.67	0.86	-0.20	ns
Mrpl4	mitochondrial ribosomal protein L4	66163	1.03	1.04	1.00	1.03	0.51	ns
Nubp2	nucleotide binding protein 2	26426	0.69	0.67	0.65	1.07	0.63	ns
Lamb2	laminin, beta 2	16779	0.39	0.35	0.41	0.97	0.40	ns
Pnpla6	patatin-like phospholipase domain containing 6	50767	0.86	1.00	0.90	0.95	-0.23	ns
LOC622534	similar to ribosomal protein L36	622534	19.51	16.99	12.54	1.55	0.75	ns
Grcc10	gene rich cluster, C10 gene	14790	2.06	1.77	2.32	0.88	-0.43	ns
Spop	speckle-type POZ protein	20747	1.84	1.60	1.62	1.13	0.64	ns

Park7	Parkinson disease (autosomal recessive, early onset) 7	57320	2.14	2.25	2.23	0.95	-0.02 ns
Rab32	RAB32, member RAS oncogene family	67844	0.31	0.22	0.53	0.59	-0.56 ns
Sh3bgrl3	SH3 domain binding glutamic acid-rich protein-like 3	73723	1.15	1.42	1.87	0.61	-0.88 *
Emp1	epithelial membrane protein 1	13730	5.86	5.58	5.73	1.02	0.07 ns
Gsto1	glutathione S-transferase omega 1	14873	5.16	5.68	5.83	0.88	-0.58 ns
Trrap	transformation/transcription domain-associated protein	100683	1.73	1.69	1.81	0.95	-0.44 ns
Egln2	EGL nine homolog 2 (C. elegans)	112406	0.86	0.95	0.90	0.95	-0.12 ns
Dpf2	D4, zinc and double PHD fingers family 2	19708	2.29	1.97	1.39	1.64	0.98 ***
LOC666215		666215	1.26	1.29	1.29	0.97	0.05 ns
Mcrs1		51812	1.26	1.29	1.29	0.97	0.05 ns
Mum1	melanoma associated antigen (mutated) 1	68114	1.20	1.17	0.95	1.25	0.21 ns
Creld1	cysteine-rich with EGF-like domains 1	171508	0.67	0.71	0.50	1.33	0.54 ns
Hgs	HGF-regulated tyrosine kinase substrate	15239	1.38	1.23	1.14	1.20	0.84 *
Clpb	ClpB caseinolytic peptidase B homolog (E. coli)	20480	0.40	0.49	0.75	0.53	-0.78 ns
Nfe2l2	nuclear factor, erythroid derived 2, like 2	18024	2.87	2.90	2.57	1.11	0.09 ns
Ezh2	enhancer of zeste homolog 2 (Drosophila)	14056	3.20	3.49	4.17	0.76	-0.61 ns
Zdhhc7	zinc finger, DHHC domain containing 7	102193	0.58	0.58	0.38	1.54	0.89 *
Rpl6	ribosomal protein L6	19988	19.26	18.11	16.38	1.17	0.66 ns
Ndufb3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	66495	2.19	2.27	1.88	1.16	0.30 ns
Stra13	stimulated by retinoic acid 13	20892	0.56	0.55	0.65	0.87	0.05 ns
Pdlim1	PDZ and LIM domain 1 (elfin)	54132	1.30	1.34	0.48	2.67	-0.29 ns
Ei24	etoposide induced 2.4 mRNA	13663	2.61	2.33	2.28	1.14	0.80 ns
Tspan31	tetraspanin 31	67125	4.37	4.33	4.57	0.95	-0.76 ns
Melk	maternal embryonic leucine zipper kinase	17279	1.18	1.23	1.75	0.67	-0.29 ns
1500003O22Rik	RIKEN cDNA 1500003O22 gene	101867	0.40	0.44	0.43	0.92	-0.25 ns
Ctps	cytidine 5'-triphosphate synthase	51797	0.94	1.05	1.50	0.62	-0.61 ns
Strap	serine/threonine kinase receptor associated protein	20901	2.33	2.31	2.73	0.85	-0.64 ns
Atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	67126	4.90	4.85	4.81	1.01	-0.31 ns
Actl6a	actin-like 6A	56456	2.31	2.83	2.30	1.00	-0.10 ns
Gfm1	G elongation factor, mitochondrial 1	28030	0.96	0.83	0.83	1.15	0.09 ns
Tox4	TOX high mobility group box family member 4	268741	0.93	1.00	0.92	1.01	0.36 ns
Cdc45l	cell division cycle 45 homolog (S. cerevisiae)-like	12544	0.91	1.01	1.31	0.70	-0.32 ns
Tacstd1	tumor-associated calcium signal transducer 1	17075	11.62	10.57	8.48	1.36	0.96 **
Stub1	STIP1 homology and U-Box containing protein 1	56424	4.53	3.88	3.19	1.41	0.99 ***
Wdr5	WD repeat domain 5	140858	1.36	1.39	1.13	1.21	0.80 ns
Bad	Bcl-associated death promoter	12015	1.49	1.36	0.95	1.56	0.35 ns
Ruvbl1	RuvB-like protein 1	56505	0.69	0.77	0.81	0.85	-0.50 ns
Xrcc1	X-ray repair complementing defective repair in Chinese hamster cells 1	22594	0.47	0.55	0.62	0.75	-0.78 ns
Rab34	RAB34, member of RAS oncogene family	19376	1.19	1.07	0.99	1.20	0.07 ns
Glrx	glutaredoxin	93692	0.18	0.18	0.49	0.36	-0.62 ns
Mrps22	mitochondrial ribosomal protein S22	64655	0.78	0.78	0.85	0.91	0.18 ns
Slc44a4	solute carrier family 44, member 4	70129	0.49	0.45	0.45	1.09	-0.29 ns
Hdgfrp2	hepatoma-derived growth factor, related protein 2	15193	0.37	0.40	0.24	1.53	0.86 *
Glis2	GLIS family zinc finger 2	83396	2.54	2.71	1.90	1.33	-0.25 ns
EG627737		627737	8.40	8.34	8.99	0.93	-0.74 ns
LOC623483		623483	8.40	8.34	8.99	0.93	-0.74 ns
LOC632026		632026	8.40	8.34	8.99	0.93	-0.74 ns
Cyc1	cytochrome c-1	66445	3.85	4.65	5.39	0.71	-0.85 *
Nola2	nucleolar protein family A, member 2	52530	4.08	4.02	3.75	1.08	0.34 ns
4931406C07Rik	RIKEN cDNA 4931406C07 gene	70984	1.17	1.09	0.53	2.20	0.79 ns
BC004004	cDNA sequence BC004004	80748	2.54	2.45	1.94	1.31	0.92 **
Scamp2	secretory carrier membrane protein 2	24044	1.10	0.83	0.90	1.21	0.76 ns
Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	13078	0.54	0.61	0.96	0.56	-0.72 ns
Clpp	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	53895	1.17	1.17	0.85	1.38	0.79 ns
Ppox	protoporphyrinogen oxidase	19044	0.35	0.36	0.38	0.93	-0.56 ns
Smarcal1	Swi/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	54380	0.44	0.38	0.35	1.24	0.62 ns
Llgl1	lethal giant larvae homolog 1 (Drosophila)	16897	2.05	1.98	2.36	0.87	-0.65 ns
Wbscr16	Williams-Beuren syndrome chromosome region 16 homolog (human)	94254	0.30	0.41	0.36	0.83	0.00 ns
Uba52		22186	29.79	26.90	21.78	1.36	0.88 *
Spint1	serine protease inhibitor, Kunitz type 1	20732	3.43	2.37	2.04	1.67	0.55 ns
0610006I08Rik	RIKEN cDNA 0610006I08 gene	66836	1.57	1.58	1.24	1.26	0.11 ns
Slc1a5	solute carrier family 1 (neutral amino acid transporter), member 5	20514	0.40	0.40	0.42	0.96	-0.45 ns
Ap4b1	adaptor-related protein complex AP-4, beta 1	67489	0.46	0.55	0.64	0.72	-0.48 ns
5730536A07Rik	RIKEN cDNA 5730536A07 gene	68250	2.13	2.28	2.47	0.86	-0.41 ns
Rheb	RAS-homolog enriched in brain	19744	5.57	5.59	5.61	0.99	0.03 ns
Slc4a2	solute carrier family 4 (anion exchanger), member 2	20535	1.87	1.63	1.68	1.11	0.02 ns
Lig1	ligase I, DNA, ATP-dependent	16881	2.84	3.19	3.29	0.86	-0.56 ns
Tpt1	tumor protein, translationally-controlled 1	22070	32.97	29.03	24.67	1.33	0.93 **
Dync1h1	dynein cytoplasmic 1 heavy chain 1	13424	3.63	3.81	4.04	0.89	0.26 ns
Znhit2	zinc finger, HIT domain containing 2	29805	0.82	0.84	0.71	1.15	0.23 ns
Stxbp3a	syntaxin binding protein 3A	20912	1.86	1.81	1.49	1.24	0.24 ns
C1galt1c1	C1GALT1-specific chaperone 1	59048	1.15	1.17	1.74	0.66	-0.57 ns
Clic1	chloride intracellular channel 1	114584	6.87	6.41	5.92	1.15	0.55 ns
Akt1	thymoma viral proto-oncogene 1	11651	3.04	3.03	3.48	0.87	-0.11 ns
Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	66108	3.47	3.41	3.85	0.90	-0.63 ns
Coq7	demethyl-Q 7	12850	0.73	0.81	0.80	0.90	-0.17 ns
Ebp	phenylalkylamine Ca2+ antagonist (emopamil) binding protein	13595	0.97	1.12	1.99	0.49	-0.17 ns
Ttc35	tetratricopeptide repeat domain 35	66736	1.76	1.90	2.05	0.85	-0.20 ns
Naca	nascent polypeptide-associated complex alpha polypeptide	17938	17.23	15.72	14.39	1.19	0.26 ns
Mcoln1	mucolipin 1	94178	0.58	0.58	0.78	0.74	-0.54 ns
Cops3	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	26572	3.35	3.27	3.50	0.95	-0.13 ns
Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	19299	3.46	3.50	3.24	1.06	-0.01 ns
Ube3a	ubiquitin protein ligase E3A	22215	3.32	3.32	3.18	1.04	0.26 ns
Plxnb2	plexin B2	140570	4.76	4.62	4.89	0.97	-0.74 ns

Fbl	fibrillarin	14113	2.18	2.87	2.29	0.95	0.30	ns
Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	26432	1.95	1.95	1.48	1.31	0.78	ns
Tuft1	tuftelin 1	22156	1.27	1.30	1.16	1.09	-0.34	ns
Gtpbp2	GTP binding protein 2	56055	0.88	0.89	0.80	1.10	0.80	ns
Coil	coilin	12812	0.58	0.47	0.47	1.22	0.66	ns
Tspo	translocator protein	12257	3.13	3.21	3.97	0.78	-0.19	ns
D17Wsu104e	DNA segment, Chr 17, Wayne State University 104, expressed	28106	0.95	1.03	0.79	1.19	0.76	ns
Cks1b	CDC28 protein kinase 1b	54124	11.52	11.70	11.84	0.97	-0.07	ns
1110008F13Rik	RIKEN cDNA 1110008F13 gene	67388	3.67	3.66	4.29	0.85	-0.46	ns
Rnd3	Rho family GTPase 3	74194	1.42	1.06	1.30	1.08	-0.11	ns
Mapk14	mitogen activated protein kinase 14	26416	2.27	1.96	0.96	2.36	0.86	*
Rpe	ribulose-5-phosphate-3-epimerase	66646	0.78	0.75	0.66	1.18	0.42	ns
Pmf1	polyamine-modulated factor 1	67037	0.51	0.64	0.57	0.88	-0.08	ns
Ngrn	neugrin, neurite outgrowth associated	83485	0.83	0.83	0.98	0.84	-0.34	ns
Pepd	peptidase D	18624	0.45	0.52	0.42	1.06	-0.07	ns
Gjb3	gap junction membrane channel protein beta 3	14620	0.66	0.72	0.56	1.17	0.21	ns
EG668457		668457	21.18	18.54	12.32	1.71	0.87	*
Sfrs6	splicing factor, arginine/serine-rich 6	67996	7.39	6.63	6.36	1.16	0.50	ns
Hmg20a	high mobility group 20A	66867	1.27	0.93	0.91	1.38	0.87	*
Tcf4	transcription factor 4	21413	0.45	0.49	0.36	1.24	-0.26	ns
Ube2s	ubiquitin-conjugating enzyme E2S	77891	5.05	5.62	6.13	0.82	-0.42	ns
Cyb5	cytochrome b-5	109672	1.42	1.24	0.84	1.69	0.57	ns
Csnk2b	casein kinase 2, beta polypeptide	13001	5.13	4.55	3.40	1.50	0.87	*
Rcl1	RNA terminal phosphate cyclase-like 1	59028	0.59	0.69	0.39	1.51	0.58	ns
Top2b	topoisomerase (DNA) II beta	21974	1.38	1.43	1.74	0.79	-0.73	ns
Mkln1	muskelin 1, intracellular mediator containing kelch motifs	27418	0.59	0.71	1.08	0.55	-0.83	*
Asah1	N-acylsphingosine amidohydrolase 1	11886	4.16	4.26	3.57	1.16	0.72	ns
Casc3	cancer susceptibility candidate 3	192160	0.98	0.90	0.82	1.19	-0.11	ns
Gys1	glycogen synthase 1, muscle	14936	0.68	0.74	0.98	0.69	-0.34	ns
Brap	BRCA1 associated protein	72399	0.63	0.54	0.55	1.14	0.72	ns
Cfdp1	craniofacial development protein 1	23837	2.72	3.24	2.22	1.22	0.56	ns
LOC640502		640502	1.50	1.61	1.54	0.97	-0.16	ns
Uap1		107652	1.50	1.61	1.54	0.97	-0.16	ns
H2afx	H2A histone family, member X	15270	3.60	3.03	2.79	1.28	0.80	ns
D15Mgi27	DNA Segment, Chr 15, Mouse Genome Informatics 27	106073	1.07	1.18	1.08	0.98	0.41	ns
Mre11a	meiotic recombination 11 homolog A (S. cerevisiae)	17535	0.81	0.77	0.34	2.39	0.89	*
Htra1	HtrA serine peptidase 1	56213	0.56	0.52	0.56	1.00	0.21	ns
Oprs1	opioid receptor, sigma 1	18391	0.47	0.47	0.48	0.98	0.08	ns
Ddx20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	53975	1.06	1.03	0.74	1.42	0.59	ns
Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	81489	2.28	2.61	2.49	0.91	0.22	ns
Zwilch	Zwilch, kinetochore associated, homolog (Drosophila)	68014	1.51	1.60	1.79	0.84	0.12	ns
Arhgap27	Rho GTPase activating protein 27	544817	0.33	0.20	0.27	1.22	0.23	ns
Hsd11b2	hydroxysteroid 11-beta dehydrogenase 2	15484	4.44	2.54	1.96	2.25	0.79	ns
S100a10	S100 calcium binding protein A10 (calpactin)	20194	4.44	4.45	4.16	1.06	0.63	ns
Cdc123	cell division cycle 123 homolog (S. cerevisiae)	98828	2.98	2.24	2.34	1.27	0.65	ns
Fis1	fission 1 (mitochondrial outer membrane) homolog (yeast)	66437	2.66	2.74	3.18	0.83	-0.51	ns
Magmas	mitochondria-associated protein involved in granulocyte-macrophage colony-stimulating factor signal transduction	66449	1.46	1.93	2.88	0.51	-0.88	*
Mosc2	MOCO sulphurase C-terminal domain containing 2	67247	1.13	1.25	1.00	1.12	0.69	ns
1110003E01Rik	RIKEN cDNA 1110003E01 gene	68552	1.12	1.21	1.86	0.60	-0.62	ns
Atp6v0b	ATPase, H+ transporting, lysosomal V0 subunit B	114143	1.97	1.99	2.65	0.74	-0.61	ns
Stk25	serine/threonine kinase 25 (yeast)	59041	2.53	2.10	1.43	1.75	0.75	ns
Trappc3	trafficking protein particle complex 3	27096	0.94	1.07	1.31	0.72	-0.30	ns
Wee1	wee 1 homolog (S. pombe)	22390	1.00	0.91	1.13	0.88	-0.48	ns
Pfkm	phosphofructokinase, muscle	18642	0.81	0.86	0.98	0.83	-0.63	ns
Praf2	PRA1 domain family 2	54637	0.54	0.65	0.98	0.55	-0.12	ns
Idh3g	isocitrate dehydrogenase 3 (NAD+), gamma	15929	1.45	1.39	1.98	0.73	-0.42	ns
Nxf1	nuclear RNA export factor 1 homolog (S. cerevisiae)	53319	2.28	1.85	1.46	1.55	0.86	*
Ppm1g	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	14208	2.41	2.79	3.21	0.75	-0.64	ns
Nck2	non-catalytic region of tyrosine kinase adaptor protein 2	17974	0.73	0.73	0.59	1.24	-0.20	ns
Trpm7	transient receptor potential cation channel, subfamily M, member 7	58800	1.56	1.55	1.40	1.11	-0.12	ns
Cdca5	cell division cycle associated 5	67849	2.97	3.04	2.66	1.11	0.69	ns
1110032E23Rik	RIKEN cDNA 1110032E23 gene	68659	0.33	0.31	0.22	1.49	0.25	ns
Rpl36a	ribosomal protein L36a	19982	13.43	14.13	13.68	0.98	0.39	ns
Mea1	male enhanced antigen 1	17256	1.72	1.69	1.22	1.40	0.79	ns
Tia1	cytotoxic granule-associated RNA binding protein 1	21841	1.53	1.51	1.57	0.97	-0.41	ns
Bub3	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	12237	3.42	3.63	3.95	0.86	0.00	ns
Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	59125	3.64	3.05	2.15	1.68	0.45	ns
Cdc37	cell division cycle 37 homolog (S. cerevisiae)	12539	3.70	3.32	3.09	1.19	0.78	ns
B230118H07Rik	RIKEN cDNA B230118H07 gene	68170	0.84	0.61	0.50	1.68	0.69	ns
Snta1	syntrophin, acidic 1	20648	0.20	0.15	0.41	0.48	-0.61	ns
Atp5b	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	11947	13.65	12.31	11.47	1.18	0.39	ns
0610031J06Rik	RIKEN cDNA 0610031J06 gene	56700	3.05	2.86	2.76	1.10	-0.17	ns
Neu1	neuraminidase 1	18010	0.63	0.57	0.44	1.42	0.30	ns
Amd2		#######	1.65	1.26	1.03	1.59	0.48	ns
Lrp10	low-density lipoprotein receptor-related protein 10	65107	1.93	1.92	2.16	0.89	-0.08	ns
Bax	Bcl2-associated X protein	12028	1.09	1.23	1.49	0.72	-0.75	ns
Mut	methylmalonyl-Coenzyme A mutase	17850	1.07	0.86	0.66	1.61	0.59	ns
Mid1ip1	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish))	68041	2.78	3.64	4.43	0.62	-0.45	ns
1110059E24Rik	RIKEN cDNA 1110059E24 gene	66206	1.49	1.72	1.25	1.18	0.69	ns
Gstm5	glutathione S-transferase, mu 5	14866	1.08	1.40	1.16	0.92	-0.49	ns
Pde6d	phosphodiesterase 6D, cGMP-specific, rod, delta	18582	0.88	0.96	0.89	0.99	0.03	ns
Tmem132a	transmembrane protein 132A	98170	2.07	2.41	1.81	1.14	0.27	ns
Ubl5	ubiquitin-like 5	66177	0.50	0.43	0.51	0.98	0.38	ns
Ncdn	neurochondrin	26562	0.49	0.49	0.46	1.07	0.62	ns
Gas1	growth arrest specific 1	14451	0.60	0.36	0.04	16.85	-0.23	ns

3230401D17Rik	RIKEN cDNA 3230401D17 gene	66680	3.05	2.89	3.20	0.95	-0.07	ns
Sdf2	stromal cell derived factor 2	20316	2.38	2.21	2.14	1.11	-0.14	ns
Fkbp3	FK506 binding protein 3	30795	3.92	4.34	5.57	0.70	-0.66	ns
Stam	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	20844	0.85	0.76	0.64	1.33	0.95	**
Abhd8	abhydrolase domain containing 8	64296	0.38	0.39	0.43	0.87	0.36	ns
Surf6	surfeit gene 6	20935	0.29	0.39	0.30	0.95	-0.21	ns
Fgd1	FYVE, RhoGEF and PH domain containing 1	14163	0.19	0.32	0.42	0.47	-0.20	ns
Bet1	blocked early in transport 1 homolog (S. cerevisiae)	12068	0.35	0.46	0.52	0.67	-0.30	ns
Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	12580	2.35	2.06	2.53	0.92	0.18	ns
Dnalc4	dynein, axonemal, light chain 4	54152	0.55	0.52	0.66	0.82	-0.70	ns
Adam8	a disintegrin and metallopeptidase domain 8	11501	0.22	0.20	0.37	0.59	-0.71	ns
Cdk2	cyclin-dependent kinase 2	12566	1.81	1.95	2.03	0.89	-0.55	ns
Mrpl51	mitochondrial ribosomal protein L51	66493	2.74	3.02	4.11	0.66	-0.74	ns
Clptm1	cleft lip and palate associated transmembrane protein 1	56457	1.38	1.19	1.35	1.02	0.38	ns
Cbx3		12417	8.80	9.10	9.50	0.92	-0.65	ns
1110038F14Rik	RIKEN cDNA 1110038F14 gene	117171	0.73	0.74	0.84	0.87	-0.31	ns
Wdr74	WD repeat domain 74	107071	1.43	1.09	0.80	1.78	0.98	***
Numb	numb gene homolog (Drosophila)	18222	1.73	1.53	1.69	1.02	0.16	ns
1500019G21Rik	RIKEN cDNA 1500019G21 gene	66245	0.60	0.58	0.57	1.04	-0.32	ns
Efna1	ephrin A1	13636	1.17	1.21	1.07	1.09	-0.32	ns
Rps6ka1	ribosomal protein S6 kinase polypeptide 1	20111	1.58	1.53	2.21	0.71	-0.79	ns
Parp9	poly (ADP-ribose) polymerase family, member 9	80285	0.58	0.63	1.38	0.42	-0.63	ns
Nucb1	nucleobindin 1	18220	1.06	1.13	1.79	0.59	-0.82	*
Mbnl1	muscleblind-like 1 (Drosophila)	56758	5.64	5.02	4.02	1.40	0.92	**
Pigyl	phosphatidylinositol glycan anchor biosynthesis, class Y-like	66268	0.88	0.75	0.69	1.27	0.70	ns
Dnajc15	DnaJ (Hsp40) homolog, subfamily C, member 15	66148	1.04	1.02	1.37	0.76	-0.48	ns
Mtvr2	mammary tumor virus receptor 2	17826	1.32	1.19	0.86	1.52	0.84	*
Msh6	mutS homolog 6 (E. coli)	17688	3.43	2.84	2.39	1.43	0.83	*
Elf3	E74-like factor 3	13710	1.67	1.81	1.11	1.49	0.19	ns
1700123O20Rik	RIKEN cDNA 1700123O20 gene	58248	1.25	1.25	1.13	1.10	0.22	ns
Dlg3	discs, large homolog 3 (Drosophila)	53310	0.45	0.35	0.50	0.90	-0.31	ns
Rbm4	RNA binding motif protein 4	19653	0.48	0.50	0.33	1.44	0.16	ns
Aldoa	aldolase 1, A isoform	11674	17.55	15.45	17.43	1.00	-0.02	ns
Bnip3l	BCL2/adenovirus E1B interacting protein 3-like	12177	7.43	6.91	8.09	0.91	0.17	ns
Bri3	brain protein I3	55950	2.11	1.84	1.91	1.10	0.04	ns
Trp53inp1	transformation related protein 53 inducible nuclear protein 1	60599	0.51	0.50	1.56	0.32	-0.86	*
Rbm12	RNA binding motif protein 12	75710	1.60	1.58	1.54	1.03	0.42	ns
Nif3l1	Ngg1 interacting factor 3-like 1 (S. pombe)	65102	0.50	0.54	0.39	1.29	-0.11	ns
Cog2	component of oligomeric golgi complex 2	76332	0.46	0.45	0.38	1.21	0.56	ns
Por	P450 (cytochrome) oxidoreductase	18984	1.24	1.28	1.75	0.70	-0.78	ns
Gabarap	gamma-aminobutyric acid receptor associated protein	56486	5.85	5.70	6.54	0.89	-0.76	ns
Chchd1	coiled-coil-helix-coiled-coil-helix domain containing 1	66121	2.73	2.89	2.86	0.95	-0.29	ns
Ppa1	pyrophosphatase (inorganic) 1	67895	0.75	0.91	0.66	1.13	0.01	ns
Ppif	peptidylprolyl isomerase F (cyclophilin F)	105675	0.62	0.63	0.48	1.30	0.81	ns
Ube2e1		22194	2.46	2.51	2.77	0.88	-0.31	ns
Acaa1a		113868	0.95	0.95	0.81	1.17	0.85	*
Acaa1b		235674	0.95	0.95	0.81	1.17	0.85	*
Mrpl23	mitochondrial ribosomal protein L23	19935	1.16	1.21	1.12	1.03	0.63	ns
Slc39a7	solute carrier family 39 (zinc transporter), member 7	14977	1.47	1.60	1.16	1.26	0.78	ns
Tnfaip8	tumor necrosis factor, alpha-induced protein 8	106869	2.84	2.90	2.19	1.29	0.64	ns
Atp6v1d	ATPase, H+ transporting, lysosomal V1 subunit D	73834	2.37	2.56	3.24	0.73	-0.85	*
Ctgf	connective tissue growth factor	14219	2.89	3.00	3.46	0.83	-0.36	ns
Slc25a10	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	27376	1.60	1.33	1.94	0.82	-0.41	ns
Nr1d2	nuclear receptor subfamily 1, group D, member 2	353187	2.71	2.51	2.59	1.04	0.35	ns
B3gat3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	72727	0.51	0.67	0.42	1.20	0.58	ns
Rcc1	regulator of chromosome condensation 1	100088	0.25	0.27	0.39	0.63	-0.90	*
Eefsec	eukaryotic elongation factor, selenocysteine-tRNA-specific	65967	0.55	0.67	0.73	0.75	-0.27	ns
Hsd3b7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	101502	0.36	0.35	0.44	0.83	-0.42	ns
Gtse1	G two S phase expressed protein 1	29870	0.54	0.52	0.70	0.77	-0.16	ns
Cox7a2	cytochrome c oxidase, subunit VIIa 2	12866	14.61	12.25	11.48	1.27	0.82	*
EG434401		434401	4.12	4.13	4.10	1.00	0.33	ns
LOC637555		637555	4.12	4.13	4.10	1.00	0.33	ns
Nhp2l1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	20826	4.45	4.11	5.39	0.82	-0.51	ns
Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	56324	1.19	1.01	0.94	1.25	0.67	ns
Pomp	proteasome maturation protein	66537	3.12	3.16	3.88	0.80	-0.46	ns
Foxo1	forkhead box O1	56458	1.40	1.42	0.98	1.42	0.61	ns
Mrps18a	mitochondrial ribosomal protein S18A	68565	1.73	1.90	1.12	1.53	0.83	*
Msh2	mutS homolog 2 (E. coli)	17685	2.83	2.69	1.22	2.32	0.90	*
Vps53	vacuolar protein sorting 53 (yeast)	68299	0.96	0.95	0.69	1.38	0.28	ns
Rxrb	retinoid X receptor beta	20182	1.92	1.51	1.38	1.38	0.87	*
Mto1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	68291	0.38	0.29	0.33	1.15	0.64	ns
Cog4	component of oligomeric golgi complex 4	102339	0.81	0.85	0.64	1.27	0.67	ns
Hap1	huntingtin-associated protein 1	15114	0.55	0.57	0.70	0.78	-0.20	ns
Rrs1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	59014	1.46	1.63	1.12	1.30	0.31	ns
Smpd2	sphingomyelin phosphodiesterase 2, neutral	20598	0.44	0.46	0.35	1.24	0.31	ns
D4Wsu53e	DNA segment, Chr 4, Wayne State University 53, expressed	27981	1.86	1.52	1.92	0.96	-0.33	ns
Tsg101	tumor susceptibility gene 101	22088	1.24	1.13	1.36	0.90	-0.45	ns
Commd4	COMM domain containing 4	66199	0.78	0.70	0.82	0.94	0.26	ns
Vps4b	vacuolar protein sorting 4b (yeast)	20479	3.83	4.40	3.55	1.08	0.42	ns
Zfp238	zinc finger protein 238	30928	3.52	4.18	3.96	0.88	-0.56	ns
Mapkapk5	MAP kinase-activated protein kinase 5	17165	0.70	0.59	0.64	1.09	0.31	ns
Efemp2	epidermal growth factor-containing fibulin-like extracellular matrix protein 2	58859	2.11	2.08	1.28	1.65	0.88	*
Cdc6	cell division cycle 6 homolog (S. cerevisiae)	23834	1.39	1.39	1.79	0.77	-0.24	ns
Pfdn1	prefoldin 1	67199	1.61	1.77	2.11	0.76	-0.07	ns

Trim2	tripartite motif protein 2	80890	0.08	0.16	0.39	0.21	-0.91	*
Ube2g2	ubiquitin-conjugating enzyme E2G 2	22213	0.69	0.68	0.59	1.16	-0.16	ns
Trappc6a	trafficking protein particle complex 6A	67091	0.61	0.79	1.31	0.46	-0.58	ns
Sac3d1	SAC3 domain containing 1	66406	0.67	0.68	0.63	1.07	0.69	ns
Orc6l	origin recognition complex, subunit 6-like (S. cerevisiae)	56452	1.12	1.33	1.54	0.73	-0.35	ns
Sept9	septin 9	53860	1.31	1.32	0.99	1.32	0.36	ns
Cul7	cullin 7	66515	1.82	1.63	0.84	2.15	0.73	ns
Bok	Bcl-2-related ovarian killer protein	51800	4.20	3.93	2.52	1.66	0.59	ns
Slc37a4	solute carrier family 37 (glucose-6-phosphate transporter), member 4	14385	0.39	0.37	0.40	0.96	0.42	ns
Lcmt1	leucine carboxyl methyltransferase 1	30949	1.06	1.34	0.95	1.11	0.07	ns
Bid	BH3 interacting domain death agonist	12122	0.85	0.85	0.66	1.28	-0.20	ns
Tusc4	tumor suppressor candidate 4	56032	0.49	0.51	0.50	0.98	0.48	ns
Prom2	prominin 2	192212	0.78	0.82	0.79	0.98	-0.44	ns
Phb		18673	2.00	1.76	1.87	1.07	0.34	ns
0610009D07Rik	RIKEN cDNA 0610009D07 gene	66055	3.56	4.78	4.49	0.79	-0.57	ns
Psme1	proteasome (prosome, macropain) 28 subunit, alpha	19186	3.62	3.77	4.31	0.84	-0.77	ns
Lamp3		239739	2.29	2.38	2.10	1.09	0.70	ns
Ppid		67738	2.29	2.38	2.10	1.09	0.70	ns
Krtcap2	keratinocyte associated protein 2	66059	2.44	2.66	2.47	0.98	-0.24	ns
Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	53945	1.50	1.28	0.88	1.70	-0.29	ns
Armc10	armadillo repeat containing 10	67211	1.33	1.40	1.10	1.20	0.17	ns
Jagn1	jagunal homolog 1 (Drosophila)	67767	1.42	1.12	1.47	0.96	-0.27	ns
Egr1	early growth response 1	13653	9.55	9.36	6.80	1.40	0.83	*
Ptpn1	protein tyrosine phosphatase, non-receptor type 1	19246	1.59	1.79	2.00	0.79	-0.71	ns
2010309E21Rik	RIKEN cDNA 2010309E21 gene	66488	1.28	1.27	1.53	0.83	-0.46	ns
Bcap29	B-cell receptor-associated protein 29	12033	0.89	1.13	1.12	0.79	-0.29	ns
Ecsit	ECSIT homolog (Drosophila)	26940	0.46	0.42	0.38	1.21	0.77	ns
Syngr2	synaptogyrin 2	20973	1.90	2.38	2.69	0.70	-0.54	ns
Anp32b	acidic nuclear phosphoprotein 32 family, member B	67628	5.51	5.86	6.77	0.81	-0.57	ns
Sec61b	Sec61 beta subunit	66212	2.11	2.05	1.83	1.15	0.57	ns
Zfp346	zinc finger protein 346	26919	0.55	0.47	0.52	1.06	0.58	ns
Ckmt1	creatine kinase, mitochondrial 1, ubiquitous	12716	0.56	0.44	0.63	0.87	-0.57	ns
Rcn1	reticulocalbin 1	19672	0.40	0.13	0.02	25.47	0.77	ns
Chuk	conserved helix-loop-helix ubiquitous kinase	12675	1.40	1.46	1.21	1.15	0.39	ns
Acot7	acyl-CoA thioesterase 7	70025	1.15	1.34	1.60	0.72	-0.10	ns
Rrp15	ribosomal RNA processing 15 homolog (S. cerevisiae)	67223	0.43	0.48	0.37	1.16	0.36	ns
Ftsj1	FtsJ homolog 1 (E. coli)	54632	0.40	0.47	0.59	0.66	-0.25	ns
Cd320	CD320 antigen	54219	0.55	0.48	0.41	1.32	0.92	**
Hspa2	heat shock protein 2	15512	0.37	0.47	0.50	0.72	-0.73	ns
Ddt	D-dopachrome tautomerase	13202	0.95	0.93	0.78	1.21	0.74	ns
Trappc2l	trafficking protein particle complex 2-like	59005	1.39	1.37	1.04	1.33	0.48	ns
Tpd52l2	tumor protein D52-like 2	66314	0.78	0.69	0.69	1.12	-0.06	ns
Klc4	kinesin light chain 4	74764	0.66	0.55	0.35	1.89	0.74	ns
Man1a	mannosidase 1, alpha	17155	0.99	0.54	0.22	4.40	0.31	ns
Arl2bp	ADP-ribosylation factor-like 2 binding protein	107566	2.38	2.41	2.58	0.92	0.13	ns
Gmcl1	germ cell-less homolog 1 (Drosophila)	23885	2.11	2.61	2.26	0.93	-0.32	ns
Slc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	102857	0.66	0.69	0.59	1.11	0.49	ns
Zfpl1	zinc finger like protein 1	81909	0.61	0.65	0.52	1.16	0.18	ns
Vav3	vav 3 oncogene	57257	0.05	0.06	0.74	0.06	-0.60	ns
Dstn	destrin	56431	14.60	13.61	11.73	1.24	0.90	*
Ahcy	S-adenosylhomocysteine hydrolase	269378	3.30	3.49	4.38	0.75	-0.47	ns
Rpl22l1	ribosomal protein L22 like 1	68028	12.48	12.36	7.24	1.72	0.56	ns
Cdc25a	cell division cycle 25 homolog A (S. pombe)	12530	0.43	0.48	0.58	0.74	-0.18	ns
Srpk2	serine/arginine-rich protein specific kinase 2	20817	0.56	0.74	0.45	1.25	0.03	ns
Polr2e	polymerase (RNA) II (DNA directed) polypeptide E	66420	2.42	2.49	2.44	0.99	-0.60	ns
Dsn1	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	66934	0.64	0.75	0.91	0.70	-0.70	ns
Igtp	interferon gamma induced GTPase	16145	0.23	0.38	0.74	0.32	-0.69	ns
Tubg1	tubulin, gamma 1	103733	1.83	1.85	2.46	0.74	-0.31	ns
Nfxl1	nuclear transcription factor, X-box binding-like 1	100978	1.21	1.17	0.99	1.22	0.13	ns
2410018C20Rik	RIKEN cDNA 2410018C20 gene	67873	0.33	0.33	0.44	0.76	-0.63	ns
B230317C12Rik	RIKEN cDNA B230317C12 gene	56279	0.37	0.42	0.34	1.08	0.18	ns
P4ha2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide	18452	0.57	0.54	2.18	0.26	-0.60	ns
Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	18109	0.33	0.39	0.66	0.50	-0.90	*
Krt19	keratin 19	16669	7.31	6.33	9.06	0.80	-0.40	ns
Actr10	ARP10 actin-related protein 10 homolog (S. cerevisiae)	56444	3.28	3.28	4.02	0.81	-0.32	ns
Cdk2ap2	CDK2-associated protein 2	52004	2.07	2.14	2.09	0.98	0.39	ns
Tmbim1	transmembrane BAX inhibitor motif containing 1	69660	0.53	0.66	0.84	0.63	-0.73	ns
Dusp10	dual specificity phosphatase 10	63953	0.25	0.25	0.29	0.84	-0.63	ns
Mbd2	methyl-CpG binding domain protein 2	17191	0.98	1.03	1.30	0.76	-0.40	ns
Exosc5	exosome component 5	27998	0.54	0.43	0.35	1.52	0.91	*
Usp2	ubiquitin specific peptidase 2	53376	0.43	0.35	0.21	2.02	0.93	**
Lztfl1	leucine zipper transcription factor-like 1	93730	0.60	0.60	0.44	1.37	0.72	ns
Crebl1	cAMP responsive element binding protein-like 1	12915	0.45	0.44	0.38	1.20	0.58	ns
Csnk1e	casein kinase 1, epsilon	27373	1.92	1.97	2.14	0.89	-0.41	ns
Galk1	galactokinase 1	14635	1.44	1.83	2.43	0.59	-0.56	ns
Gipc2	GIPC PDZ domain containing family, member 2	54120	1.96	2.27	1.46	1.33	0.37	ns
Tspan5	tetraspanin 5	56224	1.19	1.56	1.41	0.84	-0.56	ns
Pcsk7	proprotein convertase subtilisin/kexin type 7	18554	0.37	0.28	0.39	0.96	0.15	ns
Ly6a	lymphocyte antigen 6 complex, locus A	110454	0.21	0.79	5.91	0.04	-0.66	ns
Psme2	proteasome (prosome, macropain) 28 subunit, beta	19188	1.37	1.99	2.40	0.57	-0.90	*
Dnajb9	DnaJ (Hsp40) homolog, subfamily B, member 9	27362	1.27	1.52	1.90	0.67	-0.90	*
Tmem183a	transmembrane protein 183A	57439	1.10	1.09	0.93	1.18	-0.12	ns
Ethe1	ethylmalonic encephalopathy 1	66071	0.41	0.43	0.75	0.54	-0.75	ns
Kdelr2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	66913	4.42	4.44	4.77	0.92	-0.38	ns

Dvl2	dishevelled 2, dsh homolog (Drosophila)	13543	0.45	0.42	0.43	1.04	-0.22	ns
1110032A03Rik	RIKEN cDNA 1110032A03 gene	68721	0.43	0.36	0.34	1.27	0.82	*
Rab27b	RAB27b, member RAS oncogene family	80718	0.27	0.20	0.26	1.05	0.33	ns
Cd2bp2	CD2 antigen (cytoplasmic tail) binding protein 2	70233	0.92	0.96	1.01	0.91	0.04	ns
Arl6ip5	ADP-ribosylation factor-like 6 interacting protein 5	65106	1.22	0.79	1.04	1.17	0.38	ns
Fbxw4	F-box and WD-40 domain protein 4	30838	0.82	0.90	0.89	0.91	-0.45	ns
Mccc1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	72039	0.76	0.68	0.40	1.87	0.72	ns
Capn1	calpain 1	12333	1.27	1.38	0.99	1.28	0.55	ns
Chchd4	coiled-coil-helix-coiled-coil-helix domain containing 4	72170	0.93	1.00	1.06	0.88	-0.45	ns
Mmp11	matrix metallopeptidase 11	17385	0.40	0.48	0.18	2.19	0.41	ns
Cetn3	centrin 3	12626	1.88	2.76	3.06	0.61	-0.90	*
Zyx	zyxin	22793	1.31	1.26	1.50	0.87	-0.77	ns
Eif4a3	eukaryotic translation initiation factor 4A, isoform 3	192170	4.81	4.14	4.97	0.96	0.32	ns
2310065K24Rik	RIKEN cDNA 2310065K24 gene	102122	1.25	1.24	1.55	0.80	0.00	ns
Gpr180	G protein-coupled receptor 180	58245	0.68	0.59	0.72	0.95	0.03	ns
AI597479	expressed sequence AI597479	98404	0.45	0.48	0.42	1.07	0.54	ns
Rnf12	ring finger protein 12	19820	1.31	1.38	2.08	0.63	-0.63	ns
Nt5c	5',3'-nucleotidase, cytosolic	50773	0.94	1.00	1.09	0.86	-0.01	ns
Frg1	FSHD region gene 1	14300	1.63	1.67	1.71	0.95	0.06	ns
Ift140	intraflagellar transport 140 homolog (Chlamydomonas)	106633	1.07	0.97	0.63	1.67	0.94	**
Cct5	chaperonin subunit 5 (epsilon)	12465	9.00	8.89	9.39	0.95	-0.22	ns
U2af2	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2	22185	1.15	1.26	1.30	0.88	-0.70	ns
Ptgs2	prostaglandin-endoperoxide synthase 2	19225	0.93	1.15	1.15	0.80	-0.68	ns
Coq5	coenzyme Q5 homolog, methyltransferase (yeast)	52064	0.58	0.61	0.58	0.99	0.24	ns
Cd14	CD14 antigen	12475	1.17	1.45	1.44	0.81	-0.43	ns
Cdk9	cyclin-dependent kinase 9 (CDC2-related kinase)	107951	2.53	2.27	1.87	1.35	0.48	ns
Snrpa	small nuclear ribonucleoprotein polypeptide A	53607	1.55	1.73	1.51	1.02	0.42	ns
Mal	myelin and lymphocyte protein, T-cell differentiation protein	17153	17.20	14.25	15.12	1.13	-0.13	ns
Mapkap1	mitogen-activated protein kinase associated protein 1	227743	0.60	0.69	0.60	0.99	-0.47	ns
Ndufa5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	68202	2.25	2.52	2.46	0.91	-0.06	ns
H13	histocompatibility 13	14950	1.43	1.67	2.02	0.70	-0.78	ns
Plekha2	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 2	83436	3.57	3.69	4.42	0.80	0.12	ns
Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a	21937	0.90	0.95	1.25	0.72	-0.93	**
Ifi47	interferon gamma inducible protein 47	15953	0.10	0.10	0.42	0.23	-0.55	ns
Hs6st1	heparan sulfate 6-O-sulfotransferase 1	50785	0.91	0.90	0.68	1.33	-0.08	ns
Mta1	metastasis associated 1	116870	0.97	0.92	1.03	0.93	-0.56	ns
Atf1	activating transcription factor 1	11908	2.62	2.65	2.85	0.92	0.05	ns
Itpr3	inositol 1,4,5-triphosphate receptor 3	16440	1.91	1.69	1.24	1.53	0.94	**
Ebpl	emopamil binding protein-like	68177	0.52	0.39	0.22	2.31	0.82	*
Smpdl3b	sphingomyelin phosphodiesterase, acid-like 3B	100340	0.67	0.82	1.01	0.66	-0.62	ns
Fzd6	frizzled homolog 6 (Drosophila)	14368	1.41	1.30	1.06	1.33	0.62	ns
Tyk2	tyrosine kinase 2	54721	0.32	0.33	0.36	0.88	0.23	ns
Pkm2	pyruvate kinase, muscle	18746	12.34	10.92	9.95	1.23	0.80	ns
Crip2	cysteine rich protein 2	68337	7.52	6.54	6.07	1.23	0.63	ns
Lsm7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	66094	0.86	1.05	0.59	1.45	0.69	ns
Gripap1	GRIP1 associated protein 1	54645	0.47	0.47	0.64	0.73	0.01	ns
Them2	thioesterase superfamily member 2	66834	1.41	1.22	1.18	1.19	0.27	ns
Rpl35a	ribosomal protein L35a	57808	23.93	23.06	20.07	1.19	0.90	*
Grpel1	GrpE-like 1, mitochondrial	17713	1.62	1.78	1.99	0.81	-0.31	ns
Dohh	deoxyhypusine hydroxylase/monooxygenase	102115	0.86	0.73	0.79	1.09	0.45	ns
Psrc1	proline/serine-rich coiled-coil 1	56742	0.60	0.74	0.61	0.98	-0.35	ns
Mast2	microtubule associated serine/threonine kinase 2	17776	1.10	1.07	1.23	0.89	-0.21	ns
Anapc11	anaphase promoting complex subunit 11 homolog (yeast)	66156	3.25	3.03	3.72	0.87	0.22	ns
Cav2	caveolin 2	12390	5.88	4.78	7.48	0.78	-0.48	ns
Slc23a2	solute carrier family 23 (nucleobase transporters), member 2	54338	0.27	0.38	0.43	0.63	-0.32	ns
Arl6	ADP-ribosylation factor-like 6	56297	1.75	1.55	1.69	1.03	0.14	ns
Stk19	serine/threonine kinase 19	54402	0.35	0.36	0.25	1.43	0.64	ns
Sult2b1	sulfotransferase family, cytosolic, 2B, member 1	54200	0.25	0.31	0.49	0.50	-0.67	ns
Dynll1		56455	16.34	16.50	12.50	1.30	0.70	ns
EG627788		627788	16.34	16.50	12.50	1.30	0.70	ns
2900064A13Rik	RIKEN cDNA 2900064A13 gene	73024	1.96	1.65	1.98	0.98	0.37	ns
2310039H08Rik	RIKEN cDNA 2310039H08 gene	67101	1.54	1.43	1.04	1.46	0.88	*
Pldn	pallidin	18457	1.28	1.08	0.95	1.35	0.52	ns
Snrpa1	small nuclear ribonucleoprotein polypeptide A'	68981	1.36	1.82	2.17	0.62	-0.60	ns
Sil1	endoplasmic reticulum chaperone SIL1 homolog (S. cerevisiae)	81500	0.43	0.44	0.69	0.62	-0.32	ns
Emd	emerin	13726	0.62	0.75	1.33	0.46	-0.68	ns
Mlh1	mutL homolog 1 (E. coli)	17350	0.29	0.32	0.32	0.90	-0.32	ns
Asb3	ankyrin repeat and SOCS box-containing protein 3	65257	0.41	0.40	0.46	0.88	0.14	ns
Rhcg	Rhesus blood group-associated C glycoprotein	56315	1.17	0.21	0.20	5.92	0.65	ns
Eef1g	eukaryotic translation elongation factor 1 gamma	67160	16.93	15.94	11.57	1.46	0.76	ns
Ppp2ca	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	19052	6.97	6.82	7.33	0.95	-0.31	ns
Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	17991	3.62	3.95	3.91	0.92	0.28	ns
Hsd17b4	hydroxysteroid (17-beta) dehydrogenase 4	15488	1.25	1.38	1.26	0.99	0.15	ns
Peli1	pellino 1	67245	1.52	1.33	1.79	0.84	-0.59	ns
Tuba4a	tubulin, alpha 4A	22145	10.58	9.62	7.65	1.38	0.87	*
Cadm1	cell adhesion molecule 1	54725	2.85	2.18	2.36	1.20	0.35	ns
Iqgap1	IQ motif containing GTPase activating protein 1	29875	6.90	6.62	6.24	1.10	0.09	ns
Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	12499	0.95	0.98	2.44	0.39	-0.67	ns
Npepps	aminopeptidase puromycin sensitive	19155	2.20	1.81	2.34	0.93	-0.30	ns
Med31	mediator of RNA polymerase II transcription, subunit 31 homolog (yeast)	67279	1.08	0.99	1.07	1.00	0.05	ns
Gpc1	glypican 1	14733	1.01	0.67	0.38	2.67	0.96	**
Klf4	Kruppel-like factor 4 (gut)	16600	0.28	0.36	0.92	0.30	-0.85	*
Slc9a1	solute carrier family 9 (sodium/hydrogen exchanger), member 1	20544	0.28	0.28	0.30	0.93	-0.52	ns
Rras2	related RAS viral (r-ras) oncogene homolog 2	66922	1.76	1.72	2.18	0.81	-0.63	ns
Rai14	retinoic acid induced 14	75646	1.08	1.11	1.20	0.90	-0.77	ns
1190017O12Rik	RIKEN cDNA 1190017O12 gene	68936	0.85	0.87	1.09	0.78	-0.84	*

Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	170439	4.87	3.32	1.06	4.59	0.53	ns
Stard3	START domain containing 3	59045	0.86	0.66	0.93	0.92	-0.39	ns
Sertad1	SERTA domain containing 1	55942	0.71	0.82	0.96	0.73	-0.32	ns
Fbxl14	F-box and leucine-rich repeat protein 14	101358	0.74	0.76	0.70	1.05	0.28	ns
F3	coagulation factor III	14066	8.59	7.68	5.32	1.61	0.06	ns
Jun	Jun oncogene	16476	2.53	2.07	2.49	1.01	-0.41	ns
Prkci	protein kinase C, iota	18759	7.37	7.31	5.40	1.36	0.46	ns
Cox6a1	cytochrome c oxidase, subunit VI a, polypeptide 1	12861	17.68	15.50	14.60	1.21	0.72	ns
Ccnd1	cyclin D1	12443	1.23	1.44	1.58	0.78	-0.43	ns
Grina	glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutamate binding)	66168	2.18	2.08	2.28	0.95	0.18	ns
Prkrip1	Prkr interacting protein 1 (IL11 inducible)	66801	0.40	0.49	0.54	0.74	-0.49	ns
Gnb1	guanine nucleotide binding protein, beta 1	14688	4.03	3.83	5.18	0.77	-0.39	ns
Lypla2	lysophospholipase 2	26394	1.07	0.93	1.24	0.86	-0.11	ns
Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial	14571	2.18	2.19	1.61	1.35	0.07	ns
Large	like-glycosyltransferase	16795	0.48	0.44	0.10	4.61	0.70	ns
Xrcc6	X-ray repair complementing defective repair in Chinese hamster cells 6	14375	0.82	1.06	1.07	0.77	-0.29	ns
Rdh14	retinol dehydrogenase 14 (all-trans and 9-cis)	105014	0.79	0.95	1.23	0.64	-0.67	ns
Dnajc12	DnaJ (Hsp40) homolog, subfamily C, member 12	30045	0.34	0.24	0.37	0.91	-0.33	ns
E2f5	E2F transcription factor 5	13559	0.67	0.77	0.69	0.97	-0.53	ns
Ndc80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	67052	0.58	0.62	0.48	1.20	0.72	ns
Slc12a4	solute carrier family 12, member 4	20498	0.32	0.42	0.29	1.07	0.50	ns
1810008A18Rik	RIKEN cDNA 1810008A18 gene	108707	0.67	0.52	0.40	1.68	0.87	*
Acot8	acyl-CoA thioesterase 8	170789	0.63	0.59	0.69	0.91	-0.33	ns
Tacc3	transforming, acidic coiled-coil containing protein 3	21335	1.08	1.27	1.39	0.77	-0.19	ns
Ppia	peptidylprolyl isomerase A	268373	26.49	24.60	22.39	1.18	0.91	*
Fau	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)	14109	25.48	21.73	17.10	1.48	0.98	***
Cul4b	cullin 4B	72584	1.36	1.26	1.63	0.83	-0.31	ns
Gnpat	glyceronephosphate O-acyltransferase	14712	0.68	0.72	0.59	1.14	0.51	ns
Cks2	CDC28 protein kinase regulatory subunit 2	66197	5.74	6.10	5.36	1.07	0.59	ns
Ifitm2	interferon induced transmembrane protein 2	80876	3.70	3.47	3.77	0.98	-0.57	ns
Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)	12331	2.53	2.65	3.22	0.78	-0.58	ns
2400001E08Rik		66508	4.82	4.53	5.96	0.80	-0.77	ns
EG433216		433216	4.82	4.53	5.96	0.80	-0.77	ns
Tnnc2	troponin C2, fast	21925	0.13	0.21	0.37	0.36	-0.76	ns
Tada3l	transcriptional adaptor 3 (NGG1 homolog, yeast)-like	101206	0.39	0.45	0.60	0.64	-0.43	ns
Nit1	nitrilase 1	27045	0.86	0.83	0.84	1.02	-0.29	ns
Apobec3	apolipoprotein B editing complex 3	80287	0.45	0.44	0.40	1.13	-0.10	ns
D1Ertd622e	DNA segment, Chr 1, ERATO Doi 622, expressed	52392	0.97	0.94	0.56	1.72	0.44	ns
1500035H01Rik	RIKEN cDNA 1500035H01 gene	76568	1.39	1.06	0.80	1.73	0.88	*
Atp13a1	ATPase type 13A1	170759	1.37	1.22	1.34	1.02	0.53	ns
Fbxw5	F-box and WD-40 domain protein 5	30839	0.38	0.49	0.35	1.10	0.03	ns
Gtlf3b	gene trap locus F3b	24083	0.87	0.81	0.92	0.94	-0.04	ns
Ppp2r3c	protein phosphatase 2, regulatory subunit B'', gamma	59032	0.89	0.92	1.09	0.81	-0.52	ns
Fbxo9	f-box protein 9	71538	0.76	0.64	0.52	1.45	0.95	**
Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	80859	1.31	1.51	2.41	0.54	-0.89	*
Fosl1	fos-like antigen 1	14283	0.42	0.58	0.45	0.93	0.37	ns
Ctsb	cathepsin B	13030	3.89	4.45	4.89	0.79	-0.70	ns
Bmi1	Bmi1 polycomb ring finger oncogene	12151	2.00	2.07	1.44	1.38	0.51	ns
Timm10	translocase of inner mitochondrial membrane 10 homolog (yeast)	30059	1.03	0.93	0.75	1.37	0.54	ns
Fbxo6	F-box protein 6	50762	0.33	0.35	0.57	0.57	-0.76	ns
Rfc2	replication factor C (activator 1) 2	19718	2.11	2.22	2.20	0.95	0.20	ns
Gmnn	geminin	57441	2.94	3.09	3.37	0.87	0.11	ns
Cyb561	cytochrome b-561	13056	0.98	1.23	1.49	0.65	-0.68	ns
Vps4a	vacuolar protein sorting 4a (yeast)	116733	0.78	0.80	0.63	1.23	0.83	*
Lyar	Ly1 antibody reactive clone	17089	0.99	1.25	0.98	1.00	0.35	ns
Evi5	ecotropic viral integration site 5	14020	0.64	0.60	0.77	0.83	-0.81	*
Lsm10	U7 snRNP-specific Sm-like protein LSM10	116748	0.63	0.58	0.72	0.87	-0.38	ns
Ddit3	DNA-damage inducible transcript 3	13198	0.45	0.73	0.51	0.88	-0.39	ns
Plagl2	pleiomorphic adenoma gene-like 2	54711	0.31	0.35	0.36	0.85	-0.47	ns
Srp9	signal recognition particle 9	27058	1.94	2.19	2.10	0.92	-0.55	ns
Itgb5	integrin beta 5	16419	4.32	3.70	3.47	1.24	0.91	*
Fbxo25	F-box protein 25	66822	0.60	0.64	0.62	0.96	0.39	ns
Zmat2	zinc finger, matrin type 2	66492	1.04	1.28	1.30	0.79	0.01	ns
Slc35a1	solute carrier family 35 (CMP-sialic acid transporter), member 1	24060	0.82	0.74	0.80	1.02	-0.17	ns
Elf1	E74-like factor 1	13709	1.41	1.64	1.95	0.72	-0.90	*
Hells	helicase, lymphoid specific	15201	3.94	4.73	3.76	1.04	0.24	ns
Trpv4	transient receptor potential cation channel, subfamily V, member 4	63873	1.40	1.00	0.81	1.73	0.68	ns
Sart3	squamous cell carcinoma antigen recognized by T-cells 3	53890	0.94	1.00	0.99	0.95	-0.11	ns
Sfxn1	sideroflexin 1	14057	1.83	1.59	1.07	1.70	0.98	***
Mpg	N-methylpurine-DNA glycosylase	268395	0.34	0.36	0.52	0.65	-0.38	ns
2010311D03Rik	RIKEN cDNA 2010311D03 gene	109129	2.34	1.94	1.83	1.27	0.54	ns
Nup210	nucleoporin 210	54563	1.18	1.42	1.12	1.05	-0.34	ns
Timeless	timeless homolog (Drosophila)	21853	2.55	2.33	1.83	1.38	0.31	ns
Galnt3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3	14425	1.45	1.60	1.17	1.23	0.12	ns
Ptges2	prostaglandin E synthase 2	96979	0.38	0.35	0.29	1.32	-0.01	ns
Frap1	FK506 binding protein 12-rapamycin associated protein 1	56717	0.72	0.72	0.79	0.91	-0.75	ns
Tusc2	tumor suppressor candidate 2	80385	0.27	0.32	0.26	1.05	0.52	ns
Cd276	CD276 antigen	102657	0.61	0.69	0.47	1.28	0.66	ns
Per2	period homolog 2 (Drosophila)	18627	0.45	0.38	0.26	1.74	0.27	ns
Camk1		52163	0.54	0.59	0.75	0.72	-0.45	ns
Calr	calreticulin	12317	7.92	8.40	5.87	1.34	0.76	ns
Ier5	immediate early response 5	15939	1.15	1.34	0.93	1.22	-0.10	ns
Rpl11	ribosomal protein L11	67025	11.46	10.34	10.89	1.05	-0.14	ns

St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	20446	1.03	1.15	0.90	1.14	0.33	ns
Gadd45gip1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	102060	0.60	0.58	0.63	0.94	-0.29	ns
Slc12a2	solute carrier family 12, member 2	20496	2.30	3.06	3.32	0.69	-0.71	ns
Nab1	Ngfi-A binding protein 1	17936	2.69	2.83	2.47	1.08	0.02	ns
Cxcr7	chemokine (C-X-C motif) receptor 7	12778	0.68	0.85	0.07	9.19	0.51	ns
Supt6h	suppressor of Ty 6 homolog (S. cerevisiae)	20926	0.63	0.72	0.46	1.36	0.32	ns
Atp6v0a1	ATPase, H+ transporting, lysosomal V0 subunit A1	11975	0.62	0.51	0.53	1.16	0.58	ns
Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	14664	0.41	0.53	0.54	0.76	-0.87	*
Hmg20b	high mobility group 20 B	15353	0.86	0.89	0.82	1.05	-0.20	ns
Tbca	tubulin cofactor a	21371	4.56	5.73	6.62	0.69	-0.70	ns
Sdc4	syndecan 4	20971	4.86	4.92	4.05	1.19	0.58	ns
Ars2	arsenate resistance protein 2	83701	1.74	1.48	1.35	1.29	0.68	ns
Mybl2	myeloblastosis oncogene-like 2	17865	0.56	0.69	0.82	0.67	-0.34	ns
Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member 2	22791	1.22	1.57	1.45	0.84	-0.05	ns
Vps29	vacuolar protein sorting 29 (S. pombe)	56433	4.55	4.63	4.76	0.95	0.03	ns
Rdm1	RAD52 motif 1	66599	0.66	0.78	0.96	0.69	0.00	ns
Ndrg3	N-myc downstream regulated gene 3	29812	0.73	0.62	0.79	0.92	-0.21	ns
Cpsf1	cleavage and polyadenylation specific factor 1	94230	2.88	2.57	3.24	0.88	0.05	ns
Dnttip1	deoxynucleotidyltransferase, terminal, interacting protein 1	76233	2.13	2.05	2.37	0.89	-0.52	ns
Abhd12	abhydrolase domain containing 12	76192	0.79	0.82	0.66	1.18	0.08	ns
Golga4	golgi autoantigen, golgin subfamily a, 4	54214	1.49	1.37	1.53	0.97	0.31	ns
Nudt21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	68219	4.92	4.74	4.95	0.99	0.47	ns
Diablo	diablo homolog (Drosophila)	66593	1.07	0.98	1.04	1.02	-0.33	ns
Thumpd3	THUMP domain containing 3	14911	1.00	1.04	1.17	0.86	-0.90	*
Ankfy1	ankyrin repeat and FYVE domain containing 1	11736	1.25	1.26	1.46	0.85	-0.59	ns
BC004044	cDNA sequence BC004044	80752	3.24	3.14	1.58	2.04	0.30	ns
Pdzk1ip1	PDZK1 interacting protein 1	67182	4.23	4.21	4.43	0.95	-0.28	ns
Prkag1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	19082	1.26	1.13	1.18	1.06	-0.08	ns
Bin3	bridging integrator 3	57784	1.10	1.15	1.28	0.86	-0.49	ns
Drg2	developmentally regulated GTP binding protein 2	13495	1.00	0.78	0.99	1.01	0.23	ns
Gab1	growth factor receptor bound protein 2-associated protein 1	14388	0.81	0.95	0.63	1.28	0.21	ns
Soat1	sterol O-acyltransferase 1	20652	1.35	1.30	0.76	1.77	-0.22	ns
Gtf2f1	general transcription factor IIF, polypeptide 1	98053	1.09	1.20	0.71	1.53	0.79	ns
Pvrl2	poliovirus receptor-related 2	19294	1.09	1.24	1.28	0.84	-0.46	ns
Otub1	OTU domain, ubiquitin aldehyde binding 1	107260	1.32	1.14	0.89	1.47	0.83	*
Naglu	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)	27419	0.41	0.49	0.73	0.56	-0.45	ns
Mettl9	methyltransferase like 9	59052	3.38	3.06	3.77	0.89	-0.40	ns
Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	67204	12.01	11.94	12.44	0.96	0.04	ns
Got2	glutamate oxaloacetate transaminase 2, mitochondrial	14719	5.93	5.22	4.86	1.21	0.82	*
Sap30	sin3 associated polypeptide	60406	1.45	1.85	2.34	0.62	-0.30	ns
Polr2j	polymerase (RNA) II (DNA directed) polypeptide J	20022	2.19	2.04	2.17	1.00	0.35	ns
Pgls	6-phosphogluconolactonase	66171	1.60	1.78	1.93	0.83	-0.32	ns
Ube2j1	ubiquitin-conjugating enzyme E2, J1	56228	0.51	0.50	0.47	1.06	0.30	ns
Thoc4	THO complex 4	21681	5.55	5.33	5.58	0.99	0.50	ns
Sssca1	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	56390	1.87	1.66	1.27	1.47	0.95	**
Sfrs9	splicing factor, arginine/serine rich 9	108014	3.62	3.41	4.80	0.75	-0.38	ns
Mbd3	methyl-CpG binding domain protein 3	17192	0.75	0.80	0.70	1.07	0.62	ns
Ext1	exostoses (multiple) 1	14042	1.53	1.18	1.88	0.81	-0.44	ns
Rnf146	ring finger protein 146	68031	1.86	1.76	1.39	1.34	0.23	ns
Akap8l	A kinase (PRKA) anchor protein 8-like	54194	0.51	0.38	0.31	1.65	0.96	**
Mrps31	mitochondrial ribosomal protein S31	57312	0.56	0.64	0.73	0.76	-0.27	ns
Rab25	RAB25, member RAS oncogene family	53868	3.09	2.99	2.56	1.20	0.36	ns
Med11	mediator of RNA polymerase II transcription, subunit 11 homolog (S. cerevisiae)	66172	0.41	0.51	0.58	0.71	-0.83	*
Dmap1	DNA methyltransferase 1-associated protein 1	66233	0.39	0.37	0.40	0.97	0.39	ns
Clk2	CDC-like kinase 2	12748	1.77	1.88	1.50	1.17	0.15	ns
Tjp1	tight junction protein 1	21872	3.04	2.99	3.51	0.86	-0.80	ns
Slc25a37	solute carrier family 25, member 37	67712	0.75	0.93	1.25	0.60	-0.77	ns
Stk10	serine/threonine kinase 10	20868	0.35	0.44	0.57	0.62	-0.97	**
Unc13b	unc-13 homolog B (C. elegans)	22249	0.49	0.56	0.68	0.71	-0.51	ns
Itga2b	integrin alpha 2b	16399	0.38	0.36	0.26	1.46	0.86	*
Rpl8	ribosomal protein L8	26961	20.33	19.00	17.43	1.16	0.75	ns
LOC636537		636537	3.67	3.78	4.53	0.81	-0.27	ns
Ssr1		107513	3.67	3.78	4.53	0.81	-0.27	ns
Cyb5b	cytochrome b5 type B	66427	3.43	3.42	2.61	1.31	0.61	ns
Pnpla8	patatin-like phospholipase domain containing 8	67452	1.62	1.66	2.22	0.73	-0.71	ns
Psmc6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	67089	1.34	1.37	0.98	1.36	0.49	ns
Psmc6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	67089	3.28	2.92	3.48	0.94	-0.38	ns
Grhpr	glyoxylate reductase/hydroxypyruvate reductase	76238	0.61	0.63	0.79	0.77	-0.77	ns
Nans	N-acetylneuraminic acid synthase (sialic acid synthase)	94181	0.90	0.90	1.53	0.59	-0.61	ns
Zfp35	zinc finger protein 35	22694	0.53	0.67	0.50	1.05	0.42	ns
Als2	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	74018	0.40	0.38	0.33	1.20	0.90	*
Rgs19	regulator of G-protein signaling 19	56470	0.49	0.53	0.55	0.89	-0.32	ns
Zfml	zinc finger, matrin-like	18139	1.20	1.33	1.33	0.90	-0.66	ns
Gps2	G protein pathway suppressor 2	56310	0.70	0.66	0.62	1.12	0.56	ns
1810019J16Rik	RIKEN cDNA 1810019J16 gene	69073	0.48	0.66	0.76	0.63	-0.89	*
Parp2	poly (ADP-ribose) polymerase family, member 2	11546	0.87	1.02	1.01	0.86	-0.03	ns
Kcnb1		16500	5.43	5.26	4.93	1.09	0.75	ns
Pacsin2		23970	5.43	5.26	4.93	1.09	0.75	ns
Lamb3	laminin, beta 3	16780	1.59	1.86	1.25	1.27	0.67	ns
Wwtr1	WW domain containing transcription regulator 1	97064	4.53	3.63	3.42	1.32	0.74	ns
Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	26912	0.84	0.84	0.52	1.62	0.76	ns
Esd	esterase D/formylglutathione hydrolase	13885	5.92	5.34	6.21	0.95	-0.26	ns
Akr1e1	aldo-keto reductase family 1, member E1	56043	0.62	0.54	0.51	1.21	0.67	ns
Ngly1	N-glycanase 1	59007	0.74	0.68	0.73	1.01	-0.09	ns

Rab15	RAB15, member RAS oncogene family	104886	0.80	1.07	1.80	0.44	-0.87	*
Smc1a	structural maintenance of chromosomes 1A	24061	2.15	2.85	3.64	0.59	-0.03	ns
Zc3h10	zinc finger CCCH type containing 10	103284	0.40	0.39	0.36	1.09	0.42	ns
1500031L02Rik	RIKEN cDNA 1500031L02 gene	66994	1.21	1.36	1.18	1.03	-0.33	ns
Caml	calcium modulating ligand	12328	1.00	1.09	1.12	0.89	-0.18	ns
Eps8l2	EPS8-like 2	98845	1.27	1.04	0.95	1.33	0.18	ns
Med4	mediator of RNA polymerase II transcription, subunit 4 homolog (yeast)	67381	0.80	0.81	0.95	0.84	-0.03	ns
Cldn6	claudin 6	54419	4.38	3.49	2.18	2.00	0.85	*
Ulk2	Unc-51 like kinase 2 (C. elegans)	29869	0.31	0.33	0.40	0.77	-0.65	ns
Rb1	retinoblastoma 1	19645	1.08	1.05	1.82	0.59	-0.71	ns
Map2k5	mitogen activated protein kinase kinase 5	23938	0.61	0.55	0.44	1.35	0.94	**
Pgk1		18655	15.76	15.02	20.42	0.77	-0.38	ns
Ctsz	cathepsin Z	64138	1.27	2.19	2.99	0.42	-0.64	ns
Fhl1	four and a half LIM domains 1	14199	0.50	1.16	0.21	2.31	0.32	ns
Pwp1	PWP1 homolog (S. cerevisiae)	103136	1.53	1.64	1.27	1.19	0.29	ns
Ddx50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	94213	2.40	2.30	2.06	1.16	0.67	ns
Nenf	neuron derived neurotrophic factor	66208	0.57	0.55	0.50	1.14	0.72	ns
1810009A15Rik	RIKEN cDNA 1810009A15 gene	66276	1.20	1.55	1.41	0.85	-0.26	ns
Spsb3	splA/ryanodine receptor domain and SOCS box containing 3	79043	0.56	0.58	0.50	1.12	0.61	ns
Sfxn3	sideroflexin 3	94280	1.16	1.09	0.90	1.29	0.83	*
Gpr97	G protein-coupled receptor 97	54672	0.38	0.43	0.26	1.44	0.76	ns
Tmem54	transmembrane protein 54	66260	0.72	0.73	1.04	0.69	-0.63	ns
Tjp3	tight junction protein 3	27375	1.06	1.11	1.04	1.02	-0.50	ns
Brms1	breast cancer metastasis-suppressor 1	107392	0.66	0.66	0.44	1.50	0.83	*
Slc19a2	solute carrier family 19 (thiamine transporter), member 2	116914	0.33	0.31	0.43	0.76	-0.79	ns
Dclre1a	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	55947	0.65	0.70	0.70	0.92	-0.08	ns
Ccna2	cyclin A2	12428	6.44	5.97	5.72	1.12	0.71	ns
Gins4	GINS complex subunit 4 (Sld5 homolog)	109145	1.76	2.07	2.23	0.79	-0.24	ns
Rap2b	RAP2B, member of RAS oncogene family	74012	0.63	0.54	0.59	1.07	-0.45	ns
Fxc1	fractured callus expressed transcript 1	14356	1.45	1.44	1.61	0.90	-0.40	ns
Ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7	66385	0.68	0.70	0.73	0.93	-0.33	ns
2610029G23Rik	RIKEN cDNA 2610029G23 gene	67683	1.14	1.35	1.91	0.59	-0.60	ns
Kbtbd4	kelch repeat and BTB (POZ) domain containing 4	67136	0.40	0.31	0.34	1.16	0.13	ns
Ncapg2	non-SMC condensin II complex, subunit G2	76044	3.68	3.80	4.03	0.91	0.21	ns
Ddx19a	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a	13680	1.24	1.12	0.80	1.54	0.77	ns
Nab2	Ngfi-A binding protein 2	17937	1.31	0.96	1.10	1.19	-0.01	ns
Ndst2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	17423	0.49	0.35	0.37	1.29	0.79	ns
Dnajc4	DnaJ (Hsp40) homolog, subfamily C, member 4	57431	0.50	0.44	0.47	1.06	0.25	ns
Mkrn2	makorin, ring finger protein, 2	67027	0.74	0.79	0.82	0.91	-0.77	ns
Rad51ap1	RAD51 associated protein 1	19362	1.25	1.42	1.72	0.72	-0.21	ns
Nanp	N-acetylneuraminic acid phosphatase	67311	1.17	1.06	1.21	0.96	-0.29	ns
Lypd3	Ly6/Plaur domain containing 3	72434	0.30	0.32	0.79	0.37	-0.74	ns
Pcna	proliferating cell nuclear antigen	18538	18.13	16.88	16.53	1.09	0.55	ns
Ilf2	interleukin enhancer binding factor 2	67781	1.11	1.34	1.28	0.86	-0.02	ns
Eno3	enolase 3, beta muscle	13808	0.33	0.30	0.24	1.35	0.56	ns
D6Wsu176e	DNA segment, Chr 6, Wayne State University 176, expressed	27999	5.02	4.88	5.16	0.97	-0.54	ns
Ccdc71	coiled-coil domain containing 71	72454	0.62	0.48	0.56	1.10	0.58	ns
Tspan1	tetraspanin 1	66805	2.56	1.90	2.34	1.09	-0.12	ns
Ghr	growth hormone receptor	14600	1.26	0.40	0.32	3.92	0.37	ns
Ap3d1	adaptor-related protein complex 3, delta 1 subunit	11776	1.51	1.59	1.13	1.34	0.29	ns
Plekha1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	101476	1.08	1.09	1.32	0.82	-0.72	ns
Mbd1	methyl-CpG binding domain protein 1	17190	1.61	1.78	1.66	0.97	0.30	ns
Atp5s	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	68055	0.45	0.43	0.35	1.29	0.82	*
Nrm	nurim (nuclear envelope membrane protein)	106582	1.87	1.58	1.45	1.28	0.83	*
Pop5	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae)	117109	1.20	1.17	1.29	0.93	-0.02	ns
Kpna4	karyopherin (importin) alpha 4	16649	1.72	1.79	1.60	1.07	-0.21	ns
Insig2	insulin induced gene 2	72999	0.86	0.81	0.83	1.03	0.54	ns
Ube2v2	ubiquitin-conjugating enzyme E2 variant 2	70620	1.70	1.57	1.85	0.92	-0.23	ns
Nrarp	Notch-regulated ankyrin repeat protein	67122	0.57	0.63	0.67	0.84	-0.22	ns
Btd	biotinidase	26363	0.58	0.56	0.64	0.90	0.02	ns
Ptges3	prostaglandin E synthase 3 (cytosolic)	56351	9.51	9.04	8.43	1.12	0.14	ns
Itm2b	integral membrane protein 2B	16432	8.72	7.46	11.68	0.74	-0.65	ns
Higd2a	HIG1 domain family, member 2A	67044	4.57	4.28	5.60	0.81	-0.41	ns
Tmem176b	transmembrane protein 176B	65963	0.75	1.20	2.24	0.33	-0.65	ns
Sdhb	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	67680	2.53	2.72	2.60	0.97	-0.03	ns
1810007M14Rik	RIKEN cDNA 1810007M14 gene	67367	2.53	1.72	2.38	1.06	-0.24	ns
Sh3glb1	SH3-domain GRB2-like B1 (endophilin)	54673	3.50	3.24	3.37	1.03	-0.33	ns
B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	14595	0.61	0.71	0.83	0.73	-0.70	ns
Pum2	pumilio 2 (Drosophila)	80913	4.96	4.58	4.77	1.03	0.45	ns
Narg1	NMDA receptor-regulated gene 1	74838	2.73	2.78	2.39	1.13	0.41	ns
Bhlhb2	basic helix-loop-helix domain containing, class B2	20893	1.66	1.97	2.59	0.64	-0.43	ns
Exo1	exonuclease 1	26909	0.55	0.56	0.59	0.92	-0.57	ns
Faim	Fas apoptotic inhibitory molecule	23873	0.62	0.67	0.61	1.01	0.53	ns
Myo9b	myosin IXb	17925	0.74	0.71	0.85	0.87	0.21	ns
Itfg2	integrin alpha FG-GAP repeat containing 2	101142	0.38	0.33	0.27	1.44	0.78	ns
Prim2	DNA primase, p58 subunit	19076	1.09	0.98	0.89	1.22	0.81	ns
Rabl3	RAB, member of RAS oncogene family-like 3	67657	0.71	0.55	0.61	1.17	0.02	ns
Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	27416	0.44	0.40	0.34	1.31	0.74	ns
A630042L21Rik	RIKEN cDNA A630042L21 gene	106894	0.43	0.42	0.43	1.01	0.50	ns
1110059G10Rik	RIKEN cDNA 1110059G10 gene	66202	1.06	0.98	1.03	1.03	0.57	ns
Mvk	mevalonate kinase	17855	0.40	0.30	0.22	1.75	0.87	*
Tiam1	T-cell lymphoma invasion and metastasis 1	21844	2.63	2.60	2.39	1.10	0.60	ns
Mapk7	mitogen activated protein kinase 7	23939	0.25	0.25	0.37	0.68	-0.85	*
Cfl2	cofilin 2, muscle	12632	2.22	1.98	1.96	1.12	0.59	ns
Cdyl	chromodomain protein, Y chromosome-like	12593	0.58	0.60	0.76	0.76	-0.58	ns
Hist1h2bc	histone cluster 1, H2bc	68024	1.09	1.02	0.98	1.11	0.40	ns

St14	suppression of tumorigenicity 14 (colon carcinoma)	19143	5.26	5.17	4.08	1.28	0.78	ns
Psme3	proteaseome (prosome, macropain) 28 subunit, 3	19192	0.86	0.84	0.81	1.06	0.28	ns
0610009B22Rik	RIKEN cDNA 0610009B22 gene	66050	1.94	1.72	2.11	0.91	-0.53	ns
Prkcz	protein kinase C, zeta	18762	0.55	0.51	0.51	1.07	-0.17	ns
Ufd1l	ubiquitin fusion degradation 1 like	22230	1.13	1.04	1.23	0.91	-0.73	ns
Stx8	syntaxin 8	55943	0.78	0.85	0.94	0.83	-0.10	ns
Tcfcp2l1	transcription factor CP2-like 1	81879	4.44	4.31	3.19	1.38	0.85	*
Trip10	thyroid hormone receptor interactor 10	106628	1.92	2.17	1.78	1.08	0.60	ns
Rtn3	reticulon 3	20168	7.50	7.06	5.31	1.41	0.78	ns
Hes1	hairy and enhancer of split 1 (Drosophila)	15205	0.83	0.80	0.58	1.42	0.74	ns
Slc12a9	solute carrier family 12 (potassium/chloride transporters), member 9	83704	0.31	0.36	0.38	0.82	-0.33	ns
Mrpl10	mitochondrial ribosomal protein L10	107732	1.51	1.24	1.56	0.96	-0.06	ns
Ifrg15	interferon alpha responsive gene	64164	3.53	2.87	2.64	1.33	0.49	ns
Rbm8a	RNA binding motif protein 8a	60365	5.39	6.18	4.61	1.16	0.37	ns
Vrk3	vaccinia related kinase 3	101568	1.12	1.03	1.18	0.94	-0.06	ns
Unc119	unc-119 homolog (C. elegans)	22248	0.59	0.65	0.48	1.22	0.31	ns
Tmem85	transmembrane protein 85	68032	1.64	1.24	1.55	1.05	0.42	ns
Aifm1	apoptosis-inducing factor, mitochondrion-associated 1	26926	0.97	0.85	1.26	0.77	-0.45	ns
Adcy6	adenylate cyclase 6	11512	2.04	1.57	1.50	1.35	0.17	ns
Slc25a46	solute carrier family 25, member 46	67453	2.09	2.25	2.32	0.90	0.19	ns
Aff1	AF4/FMR2 family, member 1	17355	1.11	1.08	0.97	1.14	-0.10	ns
Mrp63	mitochondrial ribosomal protein 63	67840	1.45	1.50	1.84	0.78	-0.74	ns
Vps45	vacuolar protein sorting 45 (yeast)	22365	0.49	0.55	0.49	1.00	-0.27	ns
Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	18720	1.41	1.62	1.15	1.22	0.28	ns
Nsbp1	nucleosome binding protein 1	50887	1.14	1.28	1.86	0.61	-0.74	ns
BC004022	cDNA sequence BC004022	80750	0.57	0.51	0.71	0.80	-0.19	ns
Tcfcp2	transcription factor CP2	21422	0.62	0.52	0.62	0.99	-0.13	ns
Stx2	syntaxin 2	13852	0.44	0.46	0.46	0.95	0.21	ns
Tcfap4	transcription factor AP4	83383	0.41	0.43	0.42	0.96	-0.48	ns
Zcchc14	zinc finger, CCHC domain containing 14	142682	0.84	0.68	0.52	1.59	0.86	*
Sp1	trans-acting transcription factor 1	20683	5.18	5.55	4.72	1.09	0.59	ns
Cenpm	centromere protein M	66570	0.68	0.75	1.02	0.66	-0.29	ns
4733401H18Rik	RIKEN cDNA 4733401H18 gene	66706	0.67	0.64	0.72	0.92	0.00	ns
Gstt1	glutathione S-transferase, theta 1	14871	0.40	0.63	0.62	0.64	-0.16	ns
Mnt	max binding protein	17428	0.82	1.01	0.94	0.87	-0.31	ns
Tep1	telomerase associated protein 1	21745	0.32	0.26	0.30	1.06	-0.18	ns
Tm9sf1	transmembrane 9 superfamily member 1	74140	2.10	1.95	2.51	0.83	-0.65	ns
Plekhg2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	101497	0.66	0.69	0.71	0.93	-0.47	ns
Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1	58801	1.12	1.34	2.18	0.51	-0.52	ns
Sdf2l1	stromal cell-derived factor 2-like 1	64136	0.68	0.69	0.72	0.95	0.31	ns
Fxyd4	FXYD domain-containing ion transport regulator 4	108017	2.48	3.22	0.59	4.16	0.27	ns
Pax8	paired box gene 8	18510	2.39	2.24	1.82	1.31	0.73	ns
Pfn2	profilin 2	18645	1.21	1.28	0.98	1.23	-0.14	ns
Krt23	keratin 23	94179	0.22	0.25	0.14	1.57	-0.28	ns
Nme7	non-metastatic cells 7, protein expressed in	171567	1.08	0.97	0.69	1.57	0.54	ns
2610024G14Rik	RIKEN cDNA 2610024G14 gene	56412	0.37	0.41	0.43	0.87	-0.87	*
Sec11a	SEC11 homolog A (S. cerevisiae)	56529	2.74	2.70	3.03	0.90	-0.27	ns
Orc2l	origin recognition complex, subunit 2-like (S. cerevisiae)	18393	0.63	0.86	0.64	0.99	-0.11	ns
Nfu1	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	56748	1.48	1.46	1.65	0.89	-0.41	ns
Lims1	LIM and senescent cell antigen-like domains 1	110829	1.70	1.36	1.18	1.44	0.49	ns
Trappc5	trafficking protein particle complex 5	66682	0.61	0.63	0.80	0.76	-0.10	ns
Bcas2	breast carcinoma amplified sequence 2	68183	1.69	2.01	1.81	0.93	-0.32	ns
Gbp2	guanylate nucleotide binding protein 2	14469	0.02	0.06	0.54	0.04	-0.62	ns
Usf2	upstream transcription factor 2	22282	0.54	0.49	0.62	0.86	-0.57	ns
Faf1	Fas-associated factor 1	14084	1.70	1.65	1.82	0.93	-0.02	ns
Nat5	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae)	67877	2.38	2.21	2.96	0.80	-0.63	ns
Rbm9	RNA binding motif protein 9	93686	0.68	0.63	0.77	0.88	-0.53	ns
Crcp	calcitonin gene-related peptide-receptor component protein	12909	0.37	0.47	0.46	0.82	-0.62	ns
Arl4d	ADP-ribosylation factor-like 4D	80981	0.39	0.36	0.33	1.20	0.44	ns
LOC638935		638935	0.38	0.52	0.38	0.98	0.14	ns
Padi2		18600	0.38	0.52	0.38	0.98	0.14	ns
Hspa4l	heat shock protein 4 like	18415	0.89	1.00	1.10	0.80	-0.22	ns
Apip	APAF1 interacting protein	56369	0.65	0.55	0.42	1.56	0.11	ns
Srf	serum response factor	20807	0.63	0.73	0.46	1.38	0.45	ns
Slc12a7	solute carrier family 12, member 7	20499	0.71	0.94	1.12	0.63	-0.98	***
Dynll2	dynein light chain LC8-type 2	68097	2.20	2.12	2.05	1.07	0.51	ns
Entpd2	ectonucleoside triphosphate diphosphohydrolase 2	12496	0.32	0.35	0.62	0.51	-0.89	*
Cenpk	centromere protein K	60411	1.30	1.71	2.46	0.53	-0.57	ns
Irf2	interferon regulatory factor 2	16363	0.32	0.28	0.50	0.64	-0.57	ns
LOC666899		666899	18.67	18.01	17.99	1.03	-0.15	ns
Rpl30		19946	18.67	18.01	17.99	1.03	-0.15	ns
Elf2	E74-like factor 2	69257	1.30	1.12	1.20	1.08	-0.18	ns
rp9	retinitis pigmentosa 9 (human)	55934	2.24	2.11	1.87	1.19	0.78	ns
Rad51	RAD51 homolog (S. cerevisiae)	19361	1.89	1.60	1.80	1.04	0.48	ns
Cldn4	claudin 4	12740	6.76	4.57	3.19	2.11	0.81	ns
Vps72	vacuolar protein sorting 72 (yeast)	21427	2.00	2.14	1.64	1.21	0.60	ns
Asna1	arsA (bacterial) arsenite transporter, ATP-binding, homolog 1	56495	2.62	2.35	2.65	0.98	0.41	ns
Ifit2	interferon-induced protein with tetratricopeptide repeats 2	15958	1.36	1.03	1.14	1.19	0.47	ns
Epb4.1l4b	erythrocyte protein band 4.1-like 4b	54357	1.06	0.90	1.29	0.81	-0.35	ns
Dgat1	diacylglycerol O-acyltransferase 1	13350	0.84	0.72	1.05	0.80	-0.41	ns
Fxyd5	FXYD domain-containing ion transport regulator 5	18301	0.13	0.19	0.74	0.18	-0.50	ns
Mknk2	MAP kinase-interacting serine/threonine kinase 2	17347	5.26	4.39	4.14	1.26	0.58	ns
Irf6	interferon regulatory factor 6	54139	3.09	3.11	2.32	1.33	0.02	ns
Ppt2	palmitoyl-protein thioesterase 2	54397	0.59	0.82	0.67	0.88	-0.40	ns
Nola1	nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	68147	1.75	2.22	1.69	1.03	0.00	ns
Hus1	Hus1 homolog (S. pombe)	15574	0.50	0.45	0.52	0.96	-0.03	ns

Mark3	MAP/microtubule affinity-regulating kinase 3	17169	2.44	2.72	2.73	0.89	-0.33	ns
Rnf128	ring finger protein 128	66889	2.41	2.65	3.02	0.79	-0.85	*
Prss8	protease, serine, 8 (prostasin)	76560	1.00	0.89	0.76	1.32	0.57	ns
Dci	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)	13177	1.91	1.64	0.88	2.15	0.78	ns
Fem1b	feminization 1 homolog b (C. elegans)	14155	3.94	3.62	3.64	1.08	0.60	ns
Slc7a5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	20539	1.15	1.57	0.82	1.40	0.47	ns
1110058L19Rik	RIKEN cDNA 1110058L19 gene	68002	0.84	0.90	0.57	1.48	0.37	ns
Ctcf	CCCTC-binding factor	13018	2.40	2.88	2.94	0.81	-0.33	ns
1110031I02Rik	RIKEN cDNA 1110031I02 gene	66179	0.54	0.58	0.77	0.69	-0.17	ns
Agtpbp1		67269	0.73	0.66	0.54	1.35	0.73	ns
Dbf4	DBF4 homolog (S. cerevisiae)	27214	2.48	2.55	3.26	0.76	-0.69	ns
Dph1		116905	0.48	0.56	0.37	1.30	-0.06	ns
Rpia	ribose 5-phosphate isomerase A	19895	0.78	1.18	1.07	0.73	-0.13	ns
Wdr33	WD repeat domain 33	74320	0.85	0.87	0.86	0.98	0.16	ns
Recql	RecQ protein-like	19691	0.34	0.45	0.62	0.56	-0.91	*
Rfc1	replication factor C (activator 1) 1	19687	2.02	2.19	1.91	1.05	0.50	ns
Gtf2ird2	GTF2I repeat domain containing 2	114674	0.43	0.40	0.48	0.88	-0.27	ns
Ccdc22	coiled-coil domain containing 22	54638	0.57	0.59	0.92	0.61	-0.25	ns
Hbegf	heparin-binding EGF-like growth factor	15200	1.48	1.37	1.05	1.41	0.75	ns
Nucb2	nucleobindin 2	53322	0.39	0.45	0.83	0.47	-0.64	ns
Wbscr27	Williams Beuren syndrome chromosome region 27 (human)	79565	0.41	0.36	0.31	1.34	0.69	ns
Ftl1	ferritin light chain 1	14325	8.88	7.34	8.21	1.08	-0.01	ns
Ctsh	cathepsin H	13036	2.33	2.52	3.10	0.75	-0.28	ns
Adsl	adenylosuccinate lyase 1	11564	0.82	0.72	0.71	1.15	-0.05	ns
Fxyd3	FXYD domain-containing ion transport regulator 3	17178	0.16	0.26	1.60	0.10	-0.58	ns
Mbd6	methyl-CpG binding domain protein 6	110962	0.57	0.54	0.45	1.26	0.05	ns
Terf1	telomeric repeat binding factor 1	21749	0.61	0.65	0.75	0.80	-0.26	ns
Apool	apolipoprotein O-like	68117	0.32	0.26	0.39	0.81	-0.44	ns
Phf21a	PHD finger protein 21A	192285	0.52	0.48	0.50	1.05	-0.08	ns
Cd97	CD97 antigen	26364	0.56	0.63	1.11	0.51	-0.54	ns
Zfp275	zinc finger protein 275	27081	0.60	0.58	1.15	0.52	-0.69	ns
Kctd9	potassium channel tetramerisation domain containing 9	105440	0.54	0.57	0.68	0.78	-0.30	ns
Dusp16	dual specificity phosphatase 16	70686	1.37	1.66	2.16	0.63	-0.52	ns
Rad9	RAD9 homolog (S. pombe)	19367	0.85	0.79	0.58	1.44	0.97	**
Hgfac	hepatocyte growth factor activator	54426	0.61	0.60	1.14	0.53	-0.78	ns
Zfand1	zinc finger, AN1-type domain 1	66361	0.56	0.56	0.49	1.14	-0.39	ns
Jrk	jerky	16469	0.42	0.35	0.39	1.07	0.46	ns
Tpd52l1	tumor protein D52-like 1	21987	0.86	0.32	0.08	10.62	0.43	ns
Hoxb5	homeo box B5	15413	1.32	0.78	0.65	2.04	0.31	ns
Kif5b	kinesin family member 5B	16573	1.62	1.90	2.07	0.78	-0.50	ns
Cab39	calcium binding protein 39	12283	1.74	1.66	1.54	1.12	0.11	ns
Stx7	syntaxin 7	53331	2.66	2.29	2.08	1.27	0.38	ns
Mlx	MAX-like protein X	21428	0.45	0.39	0.47	0.95	0.26	ns
D10Ertd322e	DNA segment, Chr 10, ERATO Doi 322, expressed	67270	2.50	2.36	2.45	1.02	-0.30	ns
Xpo1	exportin 1, CRM1 homolog (yeast)	103573	4.02	3.88	4.62	0.87	-0.45	ns
Golga5	golgi autoantigen, golgin subfamily a, 5	27277	1.63	1.59	1.77	0.92	-0.37	ns
Rras	Harvey rat sarcoma oncogene, subgroup R	20130	0.72	0.71	1.01	0.70	-0.22	ns
Lad1	ladinin	16763	6.25	5.34	4.90	1.27	0.89	*
Anapc7	anaphase promoting complex subunit 7	56317	1.36	1.46	1.48	0.92	-0.18	ns
Exosc9	exosome component 9	50911	1.42	1.68	1.39	1.02	-0.16	ns
Pik3r2	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	18709	0.80	0.88	0.80	0.99	0.26	ns
Anxa11	annexin A11	11744	1.32	1.18	0.73	1.82	0.26	ns
Scnn1b	sodium channel, nonvoltage-gated 1 beta	20277	0.09	0.14	0.15	0.58	-0.66	ns
Crlf1	cytokine receptor-like factor 1	12931	1.04	0.79	1.00	1.03	0.38	ns
Pkmyt1	protein kinase, membrane associated tyrosine/threonine 1	268930	1.31	1.23	0.98	1.32	0.75	ns
Ggta1	glycoprotein galactosyltransferase alpha 1, 3	14594	0.49	0.63	0.40	1.23	-0.03	ns
Vnn1	vanin 1	22361	0.45	0.28	0.47	0.95	-0.43	ns
Ripk4	receptor-interacting serine-threonine kinase 4	72388	3.23	3.66	3.59	0.89	-0.71	ns
Pus3	pseudouridine synthase 3	67049	0.42	0.27	0.21	1.95	0.90	*
Foxa1	forkhead box A1	15375	1.17	1.18	1.09	1.07	-0.49	ns
Oxr1	oxidation resistance 1	170719	2.80	2.85	4.88	0.57	-0.89	*
Hspa9	heat shock protein 9	15526	3.00	3.68	3.70	0.81	-0.35	ns
Nudt4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	71207	1.67	1.37	1.01	1.64	0.28	ns
Prdx2	peroxiredoxin 2	21672	5.38	5.29	5.38	0.99	0.14	ns
Cbr2	carbonyl reductase 2	12409	0.32	0.40	0.38	0.82	-0.64	ns
Fbxo8	F-box protein 8	50753	0.75	0.72	0.92	0.81	-0.04	ns
Stk3	serine/threonine kinase 3 (Ste20, yeast homolog)	56274	1.26	1.11	1.70	0.74	-0.63	ns
Mtf2	metal response element binding transcription factor 2	17765	1.48	1.41	1.44	1.02	0.14	ns
Furin	furin (paired basic amino acid cleaving enzyme)	18550	0.59	0.49	0.53	1.10	0.48	ns
Mtx1	metaxin 1	17827	2.72	2.72	2.18	1.25	0.61	ns
Pcm1	pericentriolar material 1	18536	0.95	1.17	1.00	0.94	0.29	ns
Dad1	defender against cell death 1	13135	3.20	2.65	3.12	1.02	0.22	ns
Osgep	O-sialoglycoprotein endopeptidase	66246	0.90	0.77	0.68	1.32	0.07	ns
Nup160	nucleoporin 160	59015	1.46	1.19	1.26	1.15	0.23	ns
Fzd2	frizzled homolog 2 (Drosophila)	57265	1.04	0.70	0.35	2.93	0.90	*
Kdelr3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	105785	0.63	0.79	0.67	0.94	0.42	ns
Cenpo	centromere protein O	52504	0.37	0.36	0.41	0.91	-0.44	ns
Ccdc43	coiled-coil domain containing 43	52715	1.10	1.23	1.25	0.87	0.23	ns
Wasf1	WASP family 1	83767	0.36	0.38	0.25	1.45	0.66	ns
Stambpl1	Stam binding protein like 1	76630	0.49	0.59	0.71	0.69	-0.23	ns
Arhgef18	rho/rac guanine nucleotide exchange factor (GEF) 18	102098	1.08	1.00	1.15	0.94	0.04	ns
Pdha1	pyruvate dehydrogenase E1 alpha 1	18597	1.49	1.74	1.91	0.77	0.23	ns
Nudcd2	NudC domain containing 2	52653	2.32	2.62	3.24	0.71	-0.64	ns
Ncstn	nicastrin	59287	0.47	0.52	0.49	0.94	-0.47	ns

Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	27279	3.37	3.48	2.95	1.14	0.60	ns
Raly	hnRNP-associated with lethal yellow	19383	1.19	1.08	1.15	1.03	-0.11	ns
Shfm1	split hand/foot malformation (ectrodactyly) type 1	20422	4.19	4.09	5.08	0.82	-0.35	ns
Yipf5	Yip1 domain family, member 5	67180	1.07	1.14	1.06	1.00	0.45	ns
Trim8	tripartite motif protein 8	93679	1.59	1.55	0.92	1.73	0.79	ns
Dgka	diacylglycerol kinase, alpha	13139	0.71	0.70	0.72	0.99	-0.46	ns
Rtp4	receptor transporter protein 4	67775	0.06	0.16	2.64	0.02	-0.69	ns
Hint3	histidine triad nucleotide binding protein 3	66847	0.39	0.38	0.36	1.09	-0.04	ns
Traf3	Tnf receptor-associated factor 3	22031	0.85	0.84	0.88	0.96	0.06	ns
Taf6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	21343	0.89	0.87	0.93	0.95	-0.29	ns
Ncoa1	nuclear receptor coactivator 1	17977	0.64	0.77	0.96	0.67	-0.79	ns
Hoxd10	homeo box D10	15430	0.38	0.38	0.22	1.68	0.03	ns
Mafk	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	17135	0.41	0.50	0.52	0.79	-0.53	ns
Ybx1	Y box protein 1	22608	7.30	6.92	7.86	0.92	-0.48	ns
EG433184		433184	26.06	22.71	19.29	1.34	0.95	**
EG666342		666342	26.06	22.71	19.29	1.34	0.95	**
Gapdh		14433	26.06	22.71	19.29	1.34	0.95	**
Gclm	glutamate-cysteine ligase , modifier subunit	14630	1.14	1.32	0.84	1.36	0.51	ns
Notch1	Notch gene homolog 1 (Drosophila)	18128	1.91	1.88	1.22	1.56	0.86	*
Etv3	ets variant gene 3	27049	0.47	0.58	0.73	0.65	-0.94	**
Sirt1	sirtuin 1 ((silent mating type information regulation 2, homolog) 1 (S. cerevisiae)	93759	0.79	0.76	0.61	1.28	0.16	ns
Stk11	serine/threonine kinase 11	20869	1.34	1.08	1.04	1.28	0.66	ns
Egln3	EGL nine homolog 3 (C. elegans)	112407	1.93	2.18	5.03	0.38	-0.55	ns
B4galnt1	beta-1,4-N-acetyl-galactosaminyl transferase 1	14421	0.74	0.80	0.75	0.97	-0.34	ns
Lsm5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	66373	1.66	1.86	2.44	0.68	-0.61	ns
Clock	circadian locomoter output cycles kaput	12753	0.47	0.60	0.62	0.75	-0.34	ns
Mpdz	multiple PDZ domain protein	17475	0.64	0.59	0.56	1.13	0.53	ns
Impa2	inositol (myo)-1(or 4)-monophosphatase 2	114663	0.37	0.27	0.39	0.93	-0.24	ns
2410002O22Rik	RIKEN cDNA 2410002O22 gene	66975	0.31	0.48	0.60	0.52	-0.87	*
Hspg2	perlecan (heparan sulfate proteoglycan 2)	15530	0.65	0.76	0.56	1.16	0.18	ns
Capn5	calpain 5	12337	1.07	1.14	0.92	1.16	0.56	ns
Rab8a	RAB8A, member RAS oncogene family	17274	1.71	1.64	2.09	0.81	-0.43	ns
Kcmf1	potassium channel modulatory factor 1	74287	2.14	2.30	3.22	0.66	-0.72	ns
Inmt	indolethylamine N-methyltransferase	21743	1.09	0.59	0.09	11.82	0.68	ns
Fech	ferrochelatase	14151	0.50	0.48	0.65	0.77	-0.55	ns
2810428I15Rik	RIKEN cDNA 2810428I15 gene	66462	0.90	0.92	0.88	1.01	0.17	ns
S100a13	S100 calcium binding protein A13	20196	0.62	0.80	0.51	1.21	0.48	ns
Cd59a	CD59a antigen	12509	0.69	0.46	0.26	2.61	0.74	ns
Cdc42ep5	CDC42 effector protein (Rho GTPase binding) 5	58804	1.05	0.92	0.77	1.36	-0.05	ns
Pcbd1	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	13180	2.84	2.70	2.25	1.26	0.37	ns
Pank1	pantothenate kinase 1	75735	0.36	0.61	0.44	0.83	-0.39	ns
Cxcl16	chemokine (C-X-C motif) ligand 16	66102	0.67	1.06	1.91	0.35	-0.56	ns
2410004L22Rik	RIKEN cDNA 2410004L22 gene	76478	0.35	0.54	0.65	0.54	-0.30	ns
Cops7b	COP9 (constitutive photomorphogenic) homolog, subunit 7b (Arabidopsis thaliana)	26895	0.63	0.60	0.44	1.43	0.72	ns
Tnnt2	troponin T2, cardiac	21956	0.14	0.20	0.43	0.33	-0.55	ns
Nudt2	nudix (nucleoside diphosphate linked moiety X)-type motif 2	66401	0.72	0.67	0.79	0.90	-0.27	ns
Psd3	pleckstrin and Sec7 domain containing 3	234353	0.54	0.52	0.44	1.21	0.68	ns
Rdh11	retinol dehydrogenase 11	17252	0.89	0.98	1.55	0.57	-0.54	ns
Nit2	nitrilase family, member 2	52633	0.41	0.43	0.67	0.61	-0.81	*
BC016423	cDNA sequence BC016423	105203	1.06	1.10	1.17	0.90	-0.73	ns
Fads3	fatty acid desaturase 3	60527	0.69	0.45	0.24	2.90	0.86	*
AI837181	expressed sequence AI837181	107242	0.81	0.66	0.39	2.04	0.86	*
Rce1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	19671	0.92	0.85	0.66	1.39	0.90	*
Cyp39a1	cytochrome P450, family 39, subfamily a, polypeptide 1	56050	0.89	0.76	0.60	1.48	0.82	*
Grik5	glutamate receptor, ionotropic, kainate 5 (gamma 2)	14809	0.36	0.31	0.34	1.06	0.34	ns
Sh3gl2	SH3-domain GRB2-like 2	20404	0.63	0.34	0.06	10.17	0.98	***
Zkscan1	zinc finger with KRAB and SCAN domains 1	74570	1.09	1.06	0.93	1.17	0.65	ns
Cdh2	cadherin 2	12558	0.45	0.23	0.00	163.84	0.61	ns
Chmp1b	chromatin modifying protein 1B	67064	0.78	0.87	1.12	0.69	-0.69	ns
Aqp5	aquaporin 5	11830	0.15	0.19	0.17	0.89	-0.50	ns
Zcchc10	zinc finger, CCHC domain containing 10	67966	0.32	0.36	0.45	0.70	-0.91	*
Arf6	ADP-ribosylation factor 6	11845	8.76	9.19	9.46	0.92	-0.62	ns
Thex1	three prime histone mRNA exonuclease 1	67276	1.00	1.21	1.59	0.63	-0.39	ns
Eno2	enolase 2, gamma neuronal	13807	0.32	0.30	0.58	0.56	-0.60	ns
Pkp3	plakophilin 3	56460	0.78	0.78	0.92	0.85	-0.43	ns
Phlda1	pleckstrin homology-like domain, family A, member 1	21664	3.06	3.37	2.81	1.09	-0.12	ns
Abcd1	ATP-binding cassette, sub-family D (ALD), member 1	11666	0.48	0.34	0.29	1.64	0.86	*
Pdcd4		18569	2.90	2.66	1.15	2.52	0.67	ns
Cdc2l1	cell division cycle 2-like 1	12537	1.29	1.28	1.41	0.91	-0.07	ns
Slc30a4	solute carrier family 30 (zinc transporter), member 4	22785	1.45	1.26	1.71	0.84	-0.12	ns
Alg9	asparagine-linked glycosylation 9 homolog (yeast, alpha 1,2 mannosyltransferase)	102580	0.62	0.50	0.62	1.00	0.45	ns
Ap4m1	adaptor-related protein complex AP-4, mu 1	11781	0.37	0.26	0.33	1.11	-0.46	ns
Epc1	enhancer of polycomb homolog 1 (Drosophila)	13831	1.09	1.29	1.41	0.77	-0.29	ns
Trim39	tripartite motif protein 39	79263	0.48	0.38	0.32	1.48	0.65	ns
Birc2	baculoviral IAP repeat-containing 2	11797	0.73	0.63	0.31	2.34	0.95	**
Fanca	Fanconi anemia, complementation group A	14087	1.11	1.04	0.70	1.57	0.53	ns
Rfxap	regulatory factor X-associated protein	170767	0.40	0.45	0.58	0.69	-0.17	ns
Pias4	protein inhibitor of activated STAT 4	59004	0.59	0.52	0.49	1.18	-0.04	ns
Pus1	pseudouridine synthase 1	56361	0.71	0.54	0.50	1.41	0.77	ns
Abcb1b	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	18669	0.14	0.14	0.37	0.38	-0.72	ns
Psmd4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	19185	3.27	3.55	3.28	0.99	0.45	ns

Pabpc1	poly A binding protein, cytoplasmic 1	18458	18.40	18.58	18.99	0.96	-0.61	ns
Tuba1a	tubulin, alpha 1A	22142	9.31	10.01	11.58	0.80	-0.42	ns
Idh3b	isocitrate dehydrogenase 3 (NAD+) beta	170718	3.38	3.11	2.83	1.19	0.25	ns
Sepx1	selenoprotein X 1	27361	1.41	1.27	0.98	1.42	0.94	**
Rab3d	RAB3D, member RAS oncogene family	19340	0.71	0.66	0.63	1.12	0.67	ns
Pbx2	pre B-cell leukemia transcription factor 2	18515	0.99	0.96	0.68	1.46	0.70	ns
Skap2	src family associated phosphoprotein 2	54353	1.58	1.68	1.87	0.84	-0.61	ns
Rpn2	ribophorin II	20014	2.91	3.11	4.02	0.72	-0.52	ns
Ufm1	ubiquitin-fold modifier 1	67890	1.37	1.18	1.21	1.12	-0.05	ns
Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	12608	3.28	3.33	4.43	0.74	-0.91	*
Aqp2	aquaporin 2	11827	5.03	2.92	0.12	41.30	1.00	
Nubp1	nucleotide binding protein 1	26425	1.39	1.28	1.70	0.81	-0.78	ns
Bmp7	bone morphogenetic protein 7	12162	0.62	0.88	0.41	1.49	0.16	ns
Sgol1	shugoshin-like 1 (S. pombe)	72415	1.04	1.23	0.98	1.05	0.58	ns
Rassf7	Ras association (RalGDS/AF-6) domain family 7	66985	1.72	1.73	1.82	0.94	-0.40	ns
Celsr1	cadherin EGF LAG seven-pass G-type receptor 1	12614	1.39	1.23	1.25	1.10	0.06	ns
Ift57	intraflagellar transport 57 homolog (Chlamydomonas)	73916	0.78	0.86	1.03	0.76	-0.74	ns
Nfil3	nuclear factor, interleukin 3, regulated	18030	0.26	0.29	0.59	0.44	-0.93	**
Maff	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	17133	0.46	0.53	0.95	0.48	-0.64	ns
Ift74	intraflagellar transport 74 homolog (Chlamydomonas)	67694	0.73	0.81	0.75	0.97	-0.57	ns
B230120H23Rik	RIKEN cDNA B230120H23 gene	65964	0.44	0.45	0.41	1.07	-0.19	ns
St3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	20442	0.08	0.13	0.43	0.19	-0.61	ns
Nek3	NIMA (never in mitosis gene a)-related expressed kinase 3	23954	0.41	0.31	0.34	1.18	0.63	ns
Gdf15	growth differentiation factor 15	23886	1.80	2.25	3.13	0.57	-0.14	ns
Necap2	NECAP endocytosis associated 2	66147	0.78	0.88	1.01	0.77	-0.78	ns
2310047O13Rik	RIKEN cDNA 2310047O13 gene	66960	0.63	0.45	0.50	1.23	0.50	ns
Nosip	nitric oxide synthase interacting protein	66394	0.48	0.49	0.53	0.90	-0.23	ns
St7	Suppression of tumorigenicity 7	64213	0.38	0.43	0.36	1.07	0.26	ns
Rb1cc1	RB1-inducible coiled-coil 1	12421	0.75	0.73	0.47	1.59	0.61	ns
Skp2	S-phase kinase-associated protein 2 (p45)	27401	0.77	0.82	1.26	0.61	-0.63	ns
Bcl10	B-cell leukemia/lymphoma 10	12042	1.62	1.72	1.46	1.10	0.14	ns
Blzf1	basic leucine zipper nuclear factor 1	66352	0.51	0.44	0.35	1.47	0.84	*
Inadl	InaD-like (Drosophila)	12695	0.81	0.71	0.63	1.29	0.38	ns
Uxt	ubiquitously expressed transcript	22294	0.37	0.38	0.74	0.50	-0.56	ns
Pex7	peroxisome biogenesis factor 7	18634	0.86	0.67	0.77	1.11	-0.04	ns
Bak1	BCL2-antagonist/killer 1	12018	0.41	0.48	0.34	1.19	0.58	ns
Lyrm5	LYR motif containing 5	67636	0.73	0.90	0.69	1.05	-0.35	ns
2310033P09Rik	RIKEN cDNA 2310033P09 gene	67862	0.57	0.55	0.74	0.76	-0.55	ns
Gpatch1	G patch domain containing 1	67471	0.28	0.33	0.43	0.65	-0.94	**
EG433182		433182	20.57	17.58	18.50	1.11	0.70	ns
Eno1		13806	20.57	17.58	18.50	1.11	0.70	ns
Daxx	Fas death domain-associated protein	13163	0.79	0.69	0.60	1.31	0.85	*
Gltp	glycolipid transfer protein	56356	4.17	3.69	5.00	0.83	-0.55	ns
Fads2	fatty acid desaturase 2	56473	3.66	3.11	2.55	1.43	0.56	ns
Csnk2a1	casein kinase 2, alpha 1 polypeptide	12995	1.12	1.28	1.10	1.01	0.30	ns
Itfg1	integrin alpha FG-GAP repeat containing 1	71927	1.48	1.35	1.65	0.89	-0.23	ns
Slc25a23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	66972	0.42	0.33	0.17	2.44	0.72	ns
Pcnx	pecanex homolog (Drosophila)	54604	0.59	0.48	0.79	0.74	-0.76	ns
Ovol1	OVO homolog-like 1 (Drosophila)	18426	0.44	0.38	0.51	0.86	-0.45	ns
Pex14	peroxisomal biogenesis factor 14	56273	0.35	0.37	0.51	0.69	-0.65	ns
Ptpn21	protein tyrosine phosphatase, non-receptor type 21	24000	0.57	0.56	0.59	0.95	0.35	ns
Rhod	ras homolog gene family, member D	11854	0.78	0.60	0.41	1.92	0.89	*
Epb4.1l3	erythrocyte protein band 4.1-like 3	13823	1.87	0.78	0.03	65.05	0.84	*
Ugt8a	UDP galactosyltransferase 8A	22239	2.04	1.43	1.21	1.69	0.08	ns
Ier5l	immediate early response 5-like	72500	0.76	0.77	0.52	1.45	0.24	ns
Rabgef1	RAB guanine nucleotide exchange factor (GEF) 1	56715	1.15	1.27	1.20	0.96	-0.59	ns
Chac2	ChaC, cation transport regulator homolog 2 (E. coli)	68044	0.43	0.56	0.68	0.63	-0.69	ns
Brca2	breast cancer 2	12190	0.80	0.99	1.19	0.67	-0.37	ns
Scnn1g	sodium channel, nonvoltage-gated 1 gamma	20278	0.63	0.29	0.08	7.68	0.05	ns
Fgfbp1	fibroblast growth factor binding protein 1	14181	1.29	0.83	0.93	1.39	0.75	ns
Anxa2	annexin A2	12306	10.43	8.58	7.96	1.30	0.89	*
Abhd6	abhydrolase domain containing 6	66082	0.47	0.62	0.78	0.60	-0.51	ns
Ing2	inhibitor of growth family, member 2	69260	0.91	1.02	1.02	0.89	0.08	ns
Ap1g2	adaptor protein complex AP-1, gamma 2 subunit	11766	0.78	0.74	0.77	1.01	-0.38	ns
Alg14	asparagine-linked glycosylation 14 homolog (yeast)	66789	0.57	0.72	0.54	1.04	0.39	ns
Pdgfc	platelet-derived growth factor, C polypeptide	54635	0.39	0.28	0.23	1.70	0.07	ns
Hoxd9	homeo box D9	15438	3.44	3.06	1.65	2.07	0.64	ns
Evpl	envoplakin	14027	0.49	0.46	0.51	0.96	0.05	ns
Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	18787	0.29	0.19	0.59	0.48	-0.45	ns
2810417H13Rik	RIKEN cDNA 2810417H13 gene	68026	10.31	9.49	9.21	1.11	0.71	ns
Tmprss2	transmembrane protease, serine 2	50528	3.68	3.75	2.99	1.22	-0.27	ns
Sox4		20677	1.78	1.95	1.53	1.16	0.74	ns
Hars2	histidyl-tRNA synthetase 2, mitochondrial (putative)	70791	0.34	0.30	0.33	1.02	0.28	ns
Zfp260		26466	1.04	1.09	1.22	0.84	-0.42	ns
Mapk6	mitogen-activated protein kinase 6	50772	2.11	1.77	1.98	1.06	0.53	ns
Dhfr	dihydrofolate reductase	13361	0.80	1.43	1.30	0.61	-0.73	ns
2410004B18Rik	RIKEN cDNA 2410004B18 gene	66421	1.72	1.88	1.48	1.15	-0.05	ns
Vps37a	vacuolar protein sorting 37A (yeast)	52348	0.65	0.75	0.81	0.81	-0.18	ns
Zfp326	zinc finger protein 326	54367	0.80	1.22	1.05	0.76	-0.55	ns
Papd4	PAP associated domain containing 4	100715	0.76	0.99	1.25	0.61	-0.79	ns
Fhl2	four and a half LIM domains 2	14200	0.64	0.63	0.76	0.83	-0.37	ns
Wfdc15b	WAP four-disulfide core domain 15B	192201	0.24	0.36	0.07	3.51	-0.28	ns
Dll1	delta-like 1 (Drosophila)	13388	0.41	0.30	0.23	1.76	0.38	ns
4933424B01Rik	RIKEN cDNA 4933424B01 gene	71177	0.51	0.64	0.62	0.82	-0.59	ns
Icosl	icos ligand	50723	0.51	0.49	0.44	1.15	-0.02	ns

Nat6	N-acetyltransferase 6	56441	0.37	0.34	0.36	1.03	0.56	ns
Helb	helicase (DNA) B	117599	0.50	0.46	0.36	1.39	0.59	ns
Abca7	ATP-binding cassette, sub-family A (ABC1), member 7	27403	0.47	0.47	0.46	1.01	-0.32	ns
Rab14	RAB14, member RAS oncogene family	68365	7.11	6.75	4.73	1.50	0.89	*
Pftk1	PFTAIRE protein kinase 1	18647	0.41	0.67	0.77	0.53	-0.78	ns
Eps15	epidermal growth factor receptor pathway substrate 15	13858	0.29	0.31	0.37	0.79	-0.64	ns
Eps15	epidermal growth factor receptor pathway substrate 15	13858	2.09	1.92	2.00	1.04	0.49	ns
Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	17768	1.48	1.83	1.71	0.86	-0.49	ns
Tcea1	transcription elongation factor A (SII) 1	21399	3.21	2.98	2.29	1.39	0.64	ns
Rsu1	Ras suppressor protein 1	20163	1.65	1.36	0.71	2.32	0.70	ns
Acad8	acyl-Coenzyme A dehydrogenase family, member 8	66948	0.43	0.34	0.32	1.33	0.75	ns
Adrm1	adhesion regulating molecule 1	56436	1.15	1.37	1.25	0.92	-0.50	ns
1200014M14Rik	RIKEN cDNA 1200014M14 gene	67463	0.20	0.27	0.37	0.54	-0.74	ns
Nfyb	nuclear transcription factor-Y beta	18045	0.70	0.71	0.78	0.90	-0.51	ns
Dut	deoxyuridine triphosphatase	110074	2.37	1.74	1.95	1.21	0.66	ns
Myd88	myeloid differentiation primary response gene 88	17874	0.30	0.39	0.40	0.75	-0.20	ns
C80913	expressed sequence C80913	19777	1.62	1.68	1.49	1.08	-0.04	ns
Dazap1	DAZ associated protein 1	70248	2.21	1.89	2.50	0.88	-0.48	ns
Usp48	ubiquitin specific peptidase 48	170707	0.65	0.60	0.82	0.79	-0.26	ns
Zfp259	zinc finger protein 259	22687	0.85	0.82	0.89	0.95	0.40	ns
Ift81	intraflagellar transport 81 homolog (Chlamydomonas)	12589	0.92	0.80	0.83	1.10	-0.14	ns
Syngr1	synaptogyrin 1	20972	0.37	0.36	0.63	0.59	-0.42	ns
Mettl6	methyltransferase like 6	67011	0.26	0.40	0.31	0.82	-0.37	ns
1700011H14Rik	RIKEN cDNA 1700011H14 gene	67082	0.37	0.32	0.08	4.71	0.65	ns
2010012O05Rik	RIKEN cDNA 2010012O05 gene	66439	0.45	0.41	0.25	1.79	0.86	*
Fzd4	frizzled homolog 4 (Drosophila)	14366	0.31	0.40	0.17	1.77	0.15	ns
Fbxo36	F-box protein 36	66153	0.86	0.67	0.43	1.97	0.56	ns
Gnb1l	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	13972	0.55	0.50	0.46	1.19	0.05	ns
Pdxdc1	pyridoxal-dependent decarboxylase domain containing 1	94184	1.86	2.08	2.09	0.88	-0.16	ns
Sorbs3	sorbin and SH3 domain containing 3	20410	0.80	0.73	0.67	1.18	-0.07	ns
Hook2	hook homolog 2 (Drosophila)	170833	0.59	0.71	0.69	0.85	-0.75	ns
l7Rn6	lethal, Chr 7, Rinchik 6	67669	0.99	1.08	1.90	0.52	-0.64	ns
Isy1	ISY1 splicing factor homolog (S. cerevisiae)	57905	0.37	0.35	0.32	1.16	0.83	*
Ss18	synovial sarcoma translocation, Chromosome 18	268996	2.18	2.31	2.19	0.99	0.41	ns
Mrpl35	mitochondrial ribosomal protein L35	66223	2.19	2.39	1.91	1.14	-0.11	ns
EG624124		624124	24.53	23.55	20.46	1.19	0.79	ns
LOC634044		634044	24.53	23.55	20.46	1.19	0.79	ns
LOC670565		670565	24.53	23.55	20.46	1.19	0.79	ns
Gosr2	golgi SNAP receptor complex member 2	56494	1.31	1.33	1.32	0.99	0.44	ns
Atp6v1b1	ATPase, H+ transporting, lysosomal V1 subunit B1	110935	0.50	0.53	0.72	0.69	-0.20	ns
Wbp4	WW domain binding protein 4	22380	0.84	0.80	1.08	0.77	-0.50	ns
Fxyd2	FXYD domain-containing ion transport regulator 2	11936	1.46	0.85	0.85	1.71	-0.20	ns
Pick1	protein interacting with C kinase 1	18693	0.56	0.58	0.68	0.82	-0.69	ns
Pola1	polymerase (DNA directed), alpha 1	18968	1.17	1.19	1.95	0.60	-0.64	ns
Reep5	receptor accessory protein 5	13476	2.22	1.81	2.27	0.97	0.33	ns
Siah1b		20438	0.23	0.30	0.49	0.47	-0.87	*
Rarg	retinoic acid receptor, gamma	19411	0.73	0.84	0.84	0.87	-0.22	ns
Tbc1d1	TBC1 domain family, member 1	57915	0.77	0.69	0.62	1.23	0.81	*
Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	56371	0.70	0.78	0.75	0.93	-0.17	ns
Uchl5	ubiquitin carboxyl-terminal esterase L5	56207	1.58	1.56	1.55	1.01	0.04	ns
Il10rb	interleukin 10 receptor, beta	16155	1.30	1.11	1.34	0.96	-0.56	ns
Dcxr	dicarbonyl L-xylulose reductase	67880	0.33	0.35	0.45	0.73	-0.53	ns
Rgnef	Rho-guanine nucleotide exchange factor	110596	0.74	0.71	0.82	0.90	-0.64	ns
Rpp14	ribonuclease P 14 subunit (human)	67053	0.82	0.82	0.75	1.08	-0.01	ns
Gtl3	gene trap locus 3	14894	1.33	1.35	1.20	1.10	0.81	ns
Nudc		18221	2.54	2.75	3.32	0.76	-0.57	ns
Gbas	glioblastoma amplified sequence	14467	1.12	0.96	0.86	1.29	0.86	*
Foxc1	forkhead box C1	17300	0.54	0.45	0.44	1.21	-0.35	ns
Tpd52	tumor protein D52	21985	4.99	5.43	5.90	0.84	-0.72	ns
Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	14732	1.02	1.26	0.89	1.14	0.35	ns
Ggps1	geranylgeranyl diphosphate synthase 1	14593	0.75	0.84	0.84	0.89	-0.42	ns
Nagk	N-acetylglucosamine kinase	56174	0.86	1.14	1.19	0.71	-0.81	*
Prpf40b	PRP40 pre-mRNA processing factor 40 homolog B (yeast)	54614	0.39	0.36	0.38	1.02	0.03	ns
Ect2	ect2 oncogene	13605	2.62	3.03	3.24	0.80	-0.83	*
D0HXS9928E	DNA segment, human DXS9928E	108160	0.75	0.83	1.40	0.53	-0.59	ns
Zmynd19	zinc finger, MYND domain containing 19	67187	0.68	0.68	0.59	1.15	0.11	ns
Rela	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	19697	4.44	4.11	2.79	1.58	0.97	**
Atp6v1c1	ATPase, H+ transporting, lysosomal V1 subunit C1	66335	4.06	4.05	5.72	0.71	-0.23	ns
Echdc1	enoyl Coenzyme A hydratase domain containing 1	52665	0.80	0.66	0.64	1.24	0.07	ns
Rabggtb	RAB geranylgeranyl transferase, b subunit	19352	2.40	1.80	1.37	1.75	0.77	ns
Tmem9	transmembrane protein 9	66241	0.61	0.54	0.43	1.42	0.83	*
Birc6	baculoviral IAP repeat-containing 6	12211	2.12	2.43	1.62	1.30	0.48	ns
Isg20	interferon-stimulated protein	57444	0.38	0.37	0.91	0.42	-0.56	ns
Cbx4	chromobox homolog 4 (Drosophila Pc class)	12418	1.81	1.83	1.96	0.92	-0.73	ns
Spag1	sperm associated antigen 1	26942	0.36	0.35	0.19	1.89	0.33	ns
Krt80	keratin 80	74127	0.40	0.49	0.56	0.71	-0.88	*
4833420G17Rik	RIKEN cDNA 4833420G17 gene	67392	1.02	1.44	1.38	0.74	-0.69	ns
Efnb2	ephrin B2	13642	2.50	2.98	1.82	1.36	0.03	ns
Cstf2	cleavage stimulation factor, 3' pre-RNA subunit 2	108062	1.47	1.92	2.46	0.59	-0.19	ns
Ier3	immediate early response 3	15937	4.74	4.26	4.82	0.98	0.45	ns
Myo1c	myosin IC	17913	4.75	4.98	4.03	1.17	0.52	ns
Zfr	zinc finger RNA binding protein	22763	3.30	2.97	2.54	1.29	0.98	***
Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	13207	9.10	8.88	9.40	0.96	-0.59	ns
Tle3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	21887	0.53	0.63	0.66	0.80	-0.38	ns
Slc25a36	solute carrier family 25, member 36	192287	1.81	1.83	1.98	0.91	-0.57	ns
Chic2	cysteine-rich hydrophobic domain 2	74277	1.93	1.91	1.99	0.96	0.20	ns

1600012F09Rik	RIKEN cDNA 1600012F09 gene	67008	0.60	0.59	0.55	1.07	0.13	ns
Nupr1	nuclear protein 1	56312	0.26	0.29	0.24	1.08	-0.43	ns
Il17rc	interleukin 17 receptor C	171095	0.80	0.85	0.87	0.92	-0.45	ns
Elac2	elaC homolog 2 (E. coli)	68626	0.36	0.33	0.35	1.02	-0.49	ns
2810408M09Rik		381406	0.21	0.27	0.41	0.50	-0.49	ns
Trp53rk		76367	0.21	0.27	0.41	0.50	-0.49	ns
Upf1	UPF1 regulator of nonsense transcripts homolog (yeast)	19704	0.27	0.33	0.39	0.69	-0.61	ns
Prom1	prominin 1	19126	2.42	1.40	1.07	2.25	0.42	ns
Akap12	A kinase (PRKA) anchor protein (gravin) 12	83397	3.16	3.92	3.50	0.90	0.06	ns
Pou2f1	POU domain, class 2, transcription factor 1	18986	0.38	0.38	0.28	1.34	0.67	ns
Sema3e	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	20349	1.80	1.07	1.16	1.55	-0.01	ns
Actb	actin, beta, cytoplasmic	11461	2.39	2.57	2.04	1.17	-0.33	ns
Eif1ay	eukaryotic translation initiation factor 1A, Y-linked	66235	2.96	3.91	4.15	0.71	0.07	ns
Ldha	lactate dehydrogenase A	16828	13.60	13.41	17.54	0.77	-0.29	ns
Tpm2	tropomyosin 2, beta	22004	0.37	0.60	0.64	0.58	-0.03	ns
Supt16h	suppressor of Ty 16 homolog (S. cerevisiae)	114741	2.38	2.52	2.33	1.01	0.48	ns
Carm1	coactivator-associated arginine methyltransferase 1	59035	1.14	1.01	0.87	1.31	0.92	**
4933428G20Rik	RIKEN cDNA 4933428G20 gene	58996	0.39	0.36	0.38	1.02	0.49	ns
Myo5a	myosin Va	17918	0.44	0.37	0.24	1.79	0.97	**
Zfp628	zinc finger protein 628	232816	0.41	0.49	0.51	0.80	-0.53	ns
Ccdc12	coiled-coil domain containing 12	72654	1.47	1.56	1.40	1.04	0.60	ns
Ccdc56	coiled-coil domain containing 56	52469	4.80	5.03	6.76	0.71	-0.35	ns
S100a1	S100 calcium binding protein A1	20193	1.97	2.09	0.99	1.99	0.74	ns
Sec63	SEC63-like (S. cerevisiae)	140740	0.90	0.89	0.87	1.04	0.68	ns
Pkhd1	polycystic kidney and hepatic disease 1	241035	1.38	1.61	0.63	2.18	0.25	ns
Gab2	Growth factor receptor bound protein 2-associated protein 2	14389	0.37	0.38	0.35	1.05	0.48	ns
Plec1	plectin 1	18810	4.46	4.42	4.05	1.10	0.88	*
Plk4	polo-like kinase 4 (Drosophila)	20873	3.28	3.50	3.25	1.01	0.56	ns
Hdlbp	high density lipoprotein (HDL) binding protein	110611	3.79	3.53	2.86	1.32	0.70	ns
Csf1r	colony stimulating factor 1 receptor	12978	1.41	1.26	1.40	1.00	-0.53	ns
Trim25	tripartite motif protein 25	217069	1.61	1.63	3.20	0.50	-0.66	ns
Zc3h7a	zinc finger CCCH type containing 7 A	106205	0.35	0.38	0.40	0.87	-0.54	ns
Mphosph9	M-phase phosphoprotein 9	269702	0.73	0.81	0.71	1.03	0.55	ns
Usp7	ubiquitin specific peptidase 7	252870	3.17	3.22	2.75	1.15	0.50	ns
Atrnl1	attractin like 1	226255	1.06	1.03	0.55	1.90	0.73	ns
Txndc10	thioredoxin domain containing 10	67988	0.93	1.18	1.05	0.88	0.19	ns
Rabif	RAB interacting factor	98710	0.81	0.82	0.81	1.00	-0.54	ns
Tnpo3	transportin 3	320938	1.16	1.46	1.48	0.78	-0.77	ns
Slc35a5	solute carrier family 35, member A5	74102	0.52	0.55	0.79	0.65	-0.82	*
Scp2	Sterol carrier protein 2, liver	20280	0.31	0.31	0.38	0.80	-0.69	ns
Nfatc3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	18021	0.76	0.68	0.85	0.88	-0.08	ns
D10Ertd610e	DNA segment, Chr 10, ERATO Doi 610, expressed	52666	0.37	0.32	0.25	1.48	-0.12	ns
Zfp644	zinc finger protein 644	52397	1.49	1.23	1.64	0.91	-0.59	ns
Igbp1	immunoglobulin (CD79A) binding protein 1	18518	1.89	1.68	2.84	0.66	-0.54	ns
Wwc1	WW, C2 and coiled-coil domain containing 1	211652	5.95	4.92	4.01	1.48	0.87	*
Lss	lanosterol synthase	16987	0.88	0.65	0.63	1.39	0.39	ns
Suz12	suppressor of zeste 12 homolog (Drosophila)	52615	2.73	2.70	2.24	1.21	0.78	ns
Mcm3		17215	4.51	4.82	3.52	1.28	0.74	ns
Ppp2r2d	protein phosphatase 2, regulatory subunit B, delta isoform	52432	1.12	1.07	1.23	0.91	-0.24	ns
Maf1	MAF1 homolog (S. cerevisiae)	68877	2.45	2.33	2.92	0.83	-0.22	ns
D2Ertd750e	DNA segment, Chr 2, ERATO Doi 750, expressed	51944	1.20	1.07	1.13	1.06	0.56	ns
Nfkbia	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	18035	5.86	6.43	8.36	0.70	-0.37	ns
Morc3	microrchidia 3	338467	1.30	1.40	1.85	0.70	-0.95	**
Zscan21	zinc finger and SCAN domain containing 21	22697	0.93	0.87	0.79	1.17	-0.33	ns
2410022L05Rik	RIKEN cDNA 2410022L05 gene	66423	0.22	0.35	0.31	0.73	-0.03	ns
Tcta	T-cell leukemia translocation altered gene	102791	0.48	0.32	0.31	1.56	0.82	*
D10Wsu52e	DNA segment, Chr 10, Wayne State University 52, expressed	28088	2.96	3.04	2.63	1.12	-0.10	ns
Pttg1ip	pituitary tumor-transforming 1 interacting protein	108705	4.51	4.01	4.56	0.98	-0.42	ns
EG623356	Predicted gene, EG623356	623356	1.16	1.15	0.79	1.45	-0.07	ns
Slc19a1	solute carrier family 19 (sodium/hydrogen exchanger), member 1	20509	0.62	0.55	0.48	1.30	0.67	ns
Krr1	KRR1, small subunit (SSU) processome component, homolog (yeast)	52705	1.74	1.83	1.52	1.14	0.38	ns
Abcf1	ATP-binding cassette, sub-family F (GCN20), member 1	224742	2.00	2.07	1.46	1.36	0.83	*
Myh9	myosin, heavy polypeptide 9, non-muscle	17886	14.22	12.01	10.27	1.38	0.54	ns
Tax1bp1	Tax1 (human T-cell leukemia virus type I) binding protein 1	52440	0.43	0.36	0.58	0.75	-0.58	ns
Tbc1d14	TBC1 domain family, member 14	100855	2.06	2.18	1.77	1.16	-0.08	ns
Clcn5	chloride channel 5	12728	1.90	2.77	1.92	0.98	-0.10	ns
4930455C21Rik	RIKEN cDNA 4930455C21 gene	76916	0.40	0.37	0.41	0.97	-0.57	ns
Prss22	protease, serine, 22	70835	0.83	0.73	1.14	0.73	-0.22	ns
Denr	density-regulated protein	68184	2.24	2.30	2.22	1.00	0.03	ns
Foxj2	forkhead box J2	60611	0.59	0.63	0.80	0.74	-0.55	ns
Sftpd	surfactant associated protein D	20390	0.23	0.21	0.45	0.52	-0.66	ns
Mpv17	Mpv17 transgene, kidney disease mutant	17527	0.80	0.89	0.63	1.27	0.52	ns
Spen	SPEN homolog, transcriptional regulator (Drosophila)	56381	0.43	0.43	0.39	1.09	0.36	ns
Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	20346	0.48	0.27	0.08	5.74	0.49	ns
Dhx32	DEAH (Asp-Glu-Ala-His) box polypeptide 32	101437	0.40	0.60	0.91	0.44	-0.90	*
Cenpc1	centromere protein C1	12617	0.45	0.62	0.82	0.55	-0.76	ns
Pex11b	peroxisomal biogenesis factor 11b	18632	0.37	0.50	0.37	1.01	0.27	ns
Mtpn	myotrophin	14489	5.99	5.54	6.11	0.97	-0.39	ns
Nap1l1	nucleosome assembly protein 1-like 1	53605	7.22	7.29	5.89	1.22	0.78	ns
Nol7	nucleolar protein 7	70078	3.53	3.86	4.25	0.83	-0.25	ns
Mrps14	mitochondrial ribosomal protein S14	64659	2.48	2.23	2.04	1.21	0.17	ns
Pcyt2	phosphate cytidylyltransferase 2, ethanolamine	68671	0.84	0.82	0.95	0.88	-0.11	ns
Vps26a	vacuolar protein sorting 26 homolog A (yeast)	30930	1.42	1.24	1.23	1.15	0.24	ns
Cebpz	CCAAT/enhancer binding protein zeta	12607	1.16	1.21	0.72	1.60	0.80	*

Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	13418	0.41	0.39	0.27	1.51	0.35	ns
Sat1	spermidine/spermine N1-acetyl transferase 1	20229	1.75	2.15	5.92	0.29	-0.68	ns
Stxbp1	syntaxin binding protein 1	20910	0.42	0.45	0.28	1.48	0.52	ns
Srfbp1	serum response factor binding protein 1	67222	0.22	0.29	0.35	0.64	-0.33	ns
Igsf9	immunoglobulin superfamily, member 9	93842	0.62	0.70	0.63	0.98	-0.52	ns
Rit1	Ras-like without CAAX 1	19769	0.49	0.50	0.49	1.01	-0.38	ns
Rac3	RAS-related C3 botulinum substrate 3	170758	0.46	0.56	0.31	1.48	0.40	ns
Tcl1b3	T-cell leukemia/lymphoma 1B, 3	27378	1.39	1.35	1.12	1.24	0.66	ns
Tead3	TEA domain family member 3	21678	0.36	0.34	0.30	1.21	0.62	ns
Raet1a		19368	0.56	0.47	0.35	1.56	0.89	ns
Raet1b		19369	0.56	0.47	0.35	1.56	0.89	ns
Raet1c		19370	0.56	0.47	0.35	1.56	0.89	ns
Raet1d		56554	0.56	0.47	0.35	1.56	0.89	ns
Raet1e		379043	0.56	0.47	0.35	1.56	0.89	ns
Rbm18	RNA binding motif protein 18	67889	0.92	0.91	0.69	1.34	0.15	ns
March7	membrane-associated ring finger (C3HC4) 7	57438	5.81	4.65	3.91	1.48	0.67	ns
Prkacb	protein kinase, cAMP dependent, catalytic, beta	18749	1.44	1.55	1.10	1.31	0.18	ns
Ash2l	ash2 (absent, small, or homeotic)-like (Drosophila)	23808	1.83	1.96	1.83	0.99	0.52	ns
Cpeb4	cytoplasmic polyadenylation element binding protein 4	67579	1.82	1.77	2.91	0.62	-0.81	ns
Aes	amino-terminal enhancer of split	14797	3.27	3.04	3.35	0.97	-0.31	ns
Vamp8	vesicle-associated membrane protein 8	22320	1.99	2.33	3.16	0.63	-0.67	ns
Pura	purine rich element binding protein A	19290	2.17	2.25	1.82	1.19	0.59	ns
8430419L09Rik	RIKEN cDNA 8430419L09 gene	74525	1.64	1.61	1.45	1.13	0.05	ns
Blcap	bladder cancer associated protein homolog (human)	53619	1.06	1.04	0.99	1.06	0.65	ns
Smad2	MAD homolog 2 (Drosophila)	17126	1.02	0.86	1.03	0.99	0.31	ns
Tcirg1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3	27060	0.61	0.64	0.67	0.90	-0.27	ns
Jmy	junction-mediating and regulatory protein	57748	0.31	0.37	0.40	0.76	-0.83	ns
Sqrdl	sulfide quinone reductase-like (yeast)	59010	2.86	1.66	2.28	1.25	0.38	ns
Krt8		16691	18.85	16.97	14.62	1.28	0.66	ns
Tgfb1	transforming growth factor, beta 1	21803	0.59	0.66	0.73	0.80	0.26	ns
Gbe1	glucan (1,4-alpha-), branching enzyme 1	74185	0.44	0.36	0.52	0.84	-0.50	ns
Procr	protein C receptor, endothelial	19124	0.10	0.17	1.13	0.08	-0.56	ns
Chrnb1	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)	11443	0.95	0.85	0.77	1.22	0.77	ns
Bnipl	BCL2/adenovirus E1B 19kD interacting protein like	171388	0.19	0.28	0.42	0.46	-0.51	ns
Csrp2	cysteine and glycine-rich protein 2	13008	0.54	0.43	0.19	2.86	0.82	ns
Ccndbp1	cyclin D-type binding-protein 1	17151	1.63	1.03	1.06	1.54	0.72	ns
Dtx3	deltex 3 homolog (Drosophila)	80904	0.64	0.50	0.31	2.06	0.54	ns
Tsc22d3	TSC22 domain family 3	14605	0.74	0.68	0.68	1.09	0.58	*
Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	11992	0.48	0.43	0.50	0.97	0.08	ns
Fgf9	fibroblast growth factor 9	14180	0.25	0.30	0.10	2.58	-0.05	ns
EG627557		627557	1.60	1.52	1.44	1.11	0.00	ns
Ncoa4		27057	1.60	1.52	1.44	1.11	0.00	ns
1500003O03Rik	RIKEN cDNA 1500003O03 gene	56398	0.79	0.69	1.39	0.56	-0.87	ns
Ctnnb1	catenin (cadherin associated protein), beta 1	12387	13.77	12.80	11.23	1.22	0.97	ns
2900073G15Rik	RIKEN cDNA 2900073G15 gene	67268	9.82	9.84	8.21	1.19	0.80	ns
Sgpp1	sphingosine-1-phosphate phosphatase 1	81535	0.45	0.52	0.98	0.46	-0.63	ns
Sema4d	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	20354	1.87	1.98	1.32	1.41	0.38	ns
Letm1	leucine zipper-EF-hand containing transmembrane protein 1	56384	0.36	0.48	0.48	0.74	-0.51	ns
Ccng1	cyclin G1	12450	2.01	2.06	3.84	0.52	-0.89	ns
Vamp2	vesicle-associated membrane protein 2	22318	0.36	0.45	0.38	0.96	0.00	ns
Slc25a30	solute carrier family 25, member 30	67554	1.27	1.32	1.28	0.99	-0.47	ns
Plekha3	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	83435	0.51	0.54	0.61	0.83	-0.84	ns
Ptprf	protein tyrosine phosphatase, receptor type, F	19268	3.73	3.76	3.95	0.94	-0.43	*
Mrps2	mitochondrial ribosomal protein S2	118451	1.04	1.10	0.87	1.19	0.17	ns
Crnkl1	Crn, crooked neck-like 1 (Drosophila)	66877	0.77	0.81	0.77	0.99	0.12	ns
Pkia	protein kinase inhibitor, alpha	18767	0.41	0.48	0.17	2.40	0.74	*
Dctn4	dynactin 4	67665	0.99	1.21	1.04	0.95	0.19	ns
Zfp161	zinc finger protein 161	22666	1.01	1.11	0.77	1.32	0.43	ns
Mllt10	myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolog (Drosophila)	17354	1.29	1.19	1.01	1.26	0.49	ns
Twf1	twinfilin, actin-binding protein, homolog 1 (Drosophila)	19230	2.91	3.07	3.24	0.89	-0.61	ns
Acd		497652	0.93	0.94	0.96	0.96	0.32	ns
Nsd1		18193	0.93	0.94	0.96	0.96	0.32	ns
Bcl2l1	Bcl2-like 1	12048	1.29	1.26	1.23	1.05	0.23	ns
Hccs	holocytochrome c synthetase	15159	0.55	0.72	1.00	0.54	-0.12	ns
Wnt7b	wingless-related MMTV integration site 7B	22422	3.51	3.49	3.07	1.14	0.78	ns
Tgfbr1	transforming growth factor, beta receptor I	21812	1.00	1.34	1.81	0.55	-0.99	ns
Snap23	synaptosomal-associated protein 23	20619	0.62	0.45	0.41	1.53	0.04	ns
Rab18	RAB18, member RAS oncogene family	19330	1.62	1.77	2.07	0.78	-0.02	ns
Il17ra	interleukin 17 receptor A	16172	0.32	0.32	0.38	0.86	-0.58	ns
Cd2ap	CD2-associated protein	12488	5.52	5.66	3.55	1.55	0.46	ns
Vegfa	vascular endothelial growth factor A	22339	0.80	0.78	0.90	0.88	-0.78	ns
Mfge8	milk fat globule-EGF factor 8 protein	17304	1.42	1.29	2.23	0.63	-0.50	ns
Sgk3	serum/glucocorticoid regulated kinase 3	170755	1.48	1.14	0.72	2.05	0.72	ns
St6gal1	beta galactoside alpha 2,6 sialyltransferase 1	20440	0.27	0.37	0.19	1.44	-0.42	ns
Ctnnal1	catenin (cadherin associated protein), alpha-like 1	54366	1.01	0.96	0.78	1.29	0.00	ns
Cpsf2	cleavage and polyadenylation specific factor 2	51786	0.94	0.92	1.02	0.91	-0.60	ns
Zfp185	zinc finger protein 185	22673	0.54	0.59	1.20	0.45	-0.58	ns
Son	Son cell proliferation protein	20658	6.60	6.46	6.75	0.97	-0.22	ns
Apc	adenomatosis polyposis coli	11789	1.13	1.23	0.97	1.16	0.39	*
Enc1	ectodermal-neural cortex 1	13803	1.25	1.43	1.57	0.79	-0.58	ns
Slc25a15	solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	18408	0.43	0.50	0.52	0.83	-0.47	ns
Lmo4	LIM domain only 4	16911	2.11	2.20	1.31	1.60	-0.07	ns

Chd1	chromodomain helicase DNA binding protein 1	12648	0.42	0.34	0.35	1.18	0.33	ns
Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	107765	1.04	1.53	1.89	0.55	-0.58	ns
Pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)	59001	0.34	0.46	0.58	0.59	-0.70	ns
1700021F05Rik	RIKEN cDNA 1700021F05 gene	67851	1.01	1.03	0.86	1.16	0.31	ns
Acyp1	acylphosphatase 1, erythrocyte (common) type	66204	0.86	0.86	1.46	0.59	-0.45	ns
Pik3c2a	phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide	18704	2.50	2.21	2.01	1.24	0.42	ns
Hbs1l	Hbs1-like (S. cerevisiae)	56422	1.36	1.53	1.11	1.22	0.35	ns
Zfp64	zinc finger protein 64	22722	0.73	0.77	0.72	1.01	-0.48	ns
2310016C08Rik	RIKEN cDNA 2310016C08 gene	69573	0.18	0.27	0.39	0.46	-0.56	ns
Arhgef2	rho/rac guanine nucleotide exchange factor (GEF) 2	16800	0.90	1.08	0.78	1.15	-0.27	ns
LOC671878		671878	0.72	0.90	1.27	0.56	-0.11	ns
Sms		20603	0.72	0.90	1.27	0.56	-0.11	ns
Xpo4		57258	0.38	0.40	0.33	1.15	0.79	ns
Alg2	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)	56737	0.91	0.69	0.55	1.65	0.93	*
Clta	clathrin, light polypeptide (Lca)	12757	4.77	4.94	5.59	0.85	-0.53	ns
Jak2	Janus kinase 2	16452	0.60	0.64	0.64	0.92	0.42	ns
Banf1	barrier to autointegration factor 1	23825	6.52	5.93	5.58	1.16	0.74	ns
Zdhhc16	zinc finger, DHHC domain containing 16	74168	1.14	1.24	1.13	1.00	0.04	ns
Cbll1	Casitas B-lineage lymphoma-like 1	104836	0.89	0.88	1.01	0.88	-0.41	ns
Rpgrip1	retinitis pigmentosa GTPase regulator interacting protein 1	77945	3.17	3.80	3.46	0.91	-0.09	ns
Terf2	telomeric repeat binding factor 2	21750	0.90	0.93	0.55	1.64	0.81	*
Atn1	atrophin 1	13498	0.49	0.50	0.58	0.85	-0.43	ns
Epha2	Eph receptor A2	13836	0.46	0.43	0.49	0.93	-0.63	ns
Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1	16801	0.71	0.71	0.84	0.85	-0.88	*
Adam12	a disintegrin and metallopeptidase domain 12 (meltrin alpha)	11489	0.23	0.20	0.23	0.97	0.03	ns
Gopc	golgi associated PDZ and coiled-coil motif containing	94221	0.41	0.47	0.57	0.72	-0.74	ns
Acin1	apoptotic chromatin condensation inducer 1	56215	1.31	1.46	1.35	0.96	0.31	ns
Atm	ataxia telangiectasia mutated homolog (human)	11920	0.73	0.64	0.50	1.43	0.73	ns
Lgals9	lectin, galactose binding, soluble 9	16859	0.23	0.49	1.92	0.12	-0.66	ns
Anxa4	annexin A4	11746	4.83	5.27	6.38	0.75	-0.98	***
Srm	spermidine synthase	20810	0.88	0.90	0.87	1.01	-0.19	ns
Lipg	lipase, endothelial	16891	0.43	0.37	0.26	1.65	0.93	**
Rbm38	RNA binding motif protein 38	56190	0.59	0.52	0.81	0.72	-0.72	ns
Lamc2	laminin, gamma 2	16782	1.67	2.46	2.73	0.61	-0.45	ns
Myb	myeloblastosis oncogene	17863	0.41	0.33	0.11	3.61	0.63	ns
Net1	neuroepithelial cell transforming gene 1	56349	0.77	0.71	1.26	0.61	-0.65	ns
G3bp2	GTPase activating protein (SH3 domain) binding protein 2	23881	3.30	3.15	2.56	1.28	0.49	ns
Mynn	myoneurin	80732	0.71	0.58	0.49	1.44	0.53	ns
Map3k5		26408	0.38	0.28	0.35	1.06	-0.45	ns
Jub	ajuba	16475	4.14	4.57	3.74	1.10	0.31	ns
S100a6	S100 calcium binding protein A6 (calcyclin)	20200	17.10	16.71	14.34	1.19	0.67	ns
Nck1	non-catalytic region of tyrosine kinase adaptor protein 1	17973	0.30	0.26	0.35	0.87	0.19	ns
Zfp120	zinc finger protein 120	104348	0.27	0.28	0.37	0.71	-0.45	ns
Txnrd1	thioredoxin reductase 1	50493	3.79	4.00	3.19	1.18	-0.13	ns
Dfna5h	deafness, autosomal dominant 5 homolog (human)	54722	0.63	0.67	0.94	0.67	-0.08	ns
Txn2	thioredoxin 2	56551	0.84	0.76	0.94	0.89	-0.52	ns
Il18r1	interleukin 18 receptor 1	16182	0.18	0.22	0.20	0.88	0.08	ns
Tank	TRAF family member-associated Nf-kappa B activator	21353	0.58	0.37	0.29	2.01	0.57	ns
Lmna	lamin A	16905	3.44	3.62	3.02	1.13	0.74	ns
Tusc3	tumor suppressor candidate 3	80286	2.61	2.84	3.36	0.77	-0.12	ns
Styx	phosphoserine/threonine/tyrosine interaction protein	56291	0.82	0.88	0.65	1.25	0.59	ns
Fert2	fer (fms/fps related) protein kinase, testis specific 2	14158	0.57	0.49	0.45	1.25	0.89	*
Tpst1	protein-tyrosine sulfotransferase 1	22021	0.68	0.59	0.44	1.52	0.91	*
Pcbp2	poly(rC) binding protein 2	18521	14.94	12.49	13.53	1.10	0.63	ns
Vbp1	von Hippel-Lindau binding protein 1	22327	2.65	2.35	3.65	0.72	-0.27	ns
Psmd14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	59029	4.88	3.97	3.43	1.41	0.95	**
Gpr19	G protein-coupled receptor 19	14760	0.42	0.37	0.59	0.70	-0.55	ns
Cox7a2l	cytochrome c oxidase subunit VIIa polypeptide 2-like	20463	5.51	4.81	3.16	1.73	0.96	**
Efna4	ephrin A4	13639	0.58	0.52	0.36	1.62	0.30	ns
Dgcr2	DiGeorge syndrome critical region gene 2	13356	1.38	1.25	1.20	1.14	0.68	ns
LOC640441		640441	4.55	2.95	2.64	1.71	0.53	ns
Thbs1		21825	4.55	2.95	2.64	1.71	0.53	ns
Tapbp	TAP binding protein	21356	2.66	3.32	3.65	0.72	-0.85	*
Msn	moesin	17698	3.18	3.03	4.46	0.71	-0.28	ns
LOC630729	similar to Glutathione reductase, mitochondrial precursor (GR) (GRase)	630729	1.45	1.53	1.86	0.78	0.05	ns
Gsr	glutathione reductase 1	14782	1.74	2.00	1.95	0.89	0.26	ns
Bcl6	B-cell leukemia/lymphoma 6	12053	0.31	0.36	0.37	0.85	-0.65	ns
LOC671392		671392	5.71	5.38	4.08	1.39	0.67	ns
Nf2	neurofibromatosis 2	18016	0.93	0.85	1.13	0.81	-0.40	ns
Ldlr	low density lipoprotein receptor	16835	2.64	1.87	2.52	1.04	0.44	ns
Ppp2cb	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	19053	2.18	2.46	2.82	0.77	-0.19	ns
Mtap7	microtubule-associated protein 7	17761	0.70	0.53	0.64	1.09	0.01	ns
Mtap7	microtubule-associated protein 7	17761	1.12	1.22	1.41	0.79	-0.71	ns
Fgfr3	fibroblast growth factor receptor 3	14184	0.55	0.54	1.08	0.50	-0.41	ns
Wsb2	WD repeat and SOCS box-containing 2	59043	1.59	1.44	1.50	1.06	0.58	ns
Stag2	stromal antigen 2	20843	2.47	2.25	3.63	0.68	-0.46	ns
Kcnk5	potassium channel, subfamily K, member 5	16529	0.25	0.40	0.49	0.50	-0.85	*
Psen1	presenilin 1	19164	2.98	2.83	3.24	0.91	-0.31	ns
Adam17	a disintegrin and metallopeptidase domain 17	11491	1.91	2.06	2.33	0.82	-0.46	ns
Clstn1	calsyntenin 1	65945	1.56	1.68	1.52	1.02	0.28	ns
Nr3c1	nuclear receptor subfamily 3, group C, member 1	14815	1.61	1.81	1.12	1.43	0.50	ns
Trim44	tripartite motif-containing 44	80985	3.32	2.84	2.62	1.26	0.35	ns
Rab24	RAB24, member RAS oncogene family	19336	1.24	1.26	1.76	0.70	-0.52	ns
Mrps23	mitochondrial ribosomal protein S23	64656	0.75	0.74	0.94	0.79	-0.59	ns
Mapk9	mitogen activated protein kinase 9	26420	0.49	0.56	0.71	0.69	-0.65	ns
Mtmr1	myotubularin related protein 1	53332	0.32	0.27	0.41	0.78	-0.43	ns

Tpp2	tripeptidyl peptidase II	22019	0.77	0.85	0.84	0.92	-0.44	ns
Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	15467	0.59	0.59	0.61	0.97	-0.65	ns
Tgs1	trimethylguanosine synthase homolog (S. cerevisiae)	116940	0.73	0.71	0.67	1.09	0.11	ns
Tcf20	transcription factor 20	21411	1.21	1.06	0.65	1.87	0.82	*
Mrpl19	mitochondrial ribosomal protein L19	56284	0.90	0.88	1.04	0.86	-0.59	ns
Dapp1	dual adaptor for phosphotyrosine and 3-phosphoinositides 1	26377	0.39	0.42	0.39	1.00	-0.53	ns
Serhl	serine hydrolase-like	68607	0.45	0.52	0.45	0.99	-0.42	ns
Tgfa	transforming growth factor alpha	21802	0.88	0.89	1.25	0.70	-0.46	ns
Ccdc123	coiled-coil domain containing 123	72140	0.54	0.66	0.45	1.19	0.34	ns
Pfdn2	prefoldin 2	18637	1.75	1.56	1.39	1.25	0.85	*
Cdc25b	cell division cycle 25 homolog B (S. pombe)	12531	1.34	1.43	2.41	0.55	-0.23	ns
Notch3	Notch gene homolog 3 (Drosophila)	18131	1.53	1.47	1.13	1.35	0.28	ns
Mrps34	mitochondrial ribosomal protein S34	79044	2.06	1.83	1.58	1.29	0.61	ns
Tcfap2a	transcription factor AP-2, alpha	21418	2.48	2.01	2.19	1.13	0.31	ns
Tor3a	torsin family 3, member A	30935	0.84	0.76	0.72	1.16	0.23	ns
Abcb8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	74610	0.36	0.49	0.33	1.08	0.23	ns
Cenph	centromere protein H	26886	0.42	0.56	0.98	0.42	-0.60	ns
Hivep2	human immunodeficiency virus type I enhancer binding protein 2	15273	0.30	0.30	0.28	1.07	-0.16	ns
Zfand6	zinc finger, AN1-type domain 6	65098	4.49	4.34	5.58	0.80	-0.55	ns
Ptpn12	protein tyrosine phosphatase, non-receptor type 12	19248	2.80	3.38	3.78	0.74	-0.98	***
Stat5b	signal transducer and activator of transcription 5B	20851	0.47	0.59	0.67	0.70	-0.40	ns
Plau	plasminogen activator, urokinase	18792	0.39	0.36	0.31	1.25	0.50	ns
EG544872		544872	29.43	25.00	19.73	1.48	0.93	**
EG546164		546164	29.43	25.00	19.73	1.48	0.93	**
EG620248		620248	29.43	25.00	19.73	1.48	0.93	**
EG667279		667279	29.43	25.00	19.73	1.48	0.93	**
EG667846		667846	29.43	25.00	19.73	1.48	0.93	**
EG667847		667847	29.43	25.00	19.73	1.48	0.93	**
LOC546298		546298	29.43	25.00	19.73	1.48	0.93	**
LOC637606		637606	29.43	25.00	19.73	1.48	0.93	**
LOC671929		671929	29.43	25.00	19.73	1.48	0.93	**
LOC672594		672594	29.43	25.00	19.73	1.48	0.93	**
Rps2		16898	29.43	25.00	19.73	1.48	0.93	**
Itgb1bp1	integrin beta 1 binding protein 1	16413	0.67	0.71	0.80	0.83	-0.31	ns
Rab17	RAB17, member RAS oncogene family	19329	0.40	0.33	0.20	1.99	0.09	ns
Cyb5r3	cytochrome b5 reductase 3	109754	5.67	5.79	6.12	0.92	-0.28	ns
Gnb5	guanine nucleotide binding protein, beta 5	14697	0.44	0.36	0.32	1.38	0.68	ns
B3gnt3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	72297	0.24	0.25	0.40	0.61	-0.76	ns
Ndufa1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	54405	2.62	3.08	4.90	0.53	-0.58	ns
Rps6kb2	ribosomal protein S6 kinase, polypeptide 2	58988	0.47	0.39	0.32	1.44	0.80	ns
Tgif1	TG interacting factor 1	21815	1.14	0.99	0.73	1.55	0.41	ns
Kctd1	potassium channel tetramerisation domain containing 1	106931	0.38	0.41	0.39	0.97	-0.15	ns
EG665937		665937	7.62	7.27	7.96	0.95	-0.50	ns
Ftl2		14337	7.62	7.27	7.96	0.95	-0.50	ns
LOC634386		634386	7.62	7.27	7.96	0.95	-0.50	ns
G6pd2		14380	0.33	0.26	0.54	0.60	-0.77	ns
Hras1	Harvey rat sarcoma virus oncogene 1	15461	0.81	0.86	0.97	0.83	-0.43	ns
Supt4h1		20922	2.11	1.72	2.01	1.05	0.05	ns
Rnf14	ring finger protein 14	56736	1.13	1.23	1.28	0.88	-0.10	ns
Fignl1	fidgetin-like 1	60530	1.99	1.94	2.38	0.83	-0.01	ns
Idh1	isocitrate dehydrogenase 1 (NADP+), soluble	15926	1.59	1.98	1.66	0.95	-0.51	ns
Ephx1	epoxide hydrolase 1, microsomal	13849	0.78	0.79	1.12	0.69	-0.82	*
LOC640611		640611	3.00	3.08	2.63	1.14	-0.33	ns
Cdk4	cyclin-dependent kinase 4	12567	4.46	4.04	3.15	1.41	0.25	ns
Smu1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	74255	2.23	2.38	2.89	0.77	-0.39	ns
Xpnpep1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	170750	2.75	2.78	3.42	0.80	-0.36	ns
Itga6	integrin alpha 6	16403	1.28	1.57	1.48	0.86	-0.66	ns
Rcn2	reticulocalbin 2	26611	2.89	2.54	2.20	1.31	0.95	**
Mrps21	mitochondrial ribosomal protein S21	66292	1.93	1.98	1.89	1.01	-0.23	ns
Bag3	Bcl2-associated athanogene 3	29810	0.42	0.36	0.40	1.05	0.42	ns
Prpf8	pre-mRNA processing factor 8	192159	4.22	4.10	3.16	1.33	0.63	ns
Nsf	N-ethylmaleimide sensitive fusion protein	18195	1.10	0.93	0.94	1.17	0.67	ns
Sumo3	SMT3 suppressor of mif two 3 homolog 3 (yeast)	20610	5.31	4.89	4.85	1.09	0.11	ns
Psmd13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	23997	1.03	1.31	1.26	0.81	-0.32	ns
Mad2l1	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast)	56150	3.60	3.78	5.03	0.71	-0.29	ns
Ube2t	ubiquitin-conjugating enzyme E2T (putative)	67196	0.72	0.70	0.77	0.93	0.04	ns
Mrpl3	mitochondrial ribosomal protein L3	94062	0.85	0.74	0.78	1.08	0.64	ns
Nxn	nucleoredoxin	18230	0.34	0.37	0.25	1.33	0.34	ns
Ppt1	palmitoyl-protein thioesterase 1	19063	0.90	0.84	0.94	0.95	-0.61	ns
Bnip3	BCL2/adenovirus E1B interacting protein 1, NIP3	12176	5.31	5.66	9.69	0.55	-0.69	ns
Pex13	peroxisomal biogenesis factor 13	72129	1.08	1.02	1.05	1.02	0.22	ns
Rps3a	ribosomal protein S3a	20091	31.96	30.09	23.52	1.35	0.87	*
Ifi30	interferon gamma inducible protein 30	65972	2.28	2.17	2.20	1.03	-0.13	ns
Acss2	acyl-CoA synthetase short-chain family member 2	60525	0.17	0.17	0.46	0.37	-0.65	ns
Snx3	sorting nexin 3	54198	5.56	4.73	4.96	1.12	0.10	ns
Ruvbl2	RuvB-like protein 2	20174	2.10	2.24	2.68	0.78	-0.22	ns
Smad4	MAD homolog 4 (Drosophila)	17128	3.83	4.07	4.03	0.95	0.34	ns
Nxt1	NTF2-related export protein 1	56488	1.37	1.37	1.67	0.82	-0.31	ns
Gcs1	glucosidase 1	57377	1.17	1.30	1.28	0.91	-0.29	ns
Bnip2	BCL2/adenovirus E1B interacting protein 1, NIP2	12175	1.26	1.06	0.93	1.35	0.87	*
Cpox	coproporphyrinogen oxidase	12892	0.52	0.74	1.51	0.34	-0.85	*
Slc30a5	solute carrier family 30 (zinc transporter), member 5	69048	0.78	0.95	1.07	0.72	-0.93	**
Parp1	poly (ADP-ribose) polymerase family, member 1	11545	1.71	1.65	1.35	1.26	0.40	ns
Cstb	cystatin B	13014	10.37	9.52	8.81	1.17	0.66	ns
Atp6v1a	ATPase, H+ transporting, lysosomal V1 subunit A	11964	2.83	2.53	3.14	0.89	-0.46	ns
U2af1	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1	108121	3.63	3.68	2.69	1.34	0.86	*

Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	69274	1.58	1.51	1.19	1.32	0.80 ns
Ogfr	opioid growth factor receptor	72075	0.80	1.01	0.98	0.81	-0.45 ns
Ccnf	cyclin F	12449	0.79	0.77	0.64	1.22	0.69 ns
Fibp	fibroblast growth factor (acidic) intracellular binding protein	58249	1.28	1.29	1.00	1.28	0.33 ns
Znrd1	zinc ribbon domain containing, 1	66136	1.34	1.36	0.90	1.48	0.91 *
Cask	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	12361	0.65	0.56	0.84	0.77	0.14 ns
Fxr2	fragile X mental retardation, autosomal homolog 2	23879	0.52	0.53	0.67	0.78	-0.49 ns
Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	74104	0.65	0.71	0.56	1.16	0.59 ns
Atp5k	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e	11958	6.01	5.53	5.66	1.06	0.13 ns
Xpc	xeroderma pigmentosum, complementation group C	22591	0.50	0.49	0.55	0.90	-0.43 ns
Ccne2	cyclin E2	12448	0.45	0.57	1.01	0.45	-0.67 ns
Extl2	exotoses (multiple)-like 2	58193	0.82	0.82	0.43	1.90	0.78 ns
Ptprm	protein tyrosine phosphatase, receptor type, M	19274	0.81	0.45	0.23	3.48	0.80 ns
Ranbp1	RAN binding protein 1	19385	10.62	9.71	10.34	1.02	0.21 ns
Arl2	ADP-ribosylation factor-like 2	56327	0.90	0.77	0.66	1.37	0.91 *
Ndnl2	necdin-like 2	66647	0.35	0.38	0.56	0.63	-0.83 *
Mt1	metallothionein 1	17748	13.00	10.67	7.22	1.79	0.17 ns
Ube2n	ubiquitin-conjugating enzyme E2N	93765	3.18	2.40	2.34	1.35	0.54 ns
Adamts5	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2)	23794	2.77	1.98	2.22	1.24	0.13 ns
Ndel1	nuclear distribution gene E-like homolog 1 (A. nidulans)	83431	1.61	1.58	2.15	0.74	-0.35 ns
Yy1	YY1 transcription factor	22632	5.59	5.65	5.81	0.96	-0.19 ns
Yy1	YY1 transcription factor	22632	0.50	0.42	0.42	1.20	-0.07 ns
Rhog	ras homolog gene family, member G	56212	0.71	0.62	0.68	1.04	0.52 ns
Ampd3	AMP deaminase 3	11717	0.57	0.64	0.42	1.33	-0.03 ns
EG628438		628438	1.19	1.16	0.79	1.50	0.83 *
Pias1	protein inhibitor of activated STAT 1	56469	1.23	0.99	1.10	1.12	0.59 ns
Skiv2l	superkiller viralicidic activity 2-like (S. cerevisiae)	108077	0.63	0.55	0.34	1.86	0.95 **
Ap3s1	adaptor-related protein complex 3, sigma 1 subunit	11777	1.97	1.75	2.64	0.74	-0.20 ns
5730470L24Rik	RIKEN cDNA 5730470L24 gene	66641	0.55	0.56	0.40	1.36	0.62 ns
Zfp143	zinc finger protein 143	20841	0.35	0.38	0.46	0.76	-0.78 ns
Serpinb9	serine (or cysteine) peptidase inhibitor, clade B, member 9	20723	0.52	0.78	1.35	0.38	-0.97 **
Rnase4	ribonuclease, RNase A family 4	58809	0.41	0.87	0.53	0.77	0.14 ns
Hk2	hexokinase 2	15277	1.22	1.66	2.59	0.47	-0.94 **
Rpl7a	ribosomal protein L7a	27176	26.27	23.21	17.06	1.53	0.90 *
Bloc1s1	biogenesis of lysosome-related organelles complex-1, subunit 1	14533	1.05	1.05	1.08	0.96	-0.40 ns
Wdr54	WD repeat domain 54	75659	0.21	0.22	0.38	0.54	-0.70 ns
Ppap2a	phosphatidic acid phosphatase 2a	19012	0.43	0.54	0.65	0.66	-0.98 ***
Ranbp2	RAN binding protein 2	19386	1.61	1.51	1.46	1.10	0.13 ns
Rev1	REV1 homolog (S. cerevisiae)	56210	0.43	0.50	0.44	0.96	-0.42 ns
Mkks	McKusick-Kaufman syndrome protein	59030	0.56	0.36	0.53	1.05	0.00 ns
Shroom3	shroom family member 3	27428	1.71	1.79	2.50	0.68	-0.76 ns
Rad50	RAD50 homolog (S. cerevisiae)	19360	1.01	1.01	1.33	0.75	-0.46 ns
Ahr	aryl-hydrocarbon receptor	11622	3.30	3.58	3.82	0.86	-0.21 ns
Dmtf1	cyclin D binding myb-like transcription factor 1	23857	1.52	1.48	1.76	0.86	-0.41 ns
Rassf5	Ras association (RalGDS/AF-6) domain family 5	54354	0.37	0.30	0.21	1.75	0.15 ns
Ring1	ring finger protein 1	19763	0.71	0.50	0.40	1.78	0.64 ns
Camk2d	calcium/calmodulin-dependent protein kinase II, delta	108058	0.60	0.71	0.34	1.73	0.10 ns
Lgals8	lectin, galactose binding, soluble 8	56048	0.77	0.78	0.94	0.81	-0.48 ns
Cblc	Casitas B-lineage lymphoma c	80794	0.27	0.36	0.37	0.73	-0.66 ns
Ebag9	estrogen receptor-binding fragment-associated gene 9	55960	1.40	1.23	1.62	0.86	-0.28 ns
Smarce1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	57376	1.44	1.29	1.61	0.89	0.03 ns
Dgat2	diacylglycerol O-acyltransferase 2	67800	0.28	0.41	0.64	0.44	-0.78 ns
Ctr9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	22083	0.70	0.75	0.82	0.84	-0.02 ns
Exoc4	exocyst complex component 4	20336	1.52	1.41	1.33	1.14	-0.21 ns
Nras	neuroblastoma ras oncogene	18176	2.21	2.32	1.89	1.16	0.16 ns
Sptlc1	serine palmitoyltransferase, long chain base subunit 1	268656	1.36	0.95	1.21	1.12	0.29 ns
Sub1	SUB1 homolog (S. cerevisiae)	20024	5.70	5.72	6.31	0.90	-0.02 ns
Jarid2	jumonji, AT rich interactive domain 2	16468	0.30	0.38	0.37	0.82	-0.57 ns
Jarid2	jumonji, AT rich interactive domain 2	16468	0.57	0.68	0.61	0.93	-0.29 ns
Gyk	glycerol kinase	14933	0.46	0.46	0.67	0.68	-0.81 *
LOC676013		676013	1.30	1.46	1.47	0.88	-0.30 ns
Ube2i	ubiquitin-conjugating enzyme E2I	22196	4.53	3.81	3.68	1.22	0.80 ns
EG546265		546265	1.89	1.78	1.23	1.54	0.85 *
LOC631286		631286	3.22	3.57	3.97	0.81	-0.63 ns
Ap3s2	adaptor-related protein complex 3, sigma 2 subunit	11778	0.32	0.38	0.41	0.77	-0.66 ns
Tnk1	tyrosine kinase, non-receptor, 1	83813	0.87	0.76	0.92	0.93	-0.60 ns
Limd1	LIM domains containing 1	29806	1.40	1.48	1.24	1.12	0.81 ns
Foxq1	forkhead box Q1	15220	0.68	0.65	0.70	0.98	-0.37 ns
Ncoa3	nuclear receptor coactivator 3	17979	0.27	0.31	0.37	0.72	-0.94 **
Hivep1	human immunodeficiency virus type I enhancer binding protein 1	110521	0.21	0.19	0.49	0.43	-0.82 *
Chek2	CHK2 checkpoint homolog (S. pombe)	50883	0.54	0.56	0.61	0.87	-0.35 ns
Xpo6	exportin 6	74204	0.50	0.56	0.62	0.79	-0.43 ns
Padi4		18602	0.34	0.46	0.51	0.66	-0.39 ns
Gipc1	GIPC PDZ domain containing family, member 1	67903	1.19	1.24	1.49	0.79	-0.35 ns
Stau1	staufen (RNA binding protein) homolog 1 (Drosophila)	20853	1.08	0.70	1.19	0.90	-0.47 ns
Bysl	bystin-like	53414	0.46	0.50	0.36	1.27	0.37 ns
Taf9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	108143	2.53	3.34	3.94	0.64	-0.81 ns
Pxmp4	peroxisomal membrane protein 4	59038	0.38	0.34	0.42	0.89	-0.19 ns
Tlr3	toll-like receptor 3	142980	0.30	0.31	0.50	0.60	-0.66 ns
Rasa2	RAS p21 protein activator 2	114713	0.57	0.69	0.66	0.85	-0.03 ns
Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	18475	1.26	1.00	1.11	1.13	0.65 ns
Cul3	cullin 3	26554	2.70	2.62	2.18	1.24	0.81 *
Prep	prolyl endopeptidase	19072	1.16	0.99	0.98	1.17	-0.11 ns

Bat2	HLA-B associated transcript 2	53761	3.21	2.93	2.01	1.59	0.87 *
Serpinb6b	serine (or cysteine) peptidase inhibitor, clade B, member 6b	20708	0.16	0.06	0.77	0.20	-0.47 ns
Ing3	inhibitor of growth family, member 3	71777	0.53	0.58	0.54	0.97	0.38 ns
Arf5	ADP-ribosylation factor 5	11844	1.19	1.37	1.83	0.65	-0.53 ns
Rims2	regulating synaptic membrane exocytosis 2	116838	0.29	0.38	0.32	0.91	-0.40 ns
Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	12316	1.88	1.89	1.42	1.32	0.84 *
Mrpl36	mitochondrial ribosomal protein L36	94066	0.48	0.60	0.89	0.54	-0.78 ns
Scel	sciellin	64929	6.81	4.99	3.17	2.14	0.83 *
Wdr77	WD repeat domain 77	70465	3.35	3.72	2.29	1.45	0.23 ns
Prkcd	protein kinase C, delta	18753	1.54	1.40	1.44	1.07	0.21 ns
Pabpn1	poly(A) binding protein, nuclear 1	54196	7.18	7.50	6.93	1.03	0.65 ns
Hmga2	high mobility group AT-hook 2	15364	1.54	0.78	0.66	2.30	0.60 ns
Shc1	src homology 2 domain-containing transforming protein C1	20416	0.98	1.04	0.93	1.05	-0.41 ns
Trip4	thyroid hormone receptor interactor 4	56404	0.67	0.48	0.36	1.84	0.98 ***
Runx1	runt related transcription factor 1	12394	0.27	0.19	0.15	1.82	0.05 ns
Sypl	synaptophysin-like protein	19027	4.68	4.49	5.82	0.80	-0.61 ns
Usp8	ubiquitin specific peptidase 8	84092	1.08	1.16	0.98	1.09	0.45 ns
Snrpd3	small nuclear ribonucleoprotein D3	67332	4.28	3.93	3.84	1.11	0.13 ns
Clk4	CDC like kinase 4	12750	0.62	0.53	0.70	0.88	-0.23 ns
Rnf5	ring finger protein 5	54197	1.62	1.30	1.26	1.28	0.43 ns
Vamp4	vesicle-associated membrane protein 4	53330	1.11	1.14	0.81	1.35	0.69 ns
Hspb1	heat shock protein 1	15507	2.64	2.40	8.01	0.33	-0.39 ns
Diap3	diaphanous homolog 3 (Drosophila)	56419	0.61	0.57	0.71	0.86	0.25 ns
Dnmt1	DNA methyltransferase (cytosine-5) 1	13433	3.84	3.54	3.49	1.10	0.69 ns
Hist1h4a		326619	0.38	0.27	0.38	0.98	0.35 ns
Hist1h4b		326620	0.38	0.27	0.38	0.98	0.35 ns
Hist1h4c		319155	0.38	0.27	0.38	0.98	0.35 ns
Hist1h4h		69386	0.38	0.27	0.38	0.98	0.35 ns
Hist1h4i		319158	0.38	0.27	0.38	0.98	0.35 ns
Hist1h4j		319159	0.38	0.27	0.38	0.98	0.35 ns
Hist1h4k		319160	0.38	0.27	0.38	0.98	0.35 ns
Hist1h4m		319161	0.38	0.27	0.38	0.98	0.35 ns
Itgb6	integrin beta 6	16420	0.26	0.36	0.33	0.80	-0.05 ns
Met	met proto-oncogene	17295	0.50	0.40	0.34	1.47	0.14 ns
Refbp2		56009	3.36	3.39	3.76	0.89	0.22 ns
Glrx2	glutaredoxin 2 (thioltransferase)	69367	0.96	0.90	0.71	1.35	-0.01 ns
Espn	espin	56226	0.14	0.35	0.45	0.31	-0.66 ns
Insl3		16336	0.44	0.39	0.32	1.37	0.66 ns
Jak3		16453	0.44	0.39	0.32	1.37	0.66 ns
Schip1	schwannomin interacting protein 1	30953	1.23	1.35	1.25	0.98	0.42 ns
LOC675857		675857	4.35	4.46	5.78	0.75	-0.69 ns
Vcp		269523	4.35	4.46	5.78	0.75	-0.69 ns
Maea	macrophage erythroblast attacher	59003	1.43	1.50	1.41	1.01	0.15 ns
Bzw1	basic leucine zipper and W2 domains 1	66882	1.56	1.58	1.51	1.02	-0.30 ns
Bzw1	basic leucine zipper and W2 domains 1	66882	4.14	3.79	2.88	1.43	0.40 ns
Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	13205	5.79	6.72	7.21	0.80	-0.10 ns
Prosc	proline synthetase co-transcribed	114863	0.72	0.83	0.75	0.96	0.34 ns
Ncbp2	nuclear cap binding protein subunit 2	68092	2.84	2.74	2.56	1.11	0.34 ns
Tollip	toll interacting protein	54473	0.84	0.76	0.80	1.05	0.44 ns
Arf4	ADP-ribosylation factor 4	11843	4.32	3.96	3.87	1.11	0.47 ns
Capza2	capping protein (actin filament) muscle Z-line, alpha 2	12343	5.09	5.12	5.20	0.97	0.17 ns
Ptk2	PTK2 protein tyrosine kinase 2	14083	1.89	1.84	2.17	0.87	-0.83 *
Pa2g4	proliferation-associated 2G4	18813	2.67	2.46	1.93	1.37	0.38 ns
Dnmt3a	DNA methyltransferase 3A	13435	0.84	0.92	1.46	0.57	-0.78 ns
Cdk5rap3	CDK5 regulatory subunit associated protein 3	80280	0.90	0.97	1.10	0.81	-0.38 ns
Ift172	intraflagellar transport 172 homolog (Chlamydomonas)	67661	0.52	0.56	0.91	0.56	-0.76 ns
Adnp	activity-dependent neuroprotective protein	11538	5.62	5.24	5.36	1.04	-0.31 ns
EG270335		270335	0.76	0.69	0.31	2.44	0.27 ns
EG622782		622782	0.76	0.69	0.31	2.44	0.27 ns
EG666200		666200	0.76	0.69	0.31	2.44	0.27 ns
EG666464		666464	0.76	0.69	0.31	2.44	0.27 ns
LOC544983		544983	0.76	0.69	0.31	2.44	0.27 ns
LOC545175		545175	0.76	0.69	0.31	2.44	0.27 ns
LOC619711		619711	0.76	0.69	0.31	2.44	0.27 ns
LOC624831		624831	0.76	0.69	0.31	2.44	0.27 ns
Lman2	lectin, mannose-binding 2	66890	0.57	0.60	0.66	0.86	-0.95 **
Snx9	sorting nexin 9	66616	1.21	1.14	0.79	1.53	0.52 ns
Sc4mol	sterol-C4-methyl oxidase-like	66234	3.32	3.28	3.86	0.85	-0.71 ns
LOC546321		546321	12.32	11.07	8.97	1.37	0.88 *
Tomm20		67952	12.32	11.07	8.97	1.37	0.88 *
Rab33b	RAB33B, member of RAS oncogene family	19338	1.58	1.39	0.88	1.78	0.94 **
Tmod3	tropomodulin 3	50875	1.14	0.93	1.28	0.89	0.05 ns
Sec61g	SEC61, gamma subunit	20335	3.71	3.50	4.19	0.88	-0.10 ns
Crbn	cereblon	58799	0.91	0.81	1.05	0.86	-0.49 ns
Capn7	calpain 7	12339	1.61	1.64	1.62	0.99	-0.30 ns
Mettl3	methyltransferase-like 3	56335	0.79	0.77	0.76	1.03	0.03 ns
Fos	FBJ osteosarcoma oncogene	14281	1.21	1.49	1.39	0.87	-0.59 ns
Paqr4	progestin and adipoQ receptor family member IV	76498	0.77	0.73	0.37	2.06	0.69 ns
Rnf10	ring finger protein 10	50849	1.74	1.54	2.13	0.81	-0.68 ns
Rfx5	regulatory factor X, 5 (influences HLA class II expression)	53970	0.48	0.45	0.39	1.22	0.86 *
Irs1	insulin receptor substrate 1	16367	1.51	1.12	0.84	1.78	0.06 ns
Yeats4	YEATS domain containing 4	64050	1.65	1.37	1.15	1.42	0.53 ns
Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	22210	3.15	2.99	3.62	0.87	-0.57 ns
Slc25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	57279	1.11	1.12	1.32	0.84	-0.16 ns
Atp5a1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	11946	6.37	6.20	6.34	1.00	0.45 ns

Dom3z	DOM-3 homolog Z (C. elegans)	112403	0.60	0.56	0.44	1.35	0.86	*
1200014J11Rik	RIKEN cDNA 1200014J11 gene	66874	0.69	0.64	0.80	0.86	-0.16	ns
Rshl2a		66832	1.91	1.82	1.42	1.34	0.96	**
Rshl2b		#######	1.91	1.82	1.42	1.34	0.96	**
Avpi1	arginine vasopressin-induced 1	69534	1.10	1.20	1.30	0.85	-0.76	ns
Atp1b3	ATPase, Na+/K+ transporting, beta 3 polypeptide	11933	2.51	2.26	2.14	1.17	0.75	ns
Impa1	inositol (myo)-1(or 4)-monophosphatase 1	55980	2.03	2.26	1.88	1.08	-0.22	ns
Aip	aryl-hydrocarbon receptor-interacting protein	11632	1.40	1.43	1.18	1.18	0.84	*
Shoc2	soc-2 (suppressor of clear) homolog (C. elegans)	56392	2.58	2.01	1.73	1.48	0.82	*
Sfrs5	splicing factor, arginine/serine-rich 5 (SRp40, HRS)	20384	10.19	8.01	8.63	1.17	0.55	ns
5730427N09Rik		59050	2.32	3.07	3.32	0.70	-0.75	ns
EG433230		433230	2.32	3.07	3.32	0.70	-0.75	ns
LOC636306		636306	2.32	3.07	3.32	0.70	-0.75	ns
Rala	v-ral simian leukemia viral oncogene homolog A (ras related)	56044	1.48	1.55	2.11	0.70	-0.40	ns
Skp1a	S-phase kinase-associated protein 1A	21402	6.44	5.85	6.59	0.97	-0.07	ns
Dnajb11	DnaJ (Hsp40) homolog, subfamily B, member 11	67838	1.38	1.42	1.70	0.81	-0.44	ns
Vapb	vesicle-associated membrane protein, associated protein B and C	56491	2.42	2.24	2.27	1.06	-0.32	ns
Gnpnat1	glucosamine-phosphate N-acetyltransferase 1	54342	0.61	0.73	0.83	0.74	-0.86	*
Dld	dihydrolipoamide dehydrogenase	13382	1.23	1.23	1.59	0.77	-0.53	ns
Spred1	sprouty protein with EVH-1 domain 1, related sequence	114715	0.40	0.46	0.47	0.83	-0.22	ns
Bat4	HLA-B associated transcript 4	81845	0.47	0.40	0.37	1.27	0.89	*
Mta2	metastasis-associated gene family, member 2	23942	1.94	1.60	1.37	1.41	0.85	*
Pard6b	par-6 (partitioning defective 6) homolog beta (C. elegans)	58220	1.98	1.88	1.98	0.99	-0.56	ns
Tob1	transducer of ErbB-2.1	22057	1.43	1.30	3.03	0.47	-0.67	ns
Abi1	abl-interactor 1	11308	2.01	1.85	1.50	1.33	0.46	ns
Gabarapl2	gamma-aminobutyric acid (GABA-A) receptor-associated protein-like 2	93739	2.23	1.97	1.74	1.27	0.97	**
6720456B07Rik	RIKEN cDNA 6720456B07 gene	101314	3.42	3.51	4.68	0.73	-0.67	ns
Fnbp4	formin binding protein 4	55935	1.03	0.79	0.68	1.50	0.40	ns
Pspc1	paraspeckle protein 1	66645	2.14	2.32	1.16	1.84	0.59	ns
Hiat1	hippocampus abundant gene transcript 1	15247	1.94	1.98	1.90	1.02	-0.44	ns
Ncor1	nuclear receptor co-repressor 1	20185	2.71	2.64	2.68	1.01	-0.06	ns
Tm9sf4	transmembrane 9 superfamily protein member 4	99237	0.67	0.58	0.73	0.91	-0.27	ns
2310003F16Rik	RIKEN cDNA 2310003F16 gene	67693	2.18	1.80	1.81	1.19	0.53	ns
Tmem167	transmembrane protein 167	66074	0.34	0.44	0.59	0.58	-0.85	*
Nola3	nucleolar protein family A, member 3	66181	5.38	4.36	4.34	1.23	0.71	ns
Phc1	polyhomeotic-like 1 (Drosophila)	13619	1.00	1.18	1.39	0.71	-0.85	*
Spcs2	signal peptidase complex subunit 2 homolog (S. cerevisiae)	66624	2.35	2.33	2.44	0.96	0.21	ns
2510049I19Rik	RIKEN cDNA 2510049I19 gene	67922	1.62	1.75	1.58	1.02	0.58	ns
Mrpl49	mitochondrial ribosomal protein L49	18120	1.54	1.38	0.98	1.56	0.81	*
Prdx6	peroxiredoxin 6	11758	3.11	2.60	1.84	1.68	0.33	ns
Inpp5e	inositol polyphosphate-5-phosphatase E	64436	0.42	0.31	0.21	1.95	0.48	ns
Psmd5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	66998	1.66	1.43	1.14	1.44	0.75	ns
Ap3b1	adaptor-related protein complex 3, beta 1 subunit	11774	1.64	1.91	2.24	0.73	-0.75	ns
Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	14423	0.50	0.62	0.82	0.61	-0.59	ns
Tfdp1		21781	2.97	3.24	4.26	0.69	-0.70	ns
Mrps36	mitochondrial ribosomal protein S36	66128	0.56	0.70	0.96	0.58	-0.88	*
Cops7a	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana)	26894	1.00	1.03	1.09	0.91	-0.64	ns
Txndc4	thioredoxin domain containing 4 (endoplasmic reticulum)	76299	1.07	1.06	1.40	0.76	-0.54	ns
Nktr	natural killer tumor recognition sequence	18087	1.04	0.99	0.99	1.05	0.37	ns
Luc7l2	LUC7-like 2 (S. cerevisiae)	192196	3.66	4.09	3.54	1.03	0.11	ns
Atp6v1g1		66290	4.05	4.46	5.90	0.68	-0.78	ns
EG623365		623365	8.78	8.75	7.56	1.16	0.03	ns
LOC633468		633468	8.78	8.75	7.56	1.16	0.03	ns
Bop1	block of proliferation 1	12181	0.94	0.92	1.09	0.85	-0.25	ns
Minpp1	multiple inositol polyphosphate histidine phosphatase 1	17330	1.85	1.70	1.27	1.45	0.71	ns
Nedd4l	neural precursor cell expressed, developmentally down-regulated gene 4-like	83814	1.89	1.75	1.57	1.19	0.37	ns
Polg	polymerase (DNA directed), gamma	18975	0.65	0.51	0.71	0.91	-0.23	ns
Ints6	integrator complex subunit 6	18130	1.39	1.51	0.94	1.47	0.19	ns
Ptprk	protein tyrosine phosphatase, receptor type, K	19272	1.70	1.20	0.92	1.84	0.48	ns
Pitpna	phosphatidylinositol transfer protein, alpha	18738	2.12	2.37	1.88	1.12	0.13	ns
1810029B16Rik	RIKEN cDNA 1810029B16 gene	66282	0.38	0.40	0.40	0.95	0.27	ns
Hyou1	hypoxia up-regulated 1	12282	1.18	1.27	1.08	1.09	0.66	ns
Psmd8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	57296	2.34	2.44	3.41	0.68	-0.55	ns
Add3	adducin 3 (gamma)	27360	0.36	0.50	0.31	1.16	-0.34	ns
Copb1	coatomer protein complex, subunit beta 1	70349	1.22	1.19	1.47	0.83	-0.53	ns
Paxip1	PAX interacting (with transcription-activation domain) protein 1	55982	1.17	1.35	1.46	0.80	-0.39	ns
Rnf111	ring finger 111	93836	1.32	0.85	0.97	1.35	0.73	ns
2010002N04Rik	RIKEN cDNA 2010002N04 gene	106878	0.60	0.59	0.53	1.13	0.62	ns
Tgoln2		22135	0.50	0.58	0.79	0.62	-0.68	ns
Tgoln1	trans-golgi network protein	22134	2.48	2.68	2.57	0.96	-0.09	ns
Tpbg	trophoblast glycoprotein	21983	0.66	0.62	0.48	1.37	0.85	*
Tmem39a	transmembrane protein 39a	67846	0.59	0.68	0.81	0.72	-0.57	ns
3110001D03Rik	RIKEN cDNA 3110001D03 gene	66928	0.70	0.65	0.89	0.78	-0.53	ns
Tacstd2	tumor-associated calcium signal transducer 2	56753	2.13	2.70	3.04	0.70	-0.85	*
Pnn	pinin	18949	1.85	2.19	3.28	0.56	-0.84	*
Sdcbp	syndecan binding protein	53378	5.88	5.25	5.97	0.98	-0.22	ns
1110004F10Rik	RIKEN cDNA 1110004F10 gene	56372	1.28	1.34	1.53	0.83	-0.69	ns
Degs1	degenerative spermatocyte homolog 1 (Drosophila)	13244	1.60	1.83	1.84	0.87	-0.80	ns
Sec23a	SEC23A (S. cerevisiae)	20334	1.34	1.36	1.76	0.76	-0.42	ns
Socs5	suppressor of cytokine signaling 5	56468	0.88	0.79	0.67	1.31	0.88	*
Mrpl1	mitochondrial ribosomal protein L1	94061	0.41	0.41	0.26	1.57	0.77	ns
Snap29	synaptosomal-associated protein	67474	0.33	0.36	0.43	0.76	-0.73	ns
Sort1	sortilin 1	20661	0.76	0.85	0.11	6.68	0.00	ns
Aktip	thymoma viral proto-oncogene 1 interacting protein	14339	1.95	2.25	2.44	0.79	-0.88	*

Cacna1g	calcium channel, voltage-dependent, T type, alpha 1G subunit	12291	0.33	0.32	0.12	2.66	0.56 ns
Wnt7a	wingless-related MMTV integration site 7A	22421	0.71	0.73	0.70	1.01	0.32 ns
Laptm4a	lysosomal-associated protein transmembrane 4A	17775	8.04	6.65	8.27	0.97	-0.45 ns
Fmr1	fragile X mental retardation syndrome 1 homolog	14265	2.52	2.14	2.75	0.91	0.06 ns
Csnk1g2	casein kinase 1, gamma 2	103236	1.73	1.37	1.39	1.24	0.53 ns
Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	66979	0.75	0.88	1.15	0.65	-0.53 ns
Rpp30	ribonuclease P/MRP 30 subunit (human)	54364	1.86	1.87	1.42	1.30	0.88 *
Ncoa6	nuclear receptor coactivator 6	56406	1.83	1.70	2.07	0.88	-0.56 ns
Osbpl9	oxysterol binding protein-like 9	100273	1.82	1.68	1.90	0.95	-0.66 ns
Actr8	ARP8 actin-related protein 8 homolog (S. cerevisiae)	56249	0.80	0.78	0.95	0.84	-0.27 ns
Psmd9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	67151	0.65	0.67	0.66	0.98	0.07 ns
Smad7	MAD homolog 7 (Drosophila)	17131	0.39	0.46	0.37	1.04	0.35 ns
Siah1a	seven in absentia 1A	20437	0.87	0.99	0.99	0.87	0.30 ns
Git2	G protein-coupled receptor kinase-interactor 2	26431	1.04	0.93	1.01	1.03	0.30 ns
Tsnax	translin-associated factor X	53424	1.70	1.64	1.02	1.66	0.89 *
Taf12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor	66464	0.41	0.41	0.44	0.91	-0.68 ns
Fbln2	fibulin 2	14115	0.70	0.58	1.57	0.45	-0.15 ns
2500003M10Rik	RIKEN cDNA 2500003M10 gene	66511	3.34	4.12	3.18	1.04	0.20 ns
Fdps	farnesyl diphosphate synthetase	110196	6.29	5.95	8.18	0.76	-0.63 ns
Pdia3	protein disulfide isomerase associated 3	14827	4.86	3.81	3.98	1.22	0.25 ns
1300012G16Rik	RIKEN cDNA 1300012G16 gene	71772	0.29	0.45	0.48	0.61	-0.78 ns
Mybbp1a	MYB binding protein (P160) 1a	18432	2.81	2.85	2.75	1.02	0.48 ns
Gsta3	glutathione S-transferase, alpha 3	14859	1.14	0.78	0.15	7.77	0.29 ns
1110001A07Rik	RIKEN cDNA 1110001A07 gene	66140	1.00	0.94	0.96	1.03	-0.25 ns
Tfb2m	transcription factor B2, mitochondrial	15278	0.77	0.60	0.48	1.61	0.37 ns
Fbxw2	F-box and WD-40 domain protein 2	30050	0.55	0.45	0.46	1.18	0.62 ns
Rock1	Rho-associated coiled-coil containing protein kinase 1	19877	1.90	2.16	2.17	0.88	-0.14 ns
Dapk3	death-associated kinase 3	13144	0.86	0.66	0.77	1.11	0.09 ns
Clpx	caseinolytic peptidase X (E.coli)	270166	0.56	0.52	0.60	0.93	0.20 ns
Rab11b		19326	2.68	2.00	1.98	1.35	0.81 *
Actn4	actinin alpha 4	60595	3.87	4.14	4.30	0.90	-0.74 ns
Hs3st1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	15476	0.29	0.40	0.50	0.57	-0.94 **
Pgrmc1	progesterone receptor membrane component 1	53328	3.80	3.82	4.84	0.78	-0.61 ns
Stk17b	serine/threonine kinase 17b (apoptosis-inducing)	98267	0.74	0.66	0.44	1.65	0.97 **
Nol12	nucleolar protein 12	97961	1.20	1.14	1.32	0.91	-0.17 ns
Ptma	prothymosin alpha	19231	20.50	19.99	17.18	1.19	0.74 ns
Bzw2	basic leucine zipper and W2 domains 2	66912	0.94	0.92	0.74	1.27	0.16 ns
Cops2	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana)	12848	2.38	1.72	1.79	1.32	0.63 ns
Ubl3	ubiquitin-like 3	24109	2.37	1.91	2.09	1.13	-0.09 ns
Map3k7ip2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	68652	3.81	3.10	3.06	1.24	0.23 ns
Frrs1		20321	1.50	1.84	1.21	1.24	0.13 ns
Sept2	septin 2	18000	3.07	2.80	2.03	1.50	0.86 *
Top1	topoisomerase (DNA) I	21969	3.94	4.14	3.93	1.00	-0.51 ns
Nol11	nucleolar protein 11	68979	1.17	1.11	1.22	0.95	0.33 ns
Cript	cysteine-rich PDZ-binding protein	56724	3.05	2.42	2.07	1.47	0.96 **
Fbxo3	F-box protein 3	57443	1.24	0.77	0.64	1.93	0.77 ns
Mrpl45	mitochondrial ribosomal protein L45	67036	1.48	1.17	1.37	1.08	-0.05 ns
Decr2	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	26378	0.39	0.33	0.25	1.55	0.58 ns
Max	Max protein	17187	0.30	0.29	0.41	0.73	-0.73 ns
Sirt2	sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)	64383	0.66	0.58	0.69	0.95	-0.28 ns
Myst4	MYST histone acetyltransferase monocytic leukemia 4	54169	0.49	0.49	0.39	1.24	0.20 ns
Asf1a	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	66403	2.48	2.17	1.46	1.69	0.64 ns
AW209491	expressed sequence AW209491	105351	0.75	0.72	0.68	1.10	0.35 ns
Csk	c-src tyrosine kinase	12988	0.95	0.85	0.77	1.24	0.81 *
Lmnb1	lamin B1	16906	1.45	1.57	1.73	0.83	0.15 ns
LOC639633		639633	1.37	1.54	0.87	1.57	0.63 ns
Npm3		18150	1.37	1.54	0.87	1.57	0.63 ns
Mastl	microtubule associated serine/threonine kinase-like	67121	0.51	0.46	0.49	1.03	-0.21 ns
Rnf44	ring finger protein 44	105239	2.36	1.88	1.98	1.19	0.55 ns
Rhot1	ras homolog gene family, member T1	59040	1.48	1.50	1.25	1.17	0.18 ns
Pdcd2	programmed cell death 2	18567	0.87	0.76	0.47	1.83	0.67 ns
Strn3	striatin, calmodulin binding protein 3	94186	4.03	4.07	4.57	0.88	-0.53 ns
Pms2	postmeiotic segregation increased 2 (S. cerevisiae)	18861	0.77	0.69	0.64	1.20	0.87 *
Ergic3	ERGIC and golgi 3	66366	2.41	2.28	2.86	0.84	-0.56 ns
Leprotl1	leptin receptor overlapping transcript-like 1	68192	0.84	0.91	1.20	0.70	-0.29 ns
Ifngr2	interferon gamma receptor 2	15980	0.30	0.34	0.92	0.33	-0.76 ns
Paics	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarboxamide synthetase	67054	9.82	10.23	8.99	1.09	-0.13 ns
Psma7	proteasome (prosome, macropain) subunit, alpha type 7	26444	2.38	2.51	2.86	0.83	-0.72 ns
Bcl2l2	Bcl2-like 2	12050	0.44	0.46	0.67	0.66	-0.81 ns
Wbscr22	Williams Beuren syndrome chromosome region 22	66138	0.92	0.96	0.91	1.01	0.14 ns
Ankrd32	ankyrin repeat domain 32	105377	0.46	0.60	0.77	0.60	-0.75 ns
Igfbp7	insulin-like growth factor binding protein 7	29817	6.45	6.24	6.63	0.97	0.33 ns
Axl	AXL receptor tyrosine kinase	26362	0.47	0.44	0.48	0.98	0.43 ns
Arpc4	actin related protein 2/3 complex, subunit 4	68089	2.66	2.23	2.93	0.90	-0.53 ns
Fgfr1op2	FGFR1 oncogene partner 2	67529	3.12	2.71	2.86	1.08	0.60 ns
Rock2	Rho-associated coiled-coil containing protein kinase 2	19878	1.33	1.49	1.36	0.97	0.27 ns
Mdm2	transformed mouse 3T3 cell double minute 2	17246	0.75	0.89	1.04	0.72	-0.78 ns
Mgat1	mannoside acetylglucosaminyltransferase 1	17308	0.47	0.56	0.64	0.72	-0.77 ns
Clp1	CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	98985	0.41	0.30	0.39	1.05	-0.24 ns
Ssfa2	sperm specific antigen 2	70599	0.46	0.44	0.42	1.10	-0.34 ns
Tarbp2	TAR (HIV) RNA binding protein 2	21357	0.62	0.58	0.54	1.15	0.63 ns

Cenpq	centromere protein Q	83815	1.03	0.97	0.73	1.40	0.76 ns
Slc33a1	solute carrier family 33 (acetyl-CoA transporter), member 1	11416	0.71	0.92	0.76	0.93	-0.50 ns
Ccnl1	cyclin L1	56706	3.01	3.48	2.22	1.35	0.55 ns
Fancl	Fanconi anemia, complementation group L	67030	0.60	0.62	0.60	0.99	-0.24 ns
Dnajc19	DnaJ (Hsp40) homolog, subfamily C, member 19	67713	1.43	1.43	1.13	1.26	0.31 ns
Dst	dystonin	13518	1.07	1.00	0.24	4.48	0.30 ns
Nqo1	NAD(P)H dehydrogenase, quinone 1	18104	0.97	0.87	0.40	2.43	0.69 ns
Pcdhga1		93709	0.30	0.38	0.19	1.54	0.35 ns
Pcdhga10		93722	0.30	0.38	0.19	1.54	0.35 ns
Pcdhga11		93723	0.30	0.38	0.19	1.54	0.35 ns
Pcdhga12		93724	0.30	0.38	0.19	1.54	0.35 ns
Pcdhga2		93710	0.30	0.38	0.19	1.54	0.35 ns
Pcdhga3		93711	0.30	0.38	0.19	1.54	0.35 ns
Pcdhga4		93712	0.30	0.38	0.19	1.54	0.35 ns
Pcdhga5		93713	0.30	0.38	0.19	1.54	0.35 ns
Pcdhga6		93714	0.30	0.38	0.19	1.54	0.35 ns
Pcdhga7		93715	0.30	0.38	0.19	1.54	0.35 ns
Pcdhga8		93716	0.30	0.38	0.19	1.54	0.35 ns
Pcdhga9		93717	0.30	0.38	0.19	1.54	0.35 ns
Pcdhgb1		93699	0.30	0.38	0.19	1.54	0.35 ns
Pcdhgb2		93700	0.30	0.38	0.19	1.54	0.35 ns
Pcdhgb4		93701	0.30	0.38	0.19	1.54	0.35 ns
Pcdhgb5		93702	0.30	0.38	0.19	1.54	0.35 ns
Pcdhgb6		93703	0.30	0.38	0.19	1.54	0.35 ns
Pcdhgb7		93704	0.30	0.38	0.19	1.54	0.35 ns
Pcdhgb8		93705	0.30	0.38	0.19	1.54	0.35 ns
Pcdhgc3		93706	0.30	0.38	0.19	1.54	0.35 ns
Pcdhgc4		93707	0.30	0.38	0.19	1.54	0.35 ns
Pcdhgc5		93708	0.30	0.38	0.19	1.54	0.35 ns
Cnot7	CCR4-NOT transcription complex, subunit 7	18983	3.65	3.82	4.89	0.74	-0.41 ns
Tubb2c	tubulin, beta 2c	227613	6.98	7.20	7.77	0.89	-0.19 ns
Zdhhc3	zinc finger, DHHC domain containing 3	69035	0.55	0.59	0.58	0.94	0.37 ns
Pdia6	protein disulfide isomerase associated 6	71853	2.54	2.64	2.74	0.92	-0.31 ns
Tmem68	transmembrane protein 68	72098	0.42	0.36	0.48	0.87	-0.25 ns
Isca1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	69046	2.11	1.55	1.51	1.39	0.61 ns
Rnf4	ring finger protein 4	19822	1.81	1.69	1.99	0.91	-0.64 ns
1500010J02Rik	RIKEN cDNA 1500010J02 gene	68964	1.04	0.82	1.17	0.88	-0.24 ns
Tbc1d17	TBC1 domain family, member 17	233204	0.48	0.47	0.49	0.98	-0.20 ns
Rpl5	ribosomal protein L5	19983	28.13	25.04	21.49	1.30	0.90 *
Mat2a	methionine adenosyltransferase II, alpha	232087	3.76	4.07	3.69	1.01	-0.08 ns
Srpr	signal recognition particle receptor ('docking protein')	67398	1.95	1.66	1.53	1.27	0.86 *
Ttc30b	tetratricopeptide repeat domain 30B	72421	0.35	0.34	0.28	1.22	-0.23 ns
BC017643	cDNA sequence BC017643	217370	0.48	0.49	0.60	0.80	-0.16 ns
Fads1	fatty acid desaturase 1	76267	5.23	5.04	5.21	1.00	0.00 ns
Cdca4	cell division cycle associated 4	71963	2.77	3.22	3.75	0.73	-0.65 ns
Prr13	proline rich 13	66151	3.30	3.42	3.87	0.85	-0.74 ns
Man2c1	mannosidase, alpha, class 2C, member 1	73744	1.69	1.27	1.25	1.35	0.83 *
Ndufa8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	68375	3.03	2.72	2.45	1.23	0.25 ns
Kctd10	potassium channel tetramerisation domain containing 10	330171	1.33	1.34	1.61	0.82	-0.58 ns
Edem2	ER degradation enhancer, mannosidase alpha-like 2	108687	1.10	1.03	1.54	0.71	-0.57 ns
Psmd6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	66413	3.84	3.45	3.14	1.21	0.96 **
Ncaph2	non-SMC condensin II complex, subunit H2	52683	3.50	3.21	3.75	0.93	0.21 ns
Coasy	Coenzyme A synthase	71743	0.69	0.71	0.86	0.80	-0.16 ns
H1f0	H1 histone family, member 0	14958	13.24	11.87	8.60	1.53	0.95 **
Ppan	peter pan homolog (Drosophila)	235036	0.42	0.37	0.43	0.97	0.43 ns
Tmem50b	transmembrane protein 50B	77975	1.09	0.70	0.91	1.20	0.01 ns
Dlst	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	78920	2.26	2.35	2.58	0.87	-0.05 ns
Ndufaf1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	69702	0.79	0.56	0.45	1.72	0.64 ns
Asf1b	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	66929	1.44	1.48	1.95	0.73	-0.07 ns
Nedd8	neural precursor cell expressed, developmentally down-regulated gene 8	18002	3.55	3.18	3.97	0.89	-0.24 ns
Ak3	adenylate kinase 3	56248	2.75	2.88	1.64	1.66	0.66 ns
Tpm1	tropomyosin 1, alpha	22003	5.47	4.58	3.78	1.44	0.84 *
Tmem49	transmembrane protein 49	75909	2.41	2.58	3.46	0.69	-0.93 **
Zwint	ZW10 interactor	52696	2.63	2.28	2.53	1.03	-0.40 ns
Pls3	plastin 3 (T-isoform)	102866	2.22	2.99	2.83	0.78	-0.73 ns
Cnih	cornichon homolog (Drosophila)	12793	2.95	2.99	3.20	0.92	-0.76 ns
Clptm1l	CLPTM1-like	218335	2.70	3.79	4.49	0.60	-0.76 ns
Tram1	translocating chain-associating membrane protein 1	72265	2.72	2.36	2.45	1.10	0.24 ns
Fiz1	Flt3 interacting zinc finger protein 1	23877	0.87	0.93	0.86	1.01	-0.42 ns
Wdr36	WD repeat domain 36	225348	0.59	0.69	0.81	0.72	-0.16 ns
Dym	dymeclin	69190	0.37	0.53	0.60	0.60	-0.08 ns
Ndufs3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	68349	2.73	1.93	1.91	1.42	0.47 ns
Aplp2	amyloid beta (A4) precursor-like protein 2	11804	8.39	7.14	7.60	1.10	0.62 ns
Rbm10	RNA binding motif protein 10	236732	2.35	2.30	3.00	0.78	-0.47 ns
Eif2s3x	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	26905	2.64	3.19	3.63	0.72	-0.76 ns
Txndc5	thioredoxin domain containing 5	105245	1.55	1.40	1.57	0.99	0.27 ns
Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	228026	3.16	3.57	4.29	0.73	-0.72 ns
Rangap1	RAN GTPase activating protein 1	19387	1.26	1.46	1.64	0.77	-0.14 ns
Ddx47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	67755	1.22	1.27	1.40	0.87	0.15 ns
Ifitm3	interferon induced transmembrane protein 3	66141	0.68	1.16	5.20	0.13	-0.67 ns
Zcchc8	zinc finger, CCHC domain containing 8	70650	1.70	1.73	1.55	1.09	0.19 ns
Tmco1	transmembrane and coiled-coil domains 1	68944	5.34	5.03	4.08	1.30	0.43 ns
Mrpl37	mitochondrial ribosomal protein L37	56280	0.44	0.43	0.57	0.76	-0.16 ns
Pak1ip1	PAK1 interacting protein 1	68083	2.03	2.16	2.08	0.97	-0.01 ns
Ptcd2	pentatricopeptide repeat domain 2	68927	0.41	0.50	0.66	0.61	-0.67 ns

Gpbp1	GC-rich promoter binding protein 1	73274	2.86	3.96	3.90	0.73	-0.53	ns
Prc1	protein regulator of cytokinesis 1	233406	1.84	1.98	2.38	0.77	0.09	ns
Tbc1d22a	TBC1 domain family, member 22a	223754	0.68	0.62	0.65	1.03	-0.14	ns
Gars	glycyl-tRNA synthetase	353172	2.81	3.06	3.27	0.86	-0.63	ns
Egln1	EGL nine homolog 1 (C. elegans)	112405	2.55	2.39	2.27	1.11	0.48	ns
8430410A17Rik	RIKEN cDNA 8430410A17 gene	232210	0.84	0.81	0.78	1.07	0.71	ns
Nup133	nucleoporin 133	234865	1.40	1.49	1.07	1.30	0.71	ns
BC005624	cDNA sequence BC005624	227707	0.96	1.13	0.70	1.36	0.49	ns
D2Ertd391e	DNA segment, Chr 2, ERATO Doi 391, expressed	51897	0.32	0.28	0.29	1.11	0.05	ns
Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	71514	2.76	3.07	2.93	0.94	-0.67	ns
Eif1	eukaryotic translation initiation factor 1	20918	14.95	14.88	15.60	0.95	-0.77	ns
Dars	aspartyl-tRNA synthetase	226414	2.37	2.23	1.87	1.26	0.38	ns
Gltscr2	glioma tumor suppressor candidate region gene 2	68077	2.59	2.65	2.75	0.93	-0.51	ns
Ints4	integrator complex subunit 4	101861	0.45	0.52	0.49	0.91	-0.52	ns
Calm2	calmodulin 2	12314	16.41	14.95	12.88	1.27	0.98	***
Tcf19	transcription factor 19	106795	4.55	4.07	3.11	1.46	0.93	**
Ppme1	protein phosphatase methylesterase 1	72590	0.80	0.60	0.92	0.86	-0.26	ns
Sf3a3	splicing factor 3a, subunit 3	75062	1.18	1.27	1.37	0.85	-0.28	ns
AW146242	expressed sequence AW146242	232023	1.23	1.72	2.08	0.59	-0.99	***
Ddx41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	72935	0.66	0.69	0.81	0.81	-0.27	ns
Ddx56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	52513	0.53	0.54	0.57	0.94	-0.03	ns
Arl6ip1	ADP-ribosylation factor-like 6 interacting protein 1	54208	4.87	4.71	4.69	1.03	0.40	ns
Elof1	elongation factor 1 homolog (ELF1, S. cerevisiae)	66126	1.93	1.62	1.48	1.30	0.82	*
Tmem168	transmembrane protein 168	101118	0.49	0.54	0.62	0.79	-0.63	ns
Mrto4	MRT4, mRNA turnover 4, homolog (S. cerevisiae)	69902	0.66	0.94	0.75	0.89	0.20	ns
Gpr177	G protein-coupled receptor 177	68151	4.97	4.94	3.60	1.37	-0.02	ns
Noc4l	nucleolar complex associated 4 homolog (S. cerevisiae)	100608	0.98	0.93	0.99	0.99	-0.12	ns
Fasn	fatty acid synthase	14104	3.17	3.03	2.94	1.07	0.78	ns
0910001A06Rik	RIKEN cDNA 0910001A06 gene	223601	4.10	3.86	2.21	1.85	0.16	ns
Brp44	brain protein 44	70456	1.96	2.12	1.31	1.48	0.28	ns
Gga1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	106039	0.80	0.64	0.85	0.94	0.16	ns
2400003C14Rik	RIKEN cDNA 2400003C14 gene	71955	3.09	3.22	2.31	1.33	0.76	ns
Tuba1b	tubulin, alpha 1B	22143	27.09	24.38	20.66	1.30	0.98	***
Ncapd2	non-SMC condensin I complex, subunit D2	68298	2.06	2.25	3.12	0.66	-0.43	ns
Mphosph6	M phase phosphoprotein 6	68533	0.90	0.92	0.67	1.34	0.77	ns
Clk3	CDC-like kinase 3	102414	0.40	0.38	0.58	0.69	-0.35	ns
Nsun2	NOL1/NOP2/Sun domain family 2	28114	1.18	1.84	2.38	0.49	-0.83	*
Rasl11b	RAS-like, family 11, member B	68939	3.80	2.99	2.04	1.85	0.87	*
Mrpl30	mitochondrial ribosomal protein L30	107734	3.50	3.43	3.12	1.12	0.96	**
Abcf2	ATP-binding cassette, sub-family F (GCN20), member 2	27407	0.45	0.53	0.61	0.73	-0.67	ns
Nrbp1	nuclear receptor binding protein 1	192292	0.61	0.49	0.83	0.74	-0.57	ns
Tmem63a	transmembrane protein 63a	208795	0.34	0.40	0.43	0.79	-0.61	ns
Lsm1	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)	67207	0.68	0.74	0.79	0.85	-0.13	ns
Chaf1b	chromatin assembly factor 1, subunit B (p60)	110749	2.23	2.06	2.53	0.88	-0.66	ns
D030056L22Rik	RIKEN cDNA D030056L22 gene	225995	1.99	1.75	1.50	1.32	0.84	*
Saps3	SAPS domain family, member 3	52036	2.63	2.11	1.60	1.63	0.97	**
Rfwd3	ring finger and WD repeat domain 3	234736	1.97	2.17	1.78	1.10	0.65	ns
Acsl1	acyl-CoA synthetase long-chain family member 1	14081	0.31	0.38	0.33	0.93	-0.57	ns
Cirh1a	cirrhosis, autosomal recessive 1A (human)	21771	1.21	1.58	0.91	1.33	0.47	ns
Lamc1	laminin, gamma 1	226519	0.91	0.89	0.71	1.28	0.07	ns
Gstt3	glutathione S-transferase, theta 3	103140	0.69	0.66	0.47	1.45	0.58	ns
Dalrd3	DALR anticodon binding domain containing 3	67789	0.45	0.43	0.44	1.02	-0.11	ns
Cugbp2	CUG triplet repeat, RNA binding protein 2	14007	1.60	1.42	0.81	1.95	0.81	ns
Rnf187	ring finger protein 187	108660	3.97	4.07	4.01	0.98	-0.57	ns
Trip12	thyroid hormone receptor interactor 12	14897	4.47	4.26	3.21	1.38	0.50	ns
Arhgef12	Rho guanine nucleotide exchange factor (GEF) 12	69632	3.92	3.02	2.80	1.39	0.88	*
Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	225887	6.33	8.38	5.97	1.06	-0.35	ns
Tmem176a	transmembrane protein 176A	66058	0.31	0.55	0.89	0.34	-0.67	ns
Ppp2r5a	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	226849	1.66	1.58	1.19	1.39	0.55	ns
Aspscr1	alveolar soft part sarcoma chromosome region, candidate 1 (human)	68938	0.69	0.72	0.91	0.75	-0.61	ns
C630004H02Rik	RIKEN cDNA C630004H02 gene	217310	0.46	0.59	0.26	1.77	0.63	ns
Mlf2	myeloid leukemia factor 2	30853	3.09	3.02	3.31	0.93	-0.45	ns
Rhbdd1	rhomboid domain containing 1	76867	1.30	1.27	0.80	1.62	0.42	ns
BC023882	cDNA sequence BC023882	231123	1.31	1.33	1.64	0.79	-0.15	ns
Ints3	integrator complex subunit 3	229543	0.95	1.32	0.90	1.06	0.15	ns
Tspan14	tetraspanin 14	52588	1.34	1.46	1.61	0.83	-0.53	ns
Dhx16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	69192	1.22	1.15	0.88	1.38	0.78	ns
Slc35b2	solute carrier family 35, member B2	73836	0.95	0.83	0.60	1.58	0.99	***
Anapc4	anaphase promoting complex subunit 4	52206	1.56	1.64	1.83	0.84	-0.55	ns
1600029D21Rik	RIKEN cDNA 1600029D21 gene	76509	6.30	6.88	5.83	1.08	0.58	ns
Kctd5	potassium channel tetramerisation domain containing 5	69259	0.84	0.72	0.67	1.24	0.68	ns
Llgl2	lethal giant larvae homolog 2 (Drosophila)	217325	1.36	1.16	1.33	1.02	0.29	ns
Yif1a	Yip1 interacting factor homolog A (S. cerevisiae)	68090	3.07	2.68	1.99	1.53	0.99	***
Camk2g	calcium/calmodulin-dependent protein kinase II gamma	12325	0.69	0.73	0.65	1.05	0.15	ns
Pdlim2	PDZ and LIM domain 2	213019	0.58	0.54	0.70	0.82	-0.33	ns
1110008P14Rik	RIKEN cDNA 1110008P14 gene	73737	0.94	1.05	0.66	1.41	0.08	ns
Bag2	Bcl2-associated athanogene 2	213539	1.68	1.62	1.38	1.22	-0.16	ns
Ube2z	ubiquitin-conjugating enzyme E2Z (putative)	268470	2.10	1.90	2.45	0.85	-0.65	ns
Tm2d3	TM2 domain containing 3	68634	0.37	0.35	0.51	0.71	-0.43	ns
Krt7	keratin 7	110310	7.40	7.72	7.26	1.01	0.58	ns
Cdkal1	CDK5 regulatory subunit associated protein 1-like 1	68916	0.51	0.43	0.38	1.32	0.95	**
C3	complement component 3	12266	1.01	2.22	3.93	0.26	-0.33	ns
Lass2	longevity assurance homolog 2 (S. cerevisiae)	76893	2.25	2.24	1.98	1.13	0.04	ns
Smap1	stromal membrane-associated protein 1	98366	1.23	1.31	1.10	1.11	0.29	ns
Ttc33	tetratricopeptide repeat domain 33	67515	0.97	0.99	0.93	1.03	0.04	ns
Cpsf3l	cleavage and polyadenylation specific factor 3-like	71957	0.79	0.88	1.03	0.76	-0.44	ns

Cd99l2	Cd99 antigen-like 2	171486	0.53	0.55	0.79	0.66	-0.45	ns
Nup37	nucleoporin 37	69736	1.46	1.47	1.06	1.37	0.70	ns
Thoc3	THO complex 3	73666	1.20	1.07	1.11	1.08	0.70	ns
Etfa	electron transferring flavoprotein, alpha polypeptide	110842	3.76	2.87	3.02	1.24	0.75	ns
Numa1	nuclear mitotic apparatus protein 1	101706	1.73	1.78	2.11	0.82	-0.59	ns
4930453N24Rik	RIKEN cDNA 4930453N24 gene	67609	1.37	1.21	1.05	1.29	0.58	ns
Fusip1	FUS interacting protein (serine-arginine rich) 1	14105	2.11	2.50	2.70	0.78	-0.69	ns
Cdc26	cell division cycle 26	66440	0.68	0.82	0.88	0.77	-0.43	ns
Rab28	RAB28, member RAS oncogene family	100972	1.48	1.63	1.37	1.07	0.21	ns
Nol14	nucleolar protein 14	75416	0.56	0.67	0.62	0.91	-0.14	ns
Gatad2a	GATA zinc finger domain containing 2A	234366	2.59	2.13	2.27	1.14	0.55	ns
Atp6v1f	ATPase, H+ transporting, lysosomal V1 subunit F	66144	4.16	4.41	5.58	0.74	-0.61	ns
Kif1b	kinesin family member 1B	16561	0.41	0.44	0.61	0.67	-0.13	ns
Gtf3c5	general transcription factor IIIC, polypeptide 5	70239	0.67	0.65	0.41	1.64	0.60	ns
Abl1	v-abl Abelson murine leukemia oncogene 1	11350	0.93	0.89	0.70	1.34	0.04	ns
Rps11	ribosomal protein S11	27207	16.62	16.08	14.94	1.11	0.31	ns
Mki67ip	Mki67 (FHA domain) interacting nucleolar phosphoprotein	67949	0.83	0.80	0.57	1.45	0.58	ns
Pdcl3	phosducin-like 3	68833	1.91	2.04	1.74	1.09	0.56	ns
4930444A02Rik	RIKEN cDNA 4930444A02 gene	74653	0.68	0.53	0.35	1.96	0.97	**
B230219D22Rik	RIKEN cDNA B230219D22 gene	78521	6.20	5.21	5.33	1.16	0.81	ns
Aarsd1	alanyl-tRNA synthetase domain containing 1	69684	0.71	0.78	0.82	0.86	0.22	ns
Etf1	eukaryotic translation termination factor 1	225363	1.55	1.70	1.70	0.91	0.19	ns
2310007F21Rik	RIKEN cDNA 2310007F21 gene	66939	0.50	0.34	0.35	1.42	0.84	*
Hint1	histidine triad nucleotide binding protein 1	15254	11.78	11.89	12.98	0.90	-0.33	ns
Nol1	nucleolar protein 1	110109	0.52	0.71	0.65	0.80	-0.49	ns
Arl6ip6		65103	1.50	1.37	1.70	0.88	-0.11	ns
LOC674449		674449	1.50	1.37	1.70	0.88	-0.11	ns
Osgin1	oxidative stress induced growth inhibitor 1	71839	0.75	0.65	0.47	1.61	-0.03	ns
Atpbd3	ATP binding domain 3	233189	0.32	0.40	0.35	0.90	-0.31	ns
Mcfd2	multiple coagulation factor deficiency 2	193813	1.53	1.31	1.18	1.29	0.94	**
BC013529	cDNA sequence BC013529	215751	0.87	0.68	0.66	1.32	0.46	ns
5830457O10Rik	RIKEN cDNA 5830457O10 gene	214987	1.70	1.78	1.22	1.39	0.65	ns
Tspyl4	TSPY-like 4	72480	0.47	0.41	0.21	2.20	0.54	ns
Prpf6	PRP6 pre-mRNA splicing factor 6 homolog (yeast)	68879	1.12	1.15	1.13	0.98	-0.29	ns
2310044H10Rik	RIKEN cDNA 2310044H10 gene	69683	0.85	0.98	1.20	0.70	-0.22	ns
Tmem66	transmembrane protein 66	67887	2.40	2.57	3.10	0.77	-0.41	ns
Mtap7d1	microtubule-associated protein 7 domain containing 1	245877	0.68	0.62	0.74	0.92	0.14	ns
Tmem5	transmembrane protein 5	216395	0.72	0.74	0.64	1.13	0.04	ns
Ppil4	peptidylprolyl isomerase (cyclophilin)-like 4	67418	0.80	0.84	0.67	1.18	0.27	ns
Jmjd2b	jumonji domain containing 2B	193796	0.45	0.36	0.30	1.49	0.90	*
5730437N04Rik	RIKEN cDNA 5730437N04 gene	70544	1.17	0.92	0.53	2.20	0.86	*
Bub1	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	12235	1.83	2.10	2.79	0.65	-0.24	ns
Dera	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	232449	0.60	0.60	0.62	0.96	0.27	ns
Cyb5r1	cytochrome b5 reductase 1	72017	1.98	1.91	1.77	1.11	-0.32	ns
Lrrc42	leucine rich repeat containing 42	77809	0.56	0.47	0.64	0.86	-0.28	ns
Col4a2	procollagen, type IV, alpha 2	12827	1.04	0.80	0.81	1.27	0.48	ns
Thap4	THAP domain containing 4	67026	1.23	1.11	0.89	1.38	0.74	ns
Tcf25	transcription factor 25 (basic helix-loop-helix)	66855	2.58	2.96	1.92	1.34	0.49	ns
Btbd2	BTB (POZ) domain containing 2	208198	1.16	0.96	0.95	1.21	0.13	ns
Ncoa5	nuclear receptor coactivator 5	228869	0.43	0.46	0.42	1.04	-0.06	ns
Gdap2	ganglioside-induced differentiation-associated-protein 2	14547	0.65	0.73	0.60	1.09	0.05	ns
Suv420h2	suppressor of variegation 4-20 homolog 2 (Drosophila)	232811	0.46	0.43	0.54	0.83	-0.49	ns
Neil3	nei like 3 (E. coli)	234258	0.22	0.16	0.38	0.58	-0.09	ns
Manbal	mannosidase, beta A, lysosomal-like	69161	0.55	0.50	0.56	0.99	0.48	ns
Ube2d1	ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog (yeast)	216080	0.74	1.04	1.09	0.67	-0.85	*
Rab1b	RAB1B, member RAS oncogene family	76308	2.54	2.29	1.73	1.46	0.82	*
Napg	N-ethylmaleimide sensitive fusion protein attachment protein gamma	108123	0.61	0.59	0.87	0.70	-0.26	ns
BC018507	cDNA sequence BC018507	218333	0.73	0.96	1.22	0.59	-0.61	ns
2010107G23Rik	RIKEN cDNA 2010107G23 gene	69894	0.36	0.36	0.41	0.86	0.05	ns
5430437P03Rik	RIKEN cDNA 5430437P03 gene	68251	1.79	1.80	2.28	0.78	-0.14	ns
9430016H08Rik	RIKEN cDNA 9430016H08 gene	68115	0.96	0.95	0.67	1.42	0.32	ns
Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1	66569	0.47	0.54	0.53	0.90	-0.56	ns
Urm1	ubiquitin related modifier 1 homolog (S. cerevisiae)	68205	0.57	0.48	0.41	1.38	0.73	ns
Dcps	decapping enzyme, scavenger	69305	0.77	0.75	0.50	1.52	0.86	*
Pcgf6	polycomb group ring finger 6	71041	1.85	1.95	1.47	1.25	0.17	ns
Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	17992	6.05	5.44	5.74	1.05	-0.05	ns
Oaf	OAF homolog (Drosophila)	102644	1.08	0.80	0.69	1.56	0.94	**
Myg1	melanocyte proliferating gene 1	60315	1.79	1.70	1.43	1.25	0.83	*
AI449175	expressed sequence AI449175	234362	0.38	0.35	0.46	0.83	-0.39	ns
Epb4.1	erythrocyte protein band 4.1	269587	1.09	1.11	0.80	1.36	0.54	ns
Nek9	NIMA (never in mitosis gene a)-related expressed kinase 9	217718	2.68	2.66	2.83	0.94	0.08	ns
Rtcd1	RNA terminal phosphate cyclase domain 1	66368	1.51	1.49	1.28	1.17	0.92	**
Atg4b	autophagy-related 4B (yeast)	66615	0.53	0.47	0.49	1.07	-0.25	ns
Syf2	SYF2 homolog, RNA splicing factor (S. cerevisiae)	68592	1.02	0.92	1.00	1.02	0.21	ns
Kif18a	kinesin family member 18A	228421	0.27	0.31	0.33	0.79	-0.02	ns
Glo1	glyoxalase 1	109801	1.94	1.98	1.27	1.53	0.64	ns
Nme1	expressed in non-metastatic cells 1, protein	18102	2.28	2.14	1.97	1.15	0.22	ns
Igf2r	insulin-like growth factor 2 receptor	16004	0.90	0.83	0.71	1.27	-0.31	ns
Lamb1-1	laminin B1 subunit 1	16777	3.85	3.83	4.04	0.95	-0.74	ns
Ppp5c	protein phosphatase 5, catalytic subunit	19060	0.78	0.63	0.76	1.03	-0.26	ns
BC056474	cDNA sequence BC056474	414077	1.47	1.31	1.38	1.06	0.57	ns
Spc25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	66442	2.59	2.48	2.03	1.27	0.73	ns
Prkab1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	19079	2.35	2.41	3.50	0.67	-0.85	*
Rnf8	ring finger protein 8	58230	0.69	0.67	0.50	1.37	0.76	ns
Commd1	COMM domain containing 1	17846	0.90	1.00	1.44	0.63	-0.28	ns
Mospd2	motile sperm domain containing 2	76763	1.60	1.77	2.08	0.77	-0.13	ns
Alas1	aminolevulinic acid synthase 1	11655	0.58	0.47	0.72	0.81	-0.41	ns

Aurkb	aurora kinase B	20877	1.00	1.18	1.73	0.58	-0.33	ns
Ptrf	polymerase I and transcript release factor	19285	2.84	3.38	2.99	0.94	0.36	ns
Tmem98	transmembrane protein 98	103743	3.78	3.58	3.55	1.06	-0.43	ns
Rspry1	ring finger and SPRY domain containing 1	67610	0.69	0.69	0.74	0.93	0.39	ns
EG667598		667598	0.86	0.93	0.83	1.04	0.49	ns
LOC624822		624822	0.86	0.93	0.83	1.04	0.49	ns
Rhbdf1	rhomboid family 1 (Drosophila)	13650	2.48	2.43	2.56	0.97	0.09	ns
Rap1a	RAS-related protein-1a	109905	3.93	4.36	3.45	1.13	0.09	ns
Hectd1	HECT domain containing 1	207304	4.88	4.19	5.14	0.94	-0.43	ns
Cdt1	chromatin licensing and DNA replication factor 1	67177	6.72	6.68	4.75	1.41	0.73	ns
Ahsa1	AHA1, activator of heat shock protein ATPase homolog 1 (yeast)	217737	2.71	2.83	3.38	0.80	-0.53	ns
Nsmce2	non-SMC element 2 homolog (MMS21, S. cerevisiae)	68501	1.05	1.12	1.24	0.84	-0.27	ns
Jtv1	JTV1 gene	231872	1.41	1.58	1.66	0.84	-0.43	ns
Isca2	iron-sulfur cluster assembly 2 homolog (S. cerevisiae)	74316	1.31	1.23	1.45	0.90	-0.17	ns
Rbl1	retinoblastoma-like 1 (p107)	19650	2.81	2.67	3.17	0.88	0.11	ns
Alg5	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltransferase)	66248	1.02	1.03	1.05	0.96	-0.46	ns
Ddx27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	228889	0.71	0.83	1.07	0.66	-0.64	ns
Rmnd5b	required for meiotic nuclear division 5 homolog B (S. cerevisiae)	66089	0.64	0.63	0.98	0.65	-0.84	*
Mrpl50	mitochondrial ribosomal protein L50	28028	0.39	0.38	0.41	0.94	-0.56	ns
Sharpin	SHANK-associated RH domain interacting protein	106025	0.77	0.78	1.13	0.68	-0.71	ns
Msh3	mutS homolog 3 (E. coli)	17686	0.42	0.50	0.67	0.63	-0.96	**
Pmm1	phosphomannomutase 1	29858	1.04	1.07	1.72	0.60	-0.83	*
Capzb	capping protein (actin filament) muscle Z-line, beta	12345	3.57	3.48	3.59	0.99	0.08	ns
Phf5a	PHD finger protein 5A	68479	2.05	1.78	2.33	0.88	-0.02	ns
Hagh	hydroxyacyl glutathione hydrolase	14651	1.20	1.27	1.23	0.97	-0.12	ns
Shkbp1	Sh3kbp1 binding protein 1	192192	1.10	1.03	1.09	1.00	0.22	ns
Tef	thyrotroph embryonic factor	21685	1.00	0.96	0.95	1.05	0.45	ns
Plekhj1	pleckstrin homology domain containing, family J member 1	78670	0.60	0.50	0.55	1.09	-0.35	ns
Acat1	acetyl-Coenzyme A acetyltransferase 1	110446	1.91	1.67	1.53	1.24	0.88	*
Acadvl	acyl-Coenzyme A dehydrogenase, very long chain	11370	1.52	1.45	2.24	0.67	-0.48	ns
Rabgap1	RAB GTPase activating protein 1	227800	1.69	1.38	1.12	1.51	0.47	ns
Pigc	phosphatidylinositol glycan anchor biosynthesis, class C	67292	0.84	0.62	0.51	1.62	0.51	ns
Tmem41a	transmembrane protein 41a	66664	0.71	0.57	0.67	1.06	-0.35	ns
1500011H22Rik	RIKEN cDNA 1500011H22 gene	68948	0.96	0.99	1.04	0.92	-0.20	ns
Pwp2	PWP2 periodic tryptophan protein homolog (yeast)	110816	0.36	0.38	0.41	0.88	-0.32	ns
Yipf1	Yip1 domain family, member 1	230584	0.59	0.60	0.63	0.93	-0.49	ns
Dlg5	discs, large homolog 5 (Drosophila)	71228	1.16	1.19	0.88	1.31	0.13	ns
Seh1l	SEH1-like (S. cerevisiae	72124	2.31	2.50	2.85	0.81	-0.19	ns
Ncln	nicalin homolog (zebrafish)	103425	0.87	0.82	0.70	1.24	0.61	ns
Mrpl13	mitochondrial ribosomal protein L13	68537	3.49	3.00	3.36	1.03	0.03	ns
Smarca5		93762	4.36	4.78	4.85	0.89	-0.09	ns
Ptger4	prostaglandin E receptor 4 (subtype EP4)	19219	0.49	0.72	0.95	0.51	-0.71	ns
Rars2	arginyl-tRNA synthetase 2, mitochondrial (putative)	109093	0.66	0.75	0.62	1.06	0.35	ns
Erlin1	ER lipid raft associated 1	226144	1.66	1.80	1.19	1.38	0.78	ns
9430023L20Rik	RIKEN cDNA 9430023L20 gene	68118	0.79	0.78	0.83	0.94	0.30	ns
Ubiad1	UbiA prenyltransferase domain containing 1	71707	0.40	0.37	0.42	0.96	0.30	ns
9130213B05Rik	RIKEN cDNA 9130213B05 gene	231440	0.20	0.33	0.35	0.56	-0.71	ns
Fundc1	FUN14 domain containing 1	72018	0.73	0.66	0.88	0.82	-0.50	ns
Papola	poly (A) polymerase alpha	18789	1.10	1.21	1.84	0.60	-0.60	ns
Porcn	porcupine homolog (Drosophila)	53627	0.22	0.20	0.46	0.47	-0.31	ns
Rad23b	RAD23b homolog (S. cerevisiae)	19359	1.71	1.70	2.04	0.83	-0.79	ns
Asb8	ankyrin repeat and SOCS box-containing protein 8	78541	0.81	0.75	0.95	0.84	-0.50	ns
Polr3h	polymerase (RNA) III (DNA directed) polypeptide H	78929	0.66	0.69	0.73	0.90	-0.20	ns
Ormdl2	ORM1-like 2 (S. cerevisiae)	66844	2.06	1.82	1.75	1.18	-0.05	ns
Tbc1d10b	TBC1 domain family, member 10b	68449	1.05	1.15	1.33	0.79	-0.48	ns
Zfp639	zinc finger protein 639	67778	0.95	0.86	0.70	1.34	0.93	**
Sirt7	sirtuin 7 (silent mating type information regulation 2, homolog) 7 (S. cerevisiae)	209011	1.20	0.89	1.25	0.96	0.24	ns
2310066E14Rik	RIKEN cDNA 2310066E14 gene	75687	0.76	0.84	0.69	1.10	0.47	ns
Arfip2	ADP-ribosylation factor interacting protein 2	76932	0.57	0.62	0.76	0.75	-0.85	*
Slc30a6	solute carrier family 30 (zinc transporter), member 6	210148	1.21	0.90	0.64	1.89	0.94	**
Bphl	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	68021	0.71	0.51	0.62	1.14	-0.27	ns
Tes	testis derived transcript	21753	1.99	2.42	2.49	0.80	0.13	ns
Erc1	ELKS/RAB6-interacting/CAST family member 1	111173	0.52	0.53	0.59	0.88	-0.21	ns
Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	71704	0.19	0.28	0.29	0.63	-0.30	ns
Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	50926	7.74	6.94	5.36	1.44	0.88	*
Supt5h	suppressor of Ty 5 homolog (S. cerevisiae)	20924	1.83	1.80	1.63	1.12	0.80	ns
Polr2d	polymerase (RNA) II (DNA directed) polypeptide D	69241	0.81	0.78	0.91	0.88	0.26	ns
Zfp672	zinc finger protein 672	319475	0.48	0.36	0.39	1.22	0.23	ns
2810003C17Rik	RIKEN cDNA 2810003C17 gene	108897	1.64	1.45	1.08	1.51	0.59	ns
Med6	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)	69792	0.54	0.70	0.65	0.83	-0.26	ns
Smox	spermine oxidase	228608	0.60	0.77	1.71	0.35	-0.58	ns
Trim41	tripartite motif-containing 41	211007	0.81	0.91	1.03	0.78	-0.73	ns
Uchl5ip	UCHL5 interacting protein	73738	0.31	0.34	0.41	0.74	-0.62	ns
Birc5	baculoviral IAP repeat-containing 5	11799	3.24	3.51	4.03	0.80	0.26	ns
Mospd1	motile sperm domain containing 1	70380	0.37	0.34	0.45	0.82	-0.08	ns
Ubap2	ubiquitin-associated protein 2	68926	1.33	1.10	1.38	0.96	-0.41	ns
Jtb	jumping translocation breakpoint	23922	2.74	3.02	2.49	1.10	0.50	ns
Arl6ip4	ADP-ribosylation factor-like 6 interacting protein 4	65105	1.66	1.62	1.78	0.93	-0.01	ns
Prkx	protein kinase, X-linked	19108	0.70	0.62	0.84	0.83	0.03	ns
Nup93	nucleoporin 93	71805	1.59	1.62	2.03	0.78	0.01	ns
Depdc1a	DEP domain containing 1a	76131	0.68	0.82	0.96	0.70	-0.59	ns
Tmem55a	transmembrane protein 55A	72519	1.02	1.21	1.06	0.96	-0.16	ns
Ppp4r1	protein phosphatase 4, regulatory subunit 1	70351	2.11	2.00	1.44	1.46	0.88	*
Gclc	glutamate-cysteine ligase, catalytic subunit	14629	1.03	1.10	0.84	1.22	0.38	ns

Zfp282	zinc finger protein 282	101095	0.32	0.24	0.28	1.14	0.26	ns
Gemin6	gem (nuclear organelle) associated protein 6	67242	0.72	0.72	0.60	1.19	0.86	*
Zfp219	zinc finger protein 219	69890	0.44	0.32	0.41	1.09	-0.24	ns
Depdc7	DEP domain containing 7	211896	1.68	0.95	0.64	2.62	0.63	ns
Mocs2	molybdenum cofactor synthesis 2	17434	0.80	0.96	1.25	0.64	-0.76	ns
Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	75406	2.68	2.31	2.28	1.17	0.28	ns
Prpf3	PRP3 pre-mRNA processing factor 3 homolog (yeast)	70767	1.38	1.39	0.99	1.39	0.84	*
1110004E09Rik	RIKEN cDNA 1110004E09 gene	68001	0.41	0.44	0.60	0.68	-0.90	*
Slc25a19	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	67283	0.35	0.30	0.39	0.91	-0.56	ns
1110067D22Rik	RIKEN cDNA 1110067D22 gene	216551	1.29	1.06	1.11	1.16	0.20	ns
Traf7	Tnf receptor-associated factor 7	224619	1.15	0.96	0.73	1.57	0.99	***
Rfc4	replication factor C (activator 1) 4	106344	2.61	2.74	3.45	0.75	-0.49	ns
Noc2l	nucleolar complex associated 2 homolog (S. cerevisiae)	57741	0.48	0.42	0.44	1.09	-0.05	ns
Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	77805	1.01	1.27	1.04	0.96	0.41	ns
Lemd2	LEM domain containing 2	224640	0.40	0.41	0.36	1.09	0.54	ns
3200002M19Rik	RIKEN cDNA 3200002M19 gene	75430	0.25	0.33	0.52	0.48	-0.88	*
Prrg2	proline-rich Gla (G-carboxyglutamic acid) polypeptide 2	65116	0.29	0.43	0.44	0.66	-0.37	ns
Rab40c	Rab40c, member RAS oncogene family	224624	1.11	1.01	0.72	1.52	0.69	ns
Rg9mtd1	RNA (guanine-9-) methyltransferase domain containing 1	52575	0.39	0.44	0.54	0.71	-0.77	ns
Ppcdc	phosphopantothenoylcysteine decarboxylase	66812	0.51	0.34	0.35	1.47	0.61	ns
Snx15	sorting nexin 15	69024	0.60	0.51	0.62	0.96	-0.10	ns
Fyttd1	forty-two-three domain containing 1	69823	1.49	1.44	2.25	0.66	-0.85	*
Eif1a	eukaryotic translation initiation factor 1A	13664	1.67	2.03	1.76	0.94	-0.29	ns
Ube2m	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	22192	0.96	1.20	1.44	0.66	-0.69	ns
Ppp6c	protein phosphatase 6, catalytic subunit	67857	1.16	1.16	0.95	1.21	0.84	*
1110007A13Rik	RIKEN cDNA 1110007A13 gene	210711	0.88	0.80	1.01	0.86	-0.29	ns
Lpgat1	lysophosphatidylglycerol acyltransferase 1	226856	1.21	1.00	0.84	1.42	0.51	ns
Wfdc2	WAP four-disulfide core domain 2	67701	11.49	13.02	16.24	0.70	-0.84	*
Lrpprc	leucine-rich PPR-motif containing	72416	1.18	1.09	0.78	1.51	0.76	ns
Metrnl	meteorin, glial cell differentiation regulator-like	210029	0.30	0.32	0.43	0.70	-0.15	ns
Tmem45b	transmembrane protein 45b	235135	1.54	1.48	0.89	1.73	0.67	ns
Ube2e2	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	218793	0.53	0.57	0.53	0.98	0.30	ns
BC019943	cDNA sequence BC019943	234138	0.32	0.36	0.36	0.89	-0.26	ns
1110020P15Rik	RIKEN cDNA 1110020P15 gene	66152	2.28	2.21	2.86	0.79	-0.36	ns
1810037I17Rik	RIKEN cDNA 1810037I17 gene	67704	5.08	5.06	4.69	1.08	0.18	ns
Dolk	dolichol kinase	227697	0.76	0.75	0.50	1.51	0.89	*
Ubqln1	ubiquilin 1	56085	4.44	3.60	4.52	0.98	0.05	ns
Mrpl32	mitochondrial ribosomal protein L32	75398	1.21	1.13	1.54	0.78	-0.53	ns
Cdc42ep1	CDC42 effector protein (Rho GTPase binding) 1	104445	1.04	0.87	0.84	1.23	-0.04	ns
BC003885	cDNA sequence BC003885	225215	1.09	1.04	0.92	1.18	0.78	ns
Ldlrap1	low density lipoprotein receptor adaptor protein 1	100017	0.60	0.61	0.72	0.83	-0.58	ns
Vps37b	vacuolar protein sorting 37B (yeast)	330192	0.44	0.52	0.47	0.92	-0.49	ns
Sf4	splicing factor 4	70616	1.00	1.27	0.98	1.01	0.50	ns
Tmem51	transmembrane protein 51	214359	1.10	1.29	1.14	0.95	0.44	ns
5830417I10Rik	RIKEN cDNA 5830417I10 gene	76022	0.79	0.81	0.51	1.53	0.72	ns
Cluap1	clusterin associated protein 1	76779	0.59	0.71	0.67	0.88	-0.52	ns
Nrd1	nardilysin, N-arginine dibasic convertase, NRD convertase 1	230598	1.09	0.95	1.10	0.99	0.06	ns
Selm	selenoprotein M	114679	0.32	0.41	0.26	1.24	0.49	ns
Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	72162	1.49	1.32	0.88	1.68	0.46	ns
Uck1	uridine-cytidine kinase 1	22245	0.51	0.54	0.56	0.92	-0.62	ns
Mbip	MAP3K12 binding inhibitory protein 1	217588	0.63	0.65	0.84	0.75	-0.57	ns
Cbx6	chromobox homolog 6	494448	4.22	4.22	4.26	0.99	-0.41	ns
Cldn23	claudin 23	71908	0.50	0.51	0.30	1.63	0.29	ns
Ttc8	tetratricopeptide repeat domain 8	76260	0.65	0.68	0.49	1.32	0.43	ns
Nkiras2	NFKB inhibitor interacting Ras-like protein 2	71966	1.02	0.79	0.99	1.02	0.16	ns
Lrrc14	leucine rich repeat containing 14	223664	0.52	0.57	0.91	0.57	-0.69	ns
Ccpg1	cell cycle progression 1	72278	0.56	0.55	0.59	0.94	0.39	ns
Flad1	RFad1, flavin adenine dinucleotide synthetase, homolog (yeast)	319945	0.52	0.41	0.45	1.15	-0.13	ns
Slc39a1	solute carrier family 39 (zinc transporter), member 1	30791	1.29	1.73	1.25	1.03	0.32	ns
Mtap	methylthioadenosine phosphorylase	66902	1.40	1.20	1.47	0.95	-0.23	ns
Tada1l	transcriptional adaptor 1 (HFI1 homolog, yeast) like	27878	0.33	0.38	0.24	1.36	0.31	ns
Mterfd2	MTERF domain containing 2	69821	0.63	0.57	0.42	1.49	0.42	ns
Ubtd1	ubiquitin domain containing 1	226122	0.18	0.21	0.13	1.32	0.23	ns
BC024814	cDNA sequence BC024814	239706	0.29	0.44	0.38	0.76	-0.39	ns
Slc27a4	solute carrier family 27 (fatty acid transporter), member 4	26569	0.72	0.87	0.83	0.86	-0.68	ns
1700030K09Rik	RIKEN cDNA 1700030K09 gene	72254	0.43	0.45	0.47	0.89	0.01	ns
Gprc5c	G protein-coupled receptor, family C, group 5, member C	70355	1.19	1.22	0.81	1.45	0.53	ns
Sltm	SAFB-like, transcription modulator	66660	1.23	1.21	1.15	1.07	0.68	ns
Tmem87a	transmembrane protein 87A	211499	0.43	0.31	0.09	4.59	0.38	ns
Gprasp1	G protein-coupled receptor associated sorting protein 1	67298	0.30	0.28	0.28	1.06	0.54	ns
Dctn2	dynactin 2	69654	3.66	3.26	2.72	1.34	0.68	ns
Ergic2	ERGIC and golgi 2	67456	1.39	1.03	1.03	1.34	0.47	ns
2210010L05Rik	RIKEN cDNA 2210010L05 gene	98682	2.28	2.18	1.28	1.78	0.81	ns
Ccdc58	coiled-coil domain containing 58	381045	1.27	1.25	1.61	0.78	-0.72	ns
Phldb1	pleckstrin homology-like domain, family B, member 1	102693	0.52	0.57	0.42	1.22	0.54	ns
Cpsf4	cleavage and polyadenylation specific factor 4	54188	0.82	0.66	0.61	1.35	0.80	ns
Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	223864	0.31	0.41	0.35	0.86	-0.57	ns
Polr2h	polymerase (RNA) II (DNA directed) polypeptide H	245841	1.11	1.24	1.08	1.03	-0.13	ns
Camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	207565	1.84	1.99	1.01	1.81	0.82	*
Akt2	thymoma viral proto-oncogene 2	11652	0.62	0.66	0.75	0.83	-0.38	ns
Mobkl1b	MOB1, Mps One Binder kinase activator-like 1B (yeast)	232157	0.92	1.07	1.18	0.78	-0.50	ns
Ppa2	pyrophosphatase (inorganic) 2	74776	1.79	1.69	1.57	1.14	-0.31	ns
Trit1	tRNA isopentenyltransferase 1	66966	0.36	0.37	0.49	0.73	-0.49	ns
Utp6	UTP6, small subunit (SSU) processome component, homolog (yeast)	216987	0.76	0.76	0.66	1.13	0.34	ns
Oit1	oncoprotein induced transcript 1	18300	1.03	1.57	1.54	0.67	-0.74	ns
Rin1	Ras and Rab interactor 1	225870	0.57	0.61	0.80	0.71	-0.91	*

Ttc5	tetratricopeptide repeat domain 5	219022	1.22	0.98	1.10	1.10	-0.07 ns
Aurka	aurora kinase A	20878	1.53	1.49	2.16	0.71	-0.55 ns
Rnf126	ring finger protein 126	70294	1.60	1.20	1.45	1.10	0.28 ns
Mtg1	mitochondrial GTPase 1 homolog (S. cerevisiae)	212508	0.32	0.33	0.38	0.83	-0.44 ns
2010305A19Rik	RIKEN cDNA 2010305A19 gene	69893	0.27	0.29	0.39	0.69	-0.58 ns
Heatr1	HEAT repeat containing 1	217995	0.82	0.88	0.86	0.95	-0.29 ns
Tgds	TDP-glucose 4,6-dehydratase	76355	0.41	0.35	0.42	0.97	0.15 ns
Ylpm1	YLP motif containing 1	56531	1.15	1.14	1.07	1.07	0.85 *
Ubl4	ubiquitin-like 4	27643	0.62	0.63	0.99	0.63	-0.58 ns
Hipk1	homeodomain interacting protein kinase 1	15257	2.84	2.06	1.81	1.56	0.38 ns
Tmem70	transmembrane protein 70	70397	0.89	0.92	1.08	0.81	-0.73 ns
S100a4	S100 calcium binding protein A4	20198	0.59	0.80	0.70	0.84	-0.43 ns
Nrbp2	nuclear receptor binding protein 2	223649	0.69	0.52	0.36	1.91	-0.04 ns
BC003965	cDNA sequence BC003965	214489	1.91	1.56	1.09	1.74	0.96 **
Degs2	degenerative spermatocyte homolog 2 (Drosophila), lipid desaturase	70059	0.25	0.27	0.64	0.40	-0.61 ns
Casp8	caspase 8	12370	1.69	1.57	1.51	1.12	0.08 ns
Ppp1r8	protein phosphatase 1, regulatory (inhibitor) subunit 8	100336	0.80	0.77	0.82	0.98	-0.35 ns
9430015G10Rik	RIKEN cDNA 9430015G10 gene	230996	0.33	0.32	0.44	0.76	-0.54 ns
Zcchc9	zinc finger, CCHC domain containing 9	69085	0.45	0.53	0.70	0.65	-0.76 ns
H2afy	H2A histone family, member Y	26914	3.06	2.98	3.32	0.92	0.07 ns
Tmed5	transmembrane emp24 protein transport domain containing 5	73130	2.51	2.82	2.85	0.88	-0.87 *
Rabl5	RAB, member of RAS oncogene family-like 5	67286	0.73	0.85	0.75	0.97	-0.05 ns
Msto1	misato homolog 1 (Drosophila)	229524	0.90	1.00	0.63	1.41	0.31 ns
Arrdc1	arrestin domain containing 1	215705	1.38	1.29	0.90	1.52	0.71 ns
Ranbp10	RAN binding protein 10	74334	0.92	0.70	0.87	1.05	0.41 ns
Ehbp1	EH domain binding protein 1	216565	0.38	0.34	0.41	0.92	-0.49 ns
Ddx19b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b	234733	0.33	0.35	0.31	1.06	0.51 ns
5830433M19Rik	RIKEN cDNA 5830433M19 gene	67770	0.40	0.45	0.55	0.72	-0.78 ns
Lgals7	lectin, galactose binding, soluble 7	16858	1.00	0.92	0.70	1.43	0.82 *
F11r	F11 receptor	16456	3.41	3.60	2.85	1.19	0.02 ns
ORF19	open reading frame 19	68767	0.66	0.60	0.45	1.47	0.92 *
Ddx6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	13209	0.43	0.43	0.30	1.44	0.60 ns
Xrcc4	X-ray repair complementing defective repair in Chinese hamster cells 4	108138	0.22	0.38	0.51	0.44	-0.91 *
Sumf1	sulfatase modifying factor 1	58911	0.68	1.15	1.20	0.56	-0.86 *
BC003993		80744	2.97	3.93	3.05	0.97	-0.05 ns
LOC544818		544818	2.97	3.93	3.05	0.97	-0.05 ns
Trub2	TruB pseudouridine (psi) synthase homolog 2 (E. coli)	227682	0.61	0.72	0.56	1.10	-0.12 ns
Npal2	NIPA-like domain containing 2	223473	0.09	0.11	0.47	0.18	-0.72 ns
Frag1	FGF receptor activating protein 1	233575	1.06	0.89	0.76	1.38	0.19 ns
EG666113		666113	4.18	3.78	3.23	1.29	0.46 ns
Sf3b4		107701	4.18	3.78	3.23	1.29	0.46 ns
D13Wsu177e	DNA segment, Chr 13, Wayne State University 177, expressed	28126	0.83	0.86	1.02	0.80	-0.48 ns
Krcc1	lysine-rich coiled-coil 1	57896	0.94	1.08	1.23	0.76	-0.48 ns
Hsf1	heat shock factor 1	15499	0.62	0.56	0.67	0.92	-0.02 ns
Dennd1a	DENN/MADD domain containing 1A	227801	0.46	0.36	0.24	1.89	0.87 *
1500032D16Rik	RIKEN cDNA 1500032D16 gene	78330	3.61	3.59	3.15	1.14	0.79 ns
Brca1	breast cancer 1	12189	1.87	1.64	2.19	0.85	0.21 ns
Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	19714	4.19	3.22	2.36	1.77	0.52 ns
Eef1a1	eukaryotic translation elongation factor 1 alpha 1	13627	33.05	29.14	23.87	1.38	0.91 *
Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	12575	3.61	3.49	3.91	0.92	-0.58 ns
Hmgcl	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	15356	0.33	0.31	0.50	0.66	-0.57 ns
Arl8a	ADP-ribosylation factor-like 8A	68724	0.35	0.39	0.28	1.25	0.26 ns
Thoc1	THO complex 1	225160	0.67	1.00	0.79	0.85	0.03 ns
Tcof1	Treacher Collins Franceschetti syndrome 1, homolog	21453	0.48	0.60	0.65	0.73	0.06 ns
Tbcc	tubulin-specific chaperone c	72726	0.51	0.47	0.39	1.29	0.94 **
Tnrc6c	trinucleotide repeat containing 6C	217351	0.96	1.04	0.74	1.29	0.70 ns
Uckl1	uridine-cytidine kinase 1-like 1	68556	0.39	0.41	0.60	0.65	-0.91 *
Tspan8	tetraspanin 8	216350	6.26	7.17	7.15	0.87	-0.74 ns
Pdia5	protein disulfide isomerase associated 5	72599	0.40	0.41	0.41	0.96	0.37 ns
Acp2	acid phosphatase 2, lysosomal	11432	0.50	0.49	0.41	1.22	0.88 *
Slit2	slit homolog 2 (Drosophila)	20563	1.07	0.92	1.00	1.06	-0.36 ns
Pmpca	peptidase (mitochondrial processing) alpha	66865	1.43	1.47	1.24	1.15	0.39 ns
Zfyve21	zinc finger, FYVE domain containing 21	68520	1.22	1.33	1.46	0.84	-0.07 ns
Plekhf1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	72287	0.76	0.75	0.73	1.04	0.41 ns
Dmxl1	Dmx-like 1	240283	0.27	0.44	0.44	0.62	-0.80 ns
Slc39a6	solute carrier family 39 (metal ion transporter), member 6	106957	1.19	1.54	1.48	0.80	-0.06 ns
Rab5c	RAB5C, member RAS oncogene family	19345	2.27	2.17	2.50	0.90	-0.26 ns
Exosc4	exosome component 4	109075	0.91	0.88	0.99	0.91	-0.16 ns
Gpr89	G protein-coupled receptor 89	67549	0.88	0.90	0.70	1.24	-0.05 ns
Dtwd1	DTW domain containing 1	69185	0.66	0.53	0.51	1.30	0.50 ns
Gca	grancalcin	227960	0.37	0.45	0.31	1.18	0.36 ns
4921511K06Rik	RIKEN cDNA 4921511K06 gene	232664	0.41	0.50	0.28	1.47	0.67 ns
Rbmx2	RNA binding motif protein, X-linked 2	209003	0.27	0.33	0.54	0.49	-0.41 ns
Zfp51	zinc finger protein 51	22709	0.29	0.36	0.25	1.15	0.35 ns
Tmed10	transmembrane emp24-like trafficking protein 10 (yeast)	68581	3.64	3.47	4.56	0.79	-0.38 ns
Gorasp2	golgi reassembly stacking protein 2	70231	2.03	1.99	1.52	1.33	0.87 *
Tmem2	transmembrane protein 2	83921	0.79	0.89	0.90	0.88	-0.67 ns
Ahctf1	AT hook containing transcription factor 1	226747	1.62	1.57	1.29	1.25	0.69 ns
Calml4	calmodulin-like 4	75600	0.81	0.26	0.13	6.36	0.74 ns
Retsat	retinol saturase (all trans retinol 13,14 reductase)	67442	0.39	0.33	0.36	1.07	0.28 ns
Mis12	MIS12 homolog (yeast)	67139	0.57	0.62	0.86	0.65	-0.78 ns
Mapt	microtubule-associated protein tau	17762	0.15	0.34	0.47	0.33	-0.24 ns
Mgat4b	mannoside acetylglucosaminyltransferase 4, isoenzyme B	103534	2.20	2.32	2.85	0.77	-0.86 *
Mfap3	microfibrillar-associated protein 3	216760	1.72	1.70	1.71	1.00	0.07 ns
Cstf3	cleavage stimulation factor, 3' pre-RNA, subunit 3	228410	1.25	0.97	0.95	1.31	0.66 ns

BC011248	cDNA sequence BC011248	224823	0.78	0.79	0.57	1.35	0.87	*
Eef2	eukaryotic translation elongation factor 2	13629	19.59	17.31	14.25	1.37	0.57	ns
Creb3	cAMP responsive element binding protein 3	12913	0.81	0.77	0.78	1.04	0.17	ns
Kif1c	kinesin family member 1C	16562	1.73	1.88	2.19	0.78	-0.66	ns
Zbtb1	zinc finger and BTB domain containing 1	268564	0.66	0.63	0.88	0.75	-0.87	*
Abt1	activator of basal transcription	30946	0.71	0.82	0.78	0.91	-0.22	ns
Zfp71-rs1	zinc finger protein 71, related sequence 1	235907	0.53	0.81	0.72	0.73	-0.62	ns
Nudt14	nudix (nucleoside diphosphate linked moiety X)-type motif 14	66174	1.25	1.27	1.55	0.80	-0.27	ns
Smyd2	SET and MYND domain containing 2	226830	0.58	0.88	0.51	1.13	0.07	ns
1700027N10Rik	RIKEN cDNA 1700027N10 gene	75564	0.31	0.38	0.22	1.40	0.07	ns
Ercc6l	excision repair cross-complementing rodent repair deficiency complementation group 6 - like	236930	0.90	0.82	1.30	0.69	-0.09	ns
Cald1	caldesmon 1	109624	6.32	5.66	4.56	1.38	0.25	ns
H2afj		232440	1.11	1.02	1.26	0.87	-0.59	ns
Slc25a28	solute carrier family 25, member 28	246696	0.75	0.82	0.66	1.12	0.32	ns
Wdr21	WD repeat domain 21	73828	0.55	0.39	0.85	0.64	-0.63	ns
Reep3	receptor accessory protein 3	28193	4.10	5.23	3.44	1.18	-0.04	ns
Wdr45	WD repeat domain 45	54636	0.61	0.62	0.84	0.72	-0.33	ns
Bcam	basal cell adhesion molecule	57278	1.76	2.08	2.16	0.81	-0.66	ns
Rnf186	ring finger protein 186	66825	0.33	0.29	0.64	0.51	-0.82	*
Enah	enabled homolog (Drosophila)	13800	3.32	3.58	2.63	1.25	-0.31	ns
3300001P08Rik	RIKEN cDNA 3300001P08 gene	67684	3.32	3.31	3.00	1.10	0.49	ns
Ndfip1	Nedd4 family interacting protein 1	65113	2.44	2.84	3.19	0.76	-0.18	ns
Slain1	SLAIN motif family, member 1	105439	0.47	0.53	0.48	0.97	-0.41	ns
Csnk1a1	casein kinase 1, alpha 1	93687	4.49	4.74	4.37	1.02	0.29	ns
Fh1	fumarate hydratase 1	14194	2.83	2.43	1.93	1.46	0.73	ns
A830007P12Rik	RIKEN cDNA A830007P12 gene	227612	0.58	0.43	0.41	1.43	0.74	ns
Ccnk	cyclin K	12454	0.35	0.28	0.40	0.86	0.00	ns
Cpne2	copine II	234577	0.23	0.15	0.40	0.59	-0.66	ns
Itpr2	inositol 1,4,5-triphosphate receptor 2	16439	0.58	0.70	0.79	0.74	-0.86	*
Clasp2	CLIP associating protein 2	76499	0.66	0.80	0.84	0.78	-0.07	ns
Arhgap24	Rho GTPase activating protein 24	231532	1.36	0.97	0.38	3.55	0.35	ns
Angel1	angel homolog 1 (Drosophila)	68737	1.03	1.13	1.91	0.53	-0.61	ns
Map3k1		26401	0.52	0.79	1.05	0.50	-0.93	**
L2hgdh	L-2-hydroxyglutarate dehydrogenase	217666	0.55	0.56	0.62	0.88	-0.46	ns
D930016D06Rik	RIKEN cDNA D930016D06 gene	100662	0.33	0.39	0.34	0.98	0.25	ns
Mib2	mindbomb homolog 2 (Drosophila)	76580	0.35	0.29	0.41	0.85	-0.16	ns
Dhrs7b	dehydrogenase/reductase (SDR family) member 7B	216820	0.58	0.59	0.71	0.81	-0.30	ns
1500031H01Rik	RIKEN cDNA 1500031H01 gene	207740	0.47	0.35	0.52	0.91	-0.48	ns
LOC666849		666849	0.63	0.62	0.52	1.22	0.53	ns
Rnf2	ring finger protein 2	19821	1.67	1.81	1.65	1.01	-0.47	ns
Ptbp1	polypyrimidine tract binding protein 1	19205	7.28	6.70	6.15	1.18	0.40	ns
Spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	229285	0.82	0.76	0.61	1.33	0.82	*
Alad	aminolevulinate, delta-, dehydratase	17025	2.56	2.83	2.69	0.95	-0.13	ns
Sap25	mSin3A-binding protein	751865	0.39	0.30	0.30	1.29	-0.06	ns
Trib1	tribbles homolog 1 (Drosophila)	211770	0.42	0.43	0.47	0.89	-0.27	ns
Nt5dc2	5'-nucleotidase domain containing 2	70021	0.49	0.58	0.41	1.21	0.64	ns
Sfrs7	splicing factor, arginine/serine-rich 7	225027	5.24	5.55	5.23	1.00	0.25	ns
Klhdc8a	kelch domain containing 8A	213417	0.98	0.90	0.55	1.77	0.72	ns
Klhdc4	kelch domain containing 4	234825	0.27	0.34	0.28	0.95	0.34	ns
March2	membrane-associated ring finger (C3HC4) 2	224703	0.67	0.58	0.39	1.71	0.97	***
Zw10	ZW10 homolog (Drosophila), centromere/kinetochore protein	26951	1.17	1.21	1.01	1.15	0.72	ns
Rab13	RAB13, member RAS oncogene family	68328	0.69	0.86	0.60	1.15	0.57	ns
Gpsm2	G-protein signalling modulator 2 (AGS3-like, C. elegans)	76123	0.93	1.18	1.17	0.80	-0.10	ns
Slc39a11	solute carrier family 39 (metal ion transporter), member 11	69806	0.40	0.42	0.35	1.11	0.70	ns
Farsa	phenylalanyl-tRNA synthetase, alpha subunit	66590	0.77	0.69	0.65	1.18	0.74	ns
Slc25a17	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17	20524	0.74	0.52	0.71	1.03	0.00	ns
2310044G17Rik	RIKEN cDNA 2310044G17 gene	217732	0.81	0.65	1.18	0.68	-0.78	ns
2310044G17Rik	RIKEN cDNA 2310044G17 gene	217732	2.60	2.05	3.55	0.73	-0.64	ns
2310044G17Rik	RIKEN cDNA 2310044G17 gene	217732	6.96	5.75	8.83	0.78	-0.66	ns
Zfp764	zinc finger protein 764	233893	0.23	0.33	0.39	0.58	-0.88	*
Tbc1d19	TBC1 domain family, member 19	67249	0.87	0.75	0.75	1.15	0.39	ns
Erbb2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	13866	1.70	1.32	1.51	1.12	0.04	ns
Bst2		69550	0.17	0.27	1.65	0.10	-0.63	ns
2210018M11Rik	RIKEN cDNA 2210018M11 gene	233545	0.49	0.53	0.61	0.79	-0.68	ns
Trim26	tripartite motif protein 26	22670	0.40	0.42	0.29	1.36	0.63	ns
Egfr	epidermal growth factor receptor	13649	0.90	1.00	0.75	1.19	0.40	ns
Myo5c	myosin VC	208943	0.70	0.68	0.68	1.03	-0.47	ns
BC022687	cDNA sequence BC022687	217887	0.43	0.35	0.28	1.54	0.43	ns
Myc	myelocytomatosis oncogene	17869	1.86	1.68	1.51	1.22	-0.03	ns
Dync1li1	dynein cytoplasmic 1 light intermediate chain 1	235661	0.58	0.54	0.69	0.84	-0.36	ns
Baiap2l1	BAI1-associated protein 2-like 1	66898	0.70	0.67	0.80	0.88	-0.79	ns
Ccdc5	coiled-coil domain containing 5	225745	1.24	1.30	1.40	0.88	0.29	ns
Epn3	epsin 3	71889	1.12	0.99	0.80	1.38	0.53	ns
Purg	purine-rich element binding protein G	75029	0.29	0.32	0.40	0.72	-0.27	ns
Ccdc99	coiled-coil domain containing 99	70385	0.52	0.56	0.68	0.77	0.08	ns
Aph1a	anterior pharynx defective 1a homolog (C. elegans)	226548	1.95	1.64	1.70	1.14	0.44	ns
Mylip	myosin regulatory light chain interacting protein	218203	0.96	1.03	0.72	1.32	-0.09	ns
Tyms		22171	1.19	1.20	1.54	0.77	-0.48	ns
8430410K20Rik	RIKEN cDNA 8430410K20 gene	78100	1.70	1.24	0.57	2.98	0.95	**
Cflar	CASP8 and FADD-like apoptosis regulator	12633	0.33	0.36	0.32	1.05	-0.41	ns
Vrk1	vaccinia related kinase 1	22367	1.40	1.33	1.61	0.86	-0.09	ns
Stx18	syntaxin 18	71116	0.55	0.66	0.78	0.71	-0.75	ns
Ephb2	Eph receptor B2	13844	0.49	0.42	0.56	0.88	-0.57	ns
Mcts1	malignant T cell amplified sequence 1	68995	0.56	0.63	0.98	0.57	-0.60	ns

EG621629		621629	3.32	3.42	4.03	0.82	-0.54	ns
Pex16	peroxisome biogenesis factor 16	18633	0.43	0.27	0.33	1.28	0.16	ns
Usp3	ubiquitin specific peptidase 3	235441	0.75	0.60	0.84	0.89	0.05	ns
Mboat2	membrane bound O-acyltransferase domain containing 2	67216	1.70	1.50	1.33	1.27	0.22	ns
Pelp1	proline, glutamic acid and leucine rich protein 1	75273	1.01	0.92	0.97	1.04	0.08	ns
Pla2g4b	phospholipase A2, group IVB (cytosolic)	211429	0.49	0.36	0.32	1.51	0.55	ns
Isoc1	Isochorismatase domain containing 1	66307	0.58	0.85	0.47	1.23	0.41	ns
2510006D16Rik	RIKEN cDNA 2510006D16 gene	76799	1.18	1.07	1.18	1.00	0.31	ns
Zfp472	zinc finger protein 472	224691	0.58	0.46	0.35	1.65	0.74	ns
Mtmr14	myotubularin related protein 14	97287	0.73	0.70	0.77	0.95	-0.40	ns
Tex264	testis expressed gene 264	21767	1.08	0.81	0.81	1.32	0.86	*
Scnn1a	sodium channel, nonvoltage-gated, type I, alpha	20276	0.39	0.45	0.28	1.41	0.13	ns
BC004728	cDNA sequence BC004728	207818	2.31	1.96	2.11	1.09	-0.10	ns
Slc44a3	solute carrier family 44, member 3	213603	1.02	1.04	1.04	0.98	0.47	ns
Spire2	spire homolog 2 (Drosophila)	234857	0.46	0.62	0.33	1.39	0.42	ns
Taldo1	transaldolase 1	21351	1.67	1.99	2.85	0.59	-0.85	*
Pigx	phosphatidylinositol glycan anchor biosynthesis, class X	72084	1.42	1.37	1.59	0.89	-0.50	ns
Lactb2	lactamase, beta 2	212442	0.37	0.40	0.38	0.96	-0.29	ns
Ndufs1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	227197	1.49	1.37	1.20	1.23	-0.05	ns
Pdcl	phosducin-like	67466	1.08	1.23	1.04	1.03	-0.27	ns
Trabd	TraB domain containing	67976	0.54	0.49	0.61	0.87	-0.26	ns
AI661453	expressed sequence AI661453	224833	1.41	1.32	1.01	1.39	0.84	*
Golph3l	golgi phosphoprotein 3-like	229593	0.49	0.49	0.46	1.06	-0.16	ns
Shmt1	serine hydroxymethyltransferase 1 (soluble)	20425	0.81	0.77	0.86	0.94	-0.32	ns
Rpl4	ribosomal protein L4	67891	26.16	22.93	19.23	1.35	0.93	**
Mrpl15	mitochondrial ribosomal protein L15	27395	1.40	1.29	1.01	1.38	0.69	ns
Phospho2	phosphatase, orphan 2	73373	0.32	0.34	0.30	1.04	-0.10	ns
6330577E15Rik	RIKEN cDNA 6330577E15 gene	67788	3.65	3.69	2.96	1.23	0.54	ns
Acat3		224530	1.64	1.18	1.19	1.37	0.71	ns
Hint2	histidine triad nucleotide binding protein 2	68917	0.48	0.51	0.47	1.01	0.44	ns
Epb4.1l5	erythrocyte protein band 4.1-like 5	226352	2.17	1.90	1.06	2.04	0.53	ns
6430514L14Rik	RIKEN cDNA 6430514L14 gene	76886	0.50	0.35	0.27	1.88	0.87	*
Dguok	deoxyguanosine kinase	27369	0.53	0.63	0.68	0.78	-0.25	ns
Zfp46	zinc finger protein 46	22704	0.44	0.35	0.44	1.00	0.19	ns
Wsb1	WD repeat and SOCS box-containing 1	78889	2.14	2.70	2.15	0.99	-0.42	ns
Rgs11	regulator of G-protein signaling 11	50782	0.78	0.58	0.36	2.15	0.94	**
Mad1l1	mitotic arrest deficient 1-like 1	17120	0.31	0.39	0.25	1.23	0.26	ns
Hnrpll	heterogeneous nuclear ribonucleoprotein L-like	72692	3.13	2.86	2.55	1.22	0.96	**
Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma	12611	0.82	1.17	1.46	0.56	-0.77	ns
Mbp	myelin basic protein	17196	0.92	0.92	0.81	1.13	0.31	ns
Prnpip1	prion protein interacting protein 1	140546	0.72	0.80	0.73	0.99	-0.40	ns
Rap1gds1	RAP1, GTP-GDP dissociation stimulator 1	229877	1.12	1.21	1.19	0.94	-0.25	ns
Rgs3		50780	0.34	0.38	0.28	1.20	0.44	ns
0610038D11Rik		67674	10.03	8.04	6.54	1.53	0.94	**
EG665860		665860	10.03	8.04	6.54	1.53	0.94	**
LOC623390		623390	10.03	8.04	6.54	1.53	0.94	**
LOC627985		627985	10.03	8.04	6.54	1.53	0.94	**
BC008163	cDNA sequence BC008163	230789	0.49	0.58	0.77	0.64	-0.74	ns
Zfp106	zinc finger protein 106	20402	2.18	1.51	1.47	1.47	0.48	ns
H2-K1	histocompatibility 2, K1, K region	14972	3.30	3.34	4.30	0.76	0.14	ns
Ptpra	protein tyrosine phosphatase, receptor type, A	19262	1.37	1.41	1.71	0.80	-0.27	ns
Srprb	signal recognition particle receptor, B subunit	20818	0.58	0.51	0.57	1.01	0.53	ns
Myef2	myelin basic protein expression factor 2, repressor	17876	1.36	1.04	1.17	1.15	0.20	ns
Aggf1	angiogenic factor with G patch and FHA domains 1	66549	0.90	1.29	1.60	0.56	-0.38	ns
Slc3a2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	17254	5.05	4.59	3.79	1.33	0.74	ns
Tpk1	thiamine pyrophosphokinase	29807	0.51	0.40	0.31	1.65	0.66	ns
Raf1	v-raf-leukemia viral oncogene 1	110157	1.76	1.66	2.03	0.87	-0.43	ns
Churc1	churchill domain containing 1	211151	1.94	2.08	2.66	0.73	-0.68	ns
Mtmr2	myotubularin related protein 2	77116	1.19	0.92	0.48	2.48	0.90	*
Senp2	SUMO/sentrin specific peptidase 2	75826	1.40	1.25	1.55	0.90	-0.67	ns
Col4a5	procollagen, type IV, alpha 5	12830	2.32	2.18	2.70	0.85	-0.67	ns
Cnot6l	CCR4-NOT transcription complex, subunit 6-like	231464	2.49	2.55	2.86	0.87	-0.46	ns
Ankmy2	ankyrin repeat and MYND domain containing 2	217473	1.31	1.23	1.03	1.27	0.25	ns
Mtmr6	myotubularin related protein 6	219135	1.24	1.24	1.24	0.99	-0.07	ns
Bmpr1a	bone morphogenetic protein receptor, type 1A	12166	2.22	2.00	1.79	1.24	0.75	ns
Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	14538	0.43	0.57	1.02	0.42	-0.68	ns
Mylk	myosin, light polypeptide kinase	107589	3.20	2.07	1.47	2.16	0.10	ns
Arfrp1	ADP-ribosylation factor related protein 1	76688	0.62	0.58	0.72	0.86	-0.41	ns
P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	18438	0.40	0.43	0.49	0.80	-0.98	***
Bin1	bridging integrator 1	30948	0.18	0.34	0.33	0.55	-0.15	ns
Stx3	syntaxin 3	20908	2.55	2.75	2.28	1.11	0.65	ns
Ppp2r5c	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	26931	2.03	2.16	3.57	0.57	-0.69	ns
H2-D1	histocompatibility 2, D region locus 1	14964	3.40	3.12	4.31	0.79	0.08	ns
Hip1r	huntingtin interacting protein 1 related	29816	0.85	0.96	1.10	0.77	-0.76	ns
Cdc16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	69957	1.45	1.39	1.66	0.87	0.12	ns
Klc3	kinesin light chain 3	232943	0.90	0.91	1.03	0.88	-0.50	ns
S100a16	S100 calcium binding protein A16	67860	2.84	3.38	2.48	1.14	0.08	ns
Trnt1	tRNA nucleotidyl transferase, CCA-adding, 1	70047	0.87	0.98	1.27	0.68	-0.75	ns
Anxa5	annexin A5	11747	10.63	10.09	8.46	1.25	0.59	ns
Tmem33	transmembrane protein 33	67878	1.53	1.39	1.84	0.83	-0.65	ns
Pik3c3	phosphoinositide-3-kinase, class 3	225326	0.43	0.57	0.66	0.65	-0.56	ns
Med12	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)	59024	0.55	0.57	0.80	0.68	-0.83	*
Chmp2a	chromatin modifying protein 2A	68953	2.23	2.14	2.68	0.83	-0.72	ns
Rtkn	rhotekin	20166	0.58	0.59	0.93	0.62	-0.59	ns
Pck2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	74551	1.28	1.43	1.40	0.91	-0.75	ns
Ccdc23	coiled-coil domain containing 23	69216	0.49	0.50	0.53	0.92	-0.80	ns

Gtf2i		14886	3.71	3.37	3.06	1.21	0.46	ns
Nol6	nucleolar protein family 6 (RNA-associated)	230082	0.40	0.28	0.36	1.09	-0.22	ns
Cep290	centrosomal protein 290	216274	0.49	0.63	0.47	1.05	-0.33	ns
BC016495	cDNA sequence BC016495	225994	0.49	0.63	0.76	0.64	-0.80	ns
Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	108100	0.54	0.52	0.50	1.07	-0.09	ns
Ssu72	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	68991	1.60	1.48	1.86	0.86	-0.41	ns
Mapk8ip1	mitogen activated protein kinase 8 interacting protein 1	19099	0.47	0.36	0.38	1.21	-0.11	ns
Btrc	beta-transducin repeat containing protein	12234	0.41	0.39	0.28	1.46	0.75	ns
Tprkb	Tp53rk binding protein	69786	0.47	0.63	0.60	0.79	-0.50	ns
Enpp5	ectonucleotide pyrophosphatase/phosphodiesterase 5	83965	1.28	1.28	0.89	1.43	0.52	ns
Ddb2	damage specific DNA binding protein 2	107986	0.70	0.59	0.59	1.17	0.21	ns
Ivns1abp	influenza virus NS1A binding protein	117198	4.80	5.13	4.80	0.99	-0.55	ns
Nmi	N-myc (and STAT) interactor	64685	0.35	0.49	0.74	0.47	-0.66	ns
Tacc2	transforming, acidic coiled-coil containing protein 2	57752	1.87	1.53	1.35	1.37	0.50	ns
Ung	uracil DNA glycosylase	22256	1.05	1.08	1.24	0.84	-0.78	ns
Six4	sine oculis-related homeobox 4 homolog (Drosophila)	20474	0.70	0.63	0.67	1.03	-0.47	ns
Tmem167	transmembrane protein 167	66074	0.96	1.25	2.05	0.47	-0.64	ns
Map3k7	mitogen activated protein kinase kinase kinase 7	26409	0.43	0.34	0.39	1.09	0.49	ns
Csrp1	cysteine and glycine-rich protein 1	13007	3.09	3.44	3.34	0.92	0.24	ns
Hmmr	hyaluronan mediated motility receptor (RHAMM)	15366	1.52	1.52	2.01	0.75	-0.32	ns
2810452K22Rik		67236	0.89	1.23	1.60	0.55	-0.68	ns
LOC640972		640972	0.89	1.23	1.60	0.55	-0.68	ns
Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3 F	20350	0.73	0.53	0.63	1.16	0.50	ns
Cklf	chemokine-like factor	75458	0.60	0.78	0.86	0.70	0.00	ns
Nfkb2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100	18034	0.74	0.90	0.86	0.86	0.33	ns
1810055G02Rik	RIKEN cDNA 1810055G02 gene	72056	0.67	0.71	0.52	1.29	0.77	ns
Atf5	activating transcription factor 5	107503	0.36	0.63	0.39	0.91	0.06	ns
Nt5c2	5'-nucleotidase, cytosolic II	76952	1.61	1.57	1.45	1.10	0.73	ns
B4galt4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	56375	0.44	0.50	0.34	1.29	0.01	ns
Hexim1	hexamethylene bis-acetamide inducible 1	192231	0.77	0.89	0.85	0.90	0.30	ns
Cdadc1	cytidine and dCMP deaminase domain containing 1	71891	0.54	0.45	0.36	1.51	0.39	ns
Zfx	zinc finger protein X-linked	22764	0.63	0.70	0.88	0.72	-0.69	ns
Mapk8ip3	mitogen-activated protein kinase 8 interacting protein 3	30957	0.38	0.29	0.20	1.88	0.93	**
Fbf1	Fas (TNFRSF6) binding factor 1	217335	0.67	0.72	0.82	0.82	-0.16	ns
LOC635075		635075	0.48	0.54	0.48	0.99	0.14	ns
Rbl2		19651	0.48	0.54	0.48	0.99	0.14	ns
Cdc7	cell division cycle 7 (S. cerevisiae)	12545	1.11	1.02	0.98	1.12	0.71	ns
Ggnbp2	gametogenetin binding protein 2	217039	2.12	1.92	2.14	0.99	-0.33	ns
2610301G19Rik	RIKEN cDNA 2610301G19 gene	219158	0.88	0.91	0.84	1.04	0.54	ns
Asph	aspartate-beta-hydroxylase	65973	0.69	0.93	1.30	0.53	-0.73	ns
0610011L14Rik	RIKEN cDNA 0610011L14 gene	68295	0.45	0.52	0.45	0.99	0.18	ns
Vill	villin-like	22351	0.54	0.66	0.67	0.80	-0.39	ns
Dbn1	drebrin 1	56320	0.32	0.65	0.75	0.43	-0.79	ns
Apeh	acylpeptide hydrolase	235606	0.87	0.88	1.14	0.76	-0.18	ns
Rabggta	Rab geranylgeranyl transferase, a subunit	56187	0.56	0.46	0.66	0.84	-0.56	ns
Hrc		15464	1.91	1.73	2.01	0.95	-0.43	ns
Cenpb	centromere protein B	12616	0.87	1.06	1.34	0.65	-0.55	ns
Mlh3	mutL homolog 3 (E coli)	217716	0.50	0.50	0.48	1.02	-0.12	ns
Trib3	tribbles homolog 3 (Drosophila)	228775	0.46	0.83	0.68	0.67	-0.48	ns
Slc7a4	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	224022	0.37	0.35	0.38	0.96	-0.23	ns
Gpr108	G protein-coupled receptor 108	78308	0.61	0.56	0.55	1.11	0.72	ns
Btg1	B-cell translocation gene 1, anti-proliferative	12226	10.96	11.16	9.71	1.12	-0.01	ns
Tor1aip1	torsin A interacting protein 1	208263	0.48	0.47	0.43	1.13	0.61	ns
BC003331	cDNA sequence BC003331	226499	0.80	0.77	0.59	1.35	0.64	ns
Tnfrsf22	tumor necrosis factor receptor superfamily, member 22	79202	0.09	0.07	0.38	0.24	-0.61	ns
Irf3	interferon regulatory factor 3	54131	0.69	0.77	0.94	0.73	-0.73	ns
Tomm40	translocase of outer mitochondrial membrane 40 homolog (yeast)	53333	0.91	1.00	1.15	0.78	-0.69	ns
Clk1	CDC-like kinase 1	12747	1.62	1.51	1.15	1.40	0.47	ns
Mitd1	MIT, microtubule interacting and transport, domain containing 1	69028	0.25	0.26	0.44	0.55	-0.68	ns
Ube2j2	ubiquitin-conjugating enzyme E2, J2 homolog (yeast)	140499	1.24	1.22	1.29	0.96	0.32	ns
Stk16	serine/threonine kinase 16	20872	0.51	0.47	0.29	1.74	0.61	ns
Casp3	caspase 3	12367	0.23	0.20	0.21	1.10	0.17	ns
Cst3	cystatin C	13010	3.55	4.07	5.38	0.66	-0.49	ns
Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	19046	6.79	5.93	9.12	0.74	-0.84	*
Ikbkb	inhibitor of kappaB kinase beta	16150	1.49	1.70	1.91	0.78	-0.20	ns
Plagl1	pleiomorphic adenoma gene-like 1	22634	9.22	5.76	0.72	12.70	0.15	ns
Strn4	striatin, calmodulin binding protein 4	97387	1.68	1.32	1.79	0.94	0.14	ns
Tmem161a	transmembrane protein 161A	234371	0.77	0.66	0.81	0.95	-0.09	ns
Imp4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	27993	0.83	0.82	0.58	1.41	0.40	ns
4930471M23Rik	RIKEN cDNA 4930471M23 gene	74919	0.23	0.32	0.49	0.46	-0.81	ns
BC024479	cDNA sequence BC024479	235184	0.41	0.37	0.31	1.30	0.81	ns
BC002199	cDNA sequence BC002199	211556	3.15	3.14	2.21	1.42	0.40	ns
Sp2	Sp2 transcription factor	78912	0.33	0.23	0.38	0.85	-0.45	ns
Bmp1	bone morphogenetic protein 1	12153	0.39	0.37	0.34	1.14	0.42	ns
Arrb2	arrestin, beta 2	216869	0.63	0.64	0.72	0.88	0.23	ns
Scmh1	sex comb on midleg homolog 1	29871	0.53	0.47	0.44	1.19	-0.03	ns
Polr2a	polymerase (RNA) II (DNA directed) polypeptide A	20020	1.69	1.67	1.24	1.36	0.38	ns
Cth	cystathionase (cystathionine gamma-lyase)	107869	0.24	0.52	0.23	1.04	-0.15	ns
Stk24	serine/threonine kinase 24 (STE20 homolog, yeast)	223255	2.43	2.00	2.64	0.92	-0.17	ns
Tm2d1	TM2 domain containing 1	94043	0.57	0.53	0.70	0.81	-0.58	ns
Timm17a	translocase of inner mitochondrial membrane 17a	21854	2.93	2.79	2.25	1.30	0.78	ns
Sars	seryl-aminoacyl-tRNA synthetase	20226	4.36	5.33	3.86	1.12	0.26	ns
Sorl1	sortilin-related receptor, LDLR class A repeats-containing	20660	3.53	2.84	2.10	1.68	0.07	ns
Pank3	pantothenate kinase 3	211347	0.33	0.34	0.42	0.79	-0.18	ns

Cadm4	cell adhesion molecule 4	260299	0.49	0.71	0.82	0.59	-0.39	ns
Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	235339	1.20	0.99	0.98	1.22	0.86	*
Zbtb8os	zinc finger and BTB domain containing 8 opposite strand	67106	0.47	0.57	0.55	0.85	-0.42	ns
C130090K23Rik	RIKEN cDNA C130090K23 gene	231293	0.11	0.23	1.00	0.11	-0.53	ns
Smc5	structural maintenance of chromosomes 5	226026	1.20	1.40	1.49	0.80	-0.94	**
Lmbr1	limb region 1	56873	0.62	0.62	0.48	1.27	0.31	ns
Ifih1	interferon induced with helicase C domain 1	71586	0.24	0.42	1.10	0.21	-0.85	*
5830415L20Rik	RIKEN cDNA 5830415L20 gene	68152	0.71	0.68	0.86	0.82	-0.65	ns
Krt20	keratin 20	66809	0.99	1.77	2.42	0.41	-0.89	*
Noc3l	nucleolar complex associated 3 homolog (S. cerevisiae)	57753	0.37	0.46	0.27	1.34	0.15	ns
Qrich1	glutamine-rich 1	69232	1.24	1.11	1.15	1.07	0.61	ns
Dimt1	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	66254	0.20	0.40	0.45	0.45	-0.93	**
Tcfe2a	transcription factor E2a	21423	1.31	1.28	0.97	1.35	0.42	ns
Upk1a	uroplakin 1A	109637	0.87	0.38	0.16	5.45	0.49	ns
Cyb5r4	cytochrome b5 reductase 4	266690	1.48	1.31	1.21	1.22	0.80	ns
Zdhhc5	zinc finger, DHHC domain containing 5	228136	0.64	0.43	0.59	1.08	0.02	ns
Bre	brain and reproductive organ-expressed protein	107976	0.84	1.11	1.27	0.66	-0.95	**
Cntf		12803	0.51	0.61	0.42	1.22	0.30	ns
Stt3b	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	68292	7.79	7.71	4.93	1.57	0.85	*
Prepl	prolyl endopeptidase-like	213760	0.71	0.53	0.36	1.99	0.77	ns
2010321M09Rik	RIKEN cDNA 2010321M09 gene	69882	0.79	0.69	0.72	1.10	0.64	ns
Hspd1	heat shock protein 1 (chaperonin)	15510	6.58	6.26	4.85	1.35	0.51	ns
Stat6	signal transducer and activator of transcription 6	20852	1.13	1.09	1.17	0.96	-0.59	ns
6330578E17Rik	RIKEN cDNA 6330578E17 gene	76178	1.96	2.26	2.00	0.98	-0.48	ns
Taok1	TAO kinase 1	216965	2.40	2.24	1.67	1.43	0.71	ns
Tmem144	transmembrane protein 144	70652	0.33	0.50	0.34	0.95	0.15	ns
Mrrf	mitochondrial ribosome recycling factor	67871	0.73	0.75	0.52	1.40	0.68	ns
2810403A07Rik	RIKEN cDNA 2810403A07 gene	74200	1.22	1.09	1.11	1.10	-0.29	ns
Eif2c2	eukaryotic translation initiation factor 2C, 2	239528	0.45	0.47	0.56	0.81	-0.18	ns
Cab39l	calcium binding protein 39-like	69008	0.84	0.77	0.63	1.33	-0.02	ns
Rin2	Ras and Rab interactor 2	74030	0.11	0.21	0.54	0.21	-0.86	*
Ski	Sloan-Kettering viral oncogene homolog	20481	0.77	0.74	0.59	1.30	0.73	ns
2410166I05Rik	RIKEN cDNA 2410166I05 gene	76824	0.86	0.77	1.00	0.86	-0.65	ns
Eif4b	eukaryotic translation initiation factor 4B	75705	6.74	6.41	5.62	1.19	0.87	*
Pprc1	peroxisome proliferative activated receptor, gamma, coactivator-related 1	226169	0.95	1.27	1.07	0.88	-0.23	ns
Cry2	cryptochrome 2 (photolyase-like)	12953	0.36	0.25	0.27	1.32	-0.01	ns
Pisd		320951	2.64	3.06	3.32	0.79	-0.30	ns
Arf1	ADP-ribosylation factor 1	11840	12.69	13.23	13.46	0.94	-0.40	ns
Sdf4	stromal cell derived factor 4	20318	1.72	1.82	1.93	0.89	-0.38	ns
Tgfbr2	transforming growth factor, beta receptor II	21813	4.41	4.01	2.61	1.68	0.88	*
Ube2w	ubiquitin-conjugating enzyme E2W (putative)	66799	0.60	0.68	0.55	1.09	-0.16	ns
Capns1	calpain, small subunit 1	12336	3.20	3.62	3.81	0.84	-0.63	ns
Ppp3ca	protein phosphatase 3, catalytic subunit, alpha isoform	19055	1.58	1.46	1.15	1.37	0.11	ns
Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	56403	1.58	1.74	1.85	0.85	-0.10	ns
Actr1b	ARP1 actin-related protein 1 homolog B (yeast)	226977	0.52	0.57	0.55	0.94	-0.04	ns
Setd8	SET domain containing (lysine methyltransferase) 8	67956	1.58	1.61	1.68	0.94	-0.49	ns
Cugbp1	CUG triplet repeat, RNA binding protein 1	13046	6.42	5.85	5.45	1.17	0.28	ns
Lzts2	leucine zipper, putative tumor suppressor 2	226154	1.10	1.03	0.78	1.40	0.75	ns
Pdk3	pyruvate dehydrogenase kinase, isoenzyme 3	236900	0.72	0.71	1.03	0.69	-0.19	ns
Yipf4	Yip1 domain family, member 4	67864	2.44	2.04	1.74	1.40	0.94	**
Rbm26	RNA binding motif protein 26	74213	0.98	1.12	1.40	0.69	-0.91	*
Cc2d1a	coiled-coil and C2 domain containing 1A	212139	0.72	0.75	1.03	0.69	-0.40	ns
Sugt1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	67955	2.17	2.18	2.65	0.81	-0.59	ns
Jag2	jagged 2	16450	0.09	0.24	0.38	0.23	-0.71	ns
Tmem43	transmembrane protein 43	74122	0.79	0.84	1.73	0.45	-0.73	ns
Tmem135	transmembrane protein 135	72759	0.61	0.50	0.55	1.09	-0.03	ns
Hdac3	histone deacetylase 3	15183	1.09	1.33	1.30	0.83	0.11	ns
Dhrs7	dehydrogenase/reductase (SDR family) member 7	66375	0.35	0.47	0.70	0.50	-0.16	ns
Nup35	nucleoporin 35	69482	0.61	0.58	0.45	1.34	0.88	*
6030465E24Rik	RIKEN cDNA 6030465E24 gene	214585	0.65	0.56	0.52	1.23	0.47	ns
Pitrm1	pitrilysin metallepetidase 1	69617	1.43	1.36	1.31	1.08	0.66	ns
Arhgdib	Rho, GDP dissociation inhibitor (GDI) beta	11857	1.69	1.63	0.37	4.55	-0.05	ns
Sdccag10	serologically defined colon cancer antigen 10	67285	0.30	0.35	0.39	0.78	-0.46	ns
Slmap	sarcolemma associated protein	83997	3.11	2.70	2.95	1.05	-0.19	ns
AW549877	expressed sequence AW549877	106064	2.27	1.67	1.82	1.24	0.50	ns
Gphn	gephyrin	268566	0.92	0.88	1.01	0.90	0.02	ns
Dlgap4	discs, large homolog-associated protein 4 (Drosophila)	228836	0.67	0.68	0.93	0.72	-0.73	ns
0610037L13Rik	RIKEN cDNA 0610037L13 gene	74098	0.38	0.27	0.32	1.19	0.29	ns
Tbp	TATA box binding protein	21374	0.83	0.64	0.55	1.51	0.73	ns
Zfp52	zinc finger protein 52	22710	0.90	1.12	0.79	1.13	0.31	ns
Dnajc9	DnaJ (Hsp40) homolog, subfamily C, member 9	108671	3.26	3.16	3.38	0.96	0.17	ns
Atpaf2	ATP synthase mitochondrial F1 complex assembly factor 2	246782	0.50	0.43	0.67	0.74	-0.52	ns
Hmbs	hydroxymethylbilane synthase	15288	1.29	1.16	1.28	1.00	0.52	ns
Rasa1	RAS p21 protein activator 1	218397	1.42	1.76	2.15	0.66	-0.74	ns
Sbds	Shwachman-Bodian-Diamond syndrome homolog (human)	66711	1.07	0.92	1.25	0.86	-0.53	ns
Klhl22	kelch-like 22 (Drosophila)	224023	2.35	2.45	3.21	0.73	-0.66	ns
Prkrir	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	72981	0.83	0.84	0.79	1.05	0.40	ns
Rbbp6	retinoblastoma binding protein 6	19647	0.73	0.86	1.01	0.72	-0.69	ns
Bfar	bifunctional apoptosis regulator	67118	0.81	0.81	0.71	1.13	0.50	ns
Herc2	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 2	15204	0.48	0.46	0.58	0.83	-0.61	ns
Tdp1	tyrosyl-DNA phosphodiesterase 1	104884	0.44	0.36	0.49	0.89	0.12	ns
Rg9mtd3	RNA (guanine-9-) methyltransferase domain containing 3	69934	0.31	0.41	0.34	0.90	0.17	ns
Wdr55	WD repeat domain 55	67936	0.47	0.48	0.65	0.73	-0.26	ns

Sh3glb2	SH3-domain GRB2-like endophilin B2	227700	0.67	0.74	0.56	1.20	0.44	ns
Icmt	isoprenylcysteine carboxyl methyltransferase	57295	0.60	0.52	0.64	0.93	-0.43	ns
Rnf121	ring finger protein 121	75212	0.42	0.57	0.78	0.54	-0.98	***
Sccpdh	saccharopine dehydrogenase (putative)	109232	0.36	0.37	0.31	1.15	0.24	ns
Tor1a	torsin family 1, member A (torsin A)	30931	0.50	0.57	0.48	1.04	-0.02	ns
Lpin1	lipin 1	14245	0.65	0.64	1.00	0.65	-0.53	ns
Tubgcp5	tubulin, gamma complex associated protein 5	233276	0.43	0.40	0.46	0.94	-0.35	ns
LOC623031		623031	1.61	1.46	1.55	1.03	-0.35	ns
Arid2	AT rich interactive domain 2 (Arid-rfx like)	77044	3.62	3.13	3.10	1.16	0.88	*
Toe1	target of EGR1, member 1 (nuclear)	68276	0.37	0.35	0.44	0.84	-0.81	*
Tagln2	transgelin 2	21346	2.05	2.00	2.19	0.93	-0.08	ns
Klhl5	kelch-like 5 (Drosophila)	71778	0.39	0.38	0.87	0.45	-0.75	ns
Arfgap3	ADP-ribosylation factor GTPase activating protein 3	66251	0.40	0.49	0.58	0.69	-0.77	ns
Narg2	NMDA receptor-regulated gene 2	93697	0.62	0.55	0.47	1.31	0.60	ns
Endod1	endonuclease domain containing 1	71946	0.49	0.60	0.21	2.35	0.59	ns
Atpbd4	ATP binding domain 4	66632	0.89	0.75	0.71	1.25	0.60	ns
Pgam1		18648	9.55	9.48	10.41	0.91	-0.10	ns
Suhw4	suppressor of hairy wing homolog 4 (Drosophila)	235469	1.14	0.76	0.64	1.77	0.92	**
LOC628147		628147	1.10	1.16	1.12	0.98	-0.35	ns
Sbno1	sno, strawberry notch homolog 1 (Drosophila)	243272	1.57	1.49	1.37	1.14	0.09	ns
Il17re	interleukin 17 receptor E	57890	1.84	1.76	1.55	1.18	-0.15	ns
Frk	fyn-related kinase	14302	1.40	1.27	0.97	1.43	-0.05	ns
Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	107029	0.45	0.48	0.48	0.93	0.29	ns
Gnl2	guanine nucleotide binding protein-like 2 (nucleolar)	230737	0.49	0.58	0.67	0.73	-0.35	ns
Ptpmt1	protein tyrosine phosphatase, mitochondrial 1	66461	1.16	0.89	1.05	1.10	-0.20	ns
Atf2	activating transcription factor 2	11909	2.44	2.01	1.48	1.64	0.75	ns
Mapk1	mitogen activated protein kinase 1	26413	4.23	3.91	4.32	0.98	-0.37	ns
Slc25a11	solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11	67863	1.47	1.48	2.11	0.69	-0.81	*
Stat3	signal transducer and activator of transcription 3	20848	1.07	1.08	1.13	0.94	-0.17	ns
Fbxo22	F-box protein 22	71999	1.67	1.54	1.44	1.15	0.83	*
Smn1	survival motor neuron 1	20595	0.39	0.59	0.69	0.56	-0.80	ns
Araf	v-raf murine sarcoma 3611 viral oncogene homolog	11836	0.64	0.57	0.87	0.72	-0.70	ns
EG633640	predicted gene, EG633640	633640	0.26	0.22	0.45	0.58	-0.80	ns
Dis3	DIS3 mitotic control homolog (S. cerevisiae)	72662	1.24	1.38	1.45	0.85	-0.32	ns
Tipin	timeless interacting protein	66131	4.87	3.97	3.37	1.44	0.93	**
Snrpb2	U2 small nuclear ribonucleoprotein B	20639	2.72	2.23	2.50	1.08	-0.32	ns
Prkcbp1	protein kinase C binding protein 1	228880	0.94	1.17	1.21	0.78	-0.10	ns
Pomgnt1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	68273	0.69	0.74	0.83	0.83	-0.72	ns
Arhgap17	Rho GTPase activating protein 17	70497	0.33	0.40	0.43	0.77	-0.84	*
Ypel3	yippee-like 3 (Drosophila)	66090	1.58	1.21	1.32	1.19	0.12	ns
Zfp623	zinc finger protein 623	78834	0.77	0.75	0.92	0.83	-0.27	ns
Gtf2f2	general transcription factor IIF, polypeptide 2	68705	0.98	0.66	0.98	1.00	-0.16	ns
Dhx8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	217207	0.60	0.62	0.62	0.96	0.44	ns
Exosc2	exosome component 2	227715	0.72	0.81	0.56	1.28	0.55	ns
Pus7	pseudouridylate synthase 7 homolog (S. cerevisiae)	78697	0.50	0.53	0.48	1.05	0.35	ns
Fn1	fibronectin 1	14268	7.23	5.15	2.39	3.01	0.77	ns
Elp3	elongation protein 3 homolog (S. cerevisiae)	74195	0.85	0.74	0.71	1.18	0.54	ns
Tbc1d20	TBC1 domain family, member 20	67231	1.08	1.02	1.33	0.81	-0.47	ns
9130011J15Rik	RIKEN cDNA 9130011J15 gene	66818	1.08	1.03	1.28	0.83	-0.17	ns
Mapkapk2	MAP kinase-activated protein kinase 2	17164	0.92	1.03	0.93	0.99	-0.33	ns
Zc3hc1	zinc finger, C3HC type 1	232679	0.34	0.37	0.56	0.60	-0.51	ns
EG665189		665189	19.66	18.72	16.64	1.18	0.84	*
Rpl27a		26451	19.66	18.72	16.64	1.18	0.84	*
Cmas	cytidine monophospho-N-acetylneuraminic acid synthetase	12764	1.04	1.34	1.71	0.60	-0.71	ns
Slc45a3	solute carrier family 45, member 3	212980	0.53	0.51	0.35	1.52	0.32	ns
Katnb1	katanin p80 (WD40-containing) subunit B 1	74187	0.58	0.59	0.53	1.09	0.75	ns
Unc84a	unc-84 homolog A (C. elegans)	77053	1.71	1.47	1.58	1.08	0.45	ns
Slc30a9	solute carrier family 30 (zinc transporter), member 9	109108	1.42	1.50	1.74	0.81	-0.54	ns
C530044N13Rik	RIKEN cDNA C530044N13 gene	223978	0.21	0.22	0.38	0.55	-0.91	*
Agrn	agrin	11603	4.07	3.72	3.36	1.21	0.47	ns
Rbm39	RNA binding motif protein 39	170791	4.89	4.81	4.70	1.03	-0.30	ns
Cdh3	cadherin 3	12560	1.70	1.49	0.62	2.73	0.68	ns
Tomm70a	translocase of outer mitochondrial membrane 70 homolog A (yeast)	28185	2.76	2.42	2.52	1.09	-0.26	ns
Flna	filamin, alpha	192176	2.32	3.04	3.79	0.61	-0.87	*
Sepn1	selenoprotein N, 1	74777	0.43	0.46	0.50	0.85	-0.74	ns
Unk	unkempt homolog (Drosophila)	217331	0.59	0.60	0.52	1.12	0.80	ns
Cnot6	CCR4-NOT transcription complex, subunit 6	104625	4.74	4.54	5.21	0.91	-0.20	ns
Sdha	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	66945	3.05	3.66	4.22	0.72	-0.86	*
Srebf1	sterol regulatory element binding factor 1	20787	2.02	1.97	2.47	0.81	-0.80	ns
Tjap1	tight junction associated protein 1	74094	1.17	1.03	0.71	1.63	0.88	*
9030624J02Rik	RIKEN cDNA 9030624J02 gene	71517	0.54	0.54	0.59	0.91	-0.56	ns
Usp52	ubiquitin specific peptidase 52	103135	0.63	0.68	0.60	1.03	0.24	ns
Gak	cyclin G associated kinase	231580	1.07	1.19	1.25	0.85	-0.75	ns
Iars	isoleucine-tRNA synthetase	105148	2.34	2.50	2.57	0.91	-0.26	ns
Tubgcp3	tubulin, gamma complex associated protein 3	259279	0.72	0.80	0.89	0.80	-0.22	ns
Antxr2	anthrax toxin receptor 2	71914	0.81	0.56	0.57	1.43	0.66	ns
Usp33	ubiquitin specific peptidase 33	170822	0.87	1.06	1.19	0.72	-0.88	*
Calm3	calmodulin 3	12315	2.43	2.45	2.76	0.88	-0.16	ns
Tdrd7	tudor domain containing 7	100121	0.29	0.35	0.62	0.46	-0.58	ns
Skiv2l2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	72198	1.20	1.44	1.67	0.72	-0.52	ns
Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2	11787	0.85	0.93	0.64	1.31	0.39	ns
Tiparp	TCDD-inducible poly(ADP-ribose) polymerase	99929	2.20	2.23	2.08	1.05	0.44	ns
Slc38a2	solute carrier family 38, member 2	67760	8.07	8.81	8.56	0.94	-0.71	ns
Ppp1r10	protein phosphatase 1, regulatory subunit 10	52040	0.63	0.74	0.63	0.99	0.16	ns
Itpk1	inositol 1,3,4-triphosphate 5/6 kinase	217837	0.62	0.71	0.76	0.80	-0.55	ns
Iars2	isoleucine-tRNA synthetase 2, mitochondrial	381314	0.54	0.52	0.49	1.08	-0.25	ns

Donson	downstream neighbor of SON	60364	0.65	0.66	0.92	0.71	-0.38	ns
Fastkd2	FAST kinase domains 2	75619	0.86	0.86	0.65	1.33	0.33	ns
Appl2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	216190	0.98	0.87	0.70	1.39	0.34	ns
1810026J23Rik	RIKEN cDNA 1810026J23 gene	69773	1.09	0.78	0.74	1.47	0.74	ns
Abcf3	ATP-binding cassette, sub-family F (GCN20), member 3	27406	0.71	0.77	0.76	0.93	-0.20	ns
Prmt3	protein arginine N-methyltransferase 3	71974	0.76	0.85	0.78	0.97	-0.32	ns
Flnb	filamin, beta	286940	1.87	1.86	2.64	0.70	-0.72	ns
Nup107	nucleoporin 107	103468	1.06	0.94	1.00	1.06	0.56	ns
Phf17	PHD finger protein 17	269424	2.14	2.08	1.83	1.16	-0.31	ns
LOC675560		675560	4.06	3.45	2.44	1.65	0.79	ns
Map4k3		225028	4.06	3.45	2.44	1.65	0.79	ns
Ipo8	importin 8	320727	1.29	1.35	1.48	0.87	-0.26	ns
Aof2	amine oxidase (flavin containing) domain 2	99982	2.10	2.31	2.57	0.81	-0.58	ns
Oaz2	ornithine decarboxylase antizyme 2	18247	1.12	0.96	1.00	1.11	0.64	ns
Commd7		99311	0.78	0.77	1.01	0.77	-0.09	ns
LOC631742		631742	0.78	0.77	1.01	0.77	-0.09	ns
LOC674161		674161	0.78	0.77	1.01	0.77	-0.09	ns
Wdr90	WD repeat domain 90	106618	0.86	0.73	0.62	1.38	0.94	**
Maml1	mastermind like 1 (Drosophila)	103806	0.79	0.84	0.89	0.88	-0.86	*
Pex5	peroxisome biogenesis factor 5	19305	0.40	0.30	0.40	0.99	0.02	ns
Parp12	poly (ADP-ribose) polymerase family, member 12	243771	0.22	0.37	1.07	0.20	-0.75	ns
Scamp1	secretory carrier membrane protein 1	107767	0.96	1.41	2.04	0.47	-0.89	*
Dag1	dystroglycan 1	13138	4.15	3.59	3.54	1.16	0.81	*
D14Ertd436e	DNA segment, Chr 14, ERATO Doi 436, expressed	218978	0.61	0.51	0.44	1.37	0.76	ns
Gpr125	G protein-coupled receptor 125	70693	0.64	0.64	0.59	1.08	-0.15	ns
Trim47	tripartite motif protein 47	217333	1.30	1.16	1.41	0.91	0.40	ns
Dhx38	DEAH (Asp-Glu-Ala-His) box polypeptide 38	64340	0.29	0.28	0.22	1.29	0.63	ns
Ssrp1	structure specific recognition protein 1	20833	7.17	6.00	5.21	1.37	0.76	ns
Ptprs	protein tyrosine phosphatase, receptor type, S	19280	3.41	4.01	3.20	1.06	0.48	ns
Kpna6	karyopherin (importin) alpha 6	16650	0.54	0.53	0.74	0.73	-0.47	ns
Ppp1r15b	protein phosphatase 1, regulatory (inhibitor) subunit 15b	108954	2.71	2.60	2.03	1.33	0.72	ns
Rab8b	RAB8B, member RAS oncogene family	235442	1.27	1.16	0.96	1.31	0.90	*
Sept8	septin 8	20362	1.23	1.30	1.77	0.69	-0.49	ns
Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	20586	3.36	3.01	2.17	1.54	0.99	***
Lgals3	lectin, galactose binding, soluble 3	16854	7.43	8.68	7.78	0.95	0.03	ns
C430004E15Rik	RIKEN cDNA C430004E15 gene	97031	1.07	0.97	0.54	1.96	0.77	ns
Jmjd1a	jumonji domain containing 1A	104263	2.54	2.19	2.86	0.88	-0.48	ns
Ppp2r5b	protein phosphatase 2, regulatory subunit B (B56), beta isoform	225849	0.55	0.47	0.43	1.26	0.64	ns
Ltv1	LTV1 homolog (S. cerevisiae)	353258	1.04	1.02	0.93	1.11	-0.22	ns
Mki67		17345	6.36	6.89	8.12	0.78	0.10	ns
Hipk3	homeodomain interacting protein kinase 3	15259	4.86	3.06	3.20	1.51	0.45	ns
2610507B11Rik	RIKEN cDNA 2610507B11 gene	72503	2.38	2.30	2.04	1.16	0.07	ns
Rhot2	ras homolog gene family, member T2	214952	0.45	0.38	0.22	2.00	0.58	ns
Psme4	proteasome (prosome, macropain) activator subunit 4	103554	2.35	2.28	3.66	0.64	-0.85	*
Fmnl3	formin-like 3	22379	0.77	0.90	0.83	0.92	-0.37	ns
Rbm16	RNA binding motif protein 16	106583	1.69	1.37	0.96	1.75	0.63	ns
1300018I17Rik	RIKEN cDNA 1300018I17 gene	72325	0.38	0.40	0.26	1.45	0.74	ns
Uimc1	ubiquitin interaction motif containing 1	20184	0.93	0.89	1.06	0.87	-0.30	ns
Ahcyl1	S-adenosylhomocysteine hydrolase-like 1	229709	5.71	5.21	5.19	1.10	0.29	ns
Eif4g3	eukaryotic translation initiation factor 4 gamma, 3	230861	0.81	0.83	0.76	1.06	0.08	ns
D930015E06Rik	RIKEN cDNA D930015E06 gene	229473	0.60	0.54	0.35	1.71	-0.12	ns
Metap1	methionyl aminopeptidase 1	75624	4.48	4.87	3.37	1.32	0.20	ns
Pold3	polymerase (DNA-directed), delta 3, accessory subunit	67967	0.67	0.86	1.23	0.54	-0.79	ns
Ythdf3	YTH domain family 3	229096	2.37	2.52	2.46	0.96	-0.62	ns
Pdcd2l	programmed cell death 2-like	68079	0.34	0.34	0.38	0.89	-0.73	ns
Cenpt	centromere protein T	320394	0.71	0.67	0.75	0.94	0.33	ns
Sec24b	SEC24 related gene family, member B (S. cerevisiae)	99683	0.71	0.65	0.50	1.42	0.35	ns
Set	SET translocation	56086	9.43	10.07	7.51	1.25	0.71	ns
Hsdl2	hydroxysteroid dehydrogenase like 2	72479	0.42	0.33	0.59	0.70	-0.70	ns
Aftph	aftiphilin	216549	1.46	1.21	1.49	0.97	-0.32	ns
Chst14	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14	72136	0.38	0.30	0.30	1.23	0.49	ns
Fbxo33	F-box protein 33	70611	0.76	0.73	0.91	0.83	-0.30	ns
Fcgbp	Fc fragment of IgG binding protein	215384	1.74	2.44	0.22	7.82	0.01	ns
Jup	junction plakoglobin	16480	1.68	1.58	1.77	0.94	-0.58	ns
Edc4	enhancer of mRNA decapping 4	234699	1.29	1.39	1.35	0.95	0.46	ns
Srxn1	sulfiredoxin 1 homolog (S. cerevisiae)	76650	0.53	0.64	0.66	0.79	-0.08	ns
Pbrm1	polybromo 1	66923	3.61	4.14	3.74	0.96	0.29	ns
Etl4	enhancer trap locus 4	208618	0.78	0.73	0.52	1.50	-0.09	ns
Ube3c	ubiquitin protein ligase E3C	100763	0.72	0.61	0.73	0.97	-0.05	ns
Slc25a45	solute carrier family 25, member 45	107375	0.52	0.44	0.26	1.99	0.67	ns
Rmnd5a	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	68477	2.37	2.15	2.16	1.09	0.54	ns
Cln5	ceroid-lipofuscinosis, neuronal 5	211286	0.61	0.59	0.61	1.00	-0.21	ns
Rpap1	RNA polymerase II associated protein 1	68925	0.53	0.37	0.34	1.56	0.33	ns
Zfp191	zinc finger protein 191	59057	1.15	1.22	1.02	1.12	0.58	ns
Rcc2	regulator of chromosome condensation 2	108911	0.78	0.88	0.91	0.86	-0.34	ns
Map3k7ip1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	66513	0.37	0.44	0.43	0.87	-0.02	ns
Tbc1d23	TBC1 domain family, member 23	67581	0.60	0.70	0.62	0.96	-0.41	ns
Jmjd1c	jumonji domain containing 1C	108829	2.44	2.60	2.20	1.10	-0.36	ns
Camta2	calmodulin binding transcription activator 2	216874	0.45	0.43	0.39	1.13	0.36	ns
Coq6	coenzyme Q6 homolog (yeast)	217707	0.48	0.54	0.72	0.66	-0.66	ns
Fndc3a	fibronectin type III domain containing 3a	319448	1.48	1.42	3.55	0.42	-0.88	*
Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10	66861	2.52	2.67	1.91	1.31	0.27	ns
Dhx57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	106794	0.56	0.52	0.46	1.21	0.88	*
Pawr	PRKC, apoptosis, WT1, regulator	114774	6.25	5.17	3.49	1.78	0.49	ns
Dsc2	desmocollin 2	13506	0.59	0.82	0.70	0.85	0.17	ns

EG621205		621205	2.72	2.36	1.93	1.40	0.72	ns
Rfwd2		26374	2.72	2.36	1.93	1.40	0.72	ns
Marveld2	MARVEL (membrane-associating) domain containing 2	218518	0.60	0.94	0.99	0.61	-0.80	ns
Scrn3	secernin 3	74616	0.42	0.24	0.14	2.97	0.80	ns
Itgb1	integrin beta 1 (fibronectin receptor beta)	16412	4.00	3.14	2.96	1.35	0.72	ns
Rc3h2	ring finger and CCCH-type zinc finger domains 2	319817	2.41	2.63	2.27	1.06	-0.39	ns
Plcg2	phospholipase C, gamma 2	234779	0.58	0.59	0.25	2.36	0.45	ns
Oxsr1	oxidative-stress responsive 1	108737	0.72	0.67	0.63	1.14	0.70	ns
Nhsl1	NHS-like 1	215819	0.68	0.58	0.42	1.60	0.39	ns
LOC629242		629242	1.04	1.47	1.99	0.52	-0.39	ns
Tsr2	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	69499	0.35	0.36	0.47	0.75	0.21	ns
Sidt2	SID1 transmembrane family, member 2	214597	1.01	0.73	0.73	1.37	0.77	ns
Aim1	absent in melanoma 1	11630	0.39	0.49	0.21	1.81	-0.17	ns
Ints1	integrator complex subunit 1	68510	0.63	0.79	0.69	0.90	0.01	ns
Fbxw8	F-box and WD-40 domain protein 8	231672	1.18	1.02	1.18	1.00	0.30	ns
Tpr	translocated promoter region	108989	2.74	2.47	2.07	1.31	0.47	ns
Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)	50766	0.45	0.40	0.22	2.05	0.72	ns
Arhgap18	Rho GTPase activating protein 18	73910	0.37	0.40	0.48	0.77	-0.86	*
Hmgb2l1	high mobility group box 2-like 1	70823	0.90	0.87	0.83	1.08	0.57	ns
Trim33	tripartite motif protein 33	94093	2.23	2.55	1.79	1.24	0.54	ns
Col18a1	procollagen, type XVIII, alpha 1	12822	3.92	3.46	2.06	1.89	0.70	ns
Trp53bp1	transformation related protein 53 binding protein 1	27223	2.98	2.35	2.07	1.43	0.57	ns
Phf20	PHD finger protein 20	228829	2.14	2.08	1.79	1.19	0.36	ns
Pacs2	phosphofurin acidic cluster sorting protein 2	217893	1.61	1.84	1.28	1.25	0.66	ns
3110003A17Rik	RIKEN cDNA 3110003A17 gene	73112	3.16	3.21	3.23	0.97	-0.52	ns
Rap2a	RAS related protein 2a	76108	0.34	0.39	0.52	0.65	-0.33	ns
Axin1	axin 1	12005	1.40	1.31	0.90	1.54	0.94	**
Rdh10	retinol dehydrogenase 10 (all-trans)	98711	2.43	1.86	1.24	1.95	0.29	ns
Trim23	tripartite motif protein 23	81003	0.44	0.50	0.89	0.49	-0.91	*
Sec24d	SEC24 related gene family, member D (S. cerevisiae)	69608	0.29	0.28	0.16	1.78	0.63	ns
Os9	amplified in osteosarcoma	216440	0.62	0.67	0.67	0.93	-0.27	ns
Usp47	ubiquitin specific peptidase 47	74996	1.38	1.17	1.48	0.93	0.09	ns
Klhl2	kelch-like 2, Mayven (Drosophila)	77113	1.16	1.30	2.05	0.56	-0.63	ns
Mlxip	MLX interacting protein	208104	0.78	0.75	0.70	1.10	0.20	ns
Flywch1	FLYWCH-type zinc finger 1	224613	0.59	0.46	0.31	1.90	0.94	**
2310067B10Rik	RIKEN cDNA 2310067B10 gene	71947	0.32	0.36	0.41	0.78	-0.55	ns
2810485I05Rik	RIKEN cDNA 2810485I05 gene	72826	2.54	2.05	1.04	2.43	0.95	**
Xpr1	xenotropic and polytropic retrovirus receptor 1	19775	0.72	0.82	0.47	1.51	0.75	ns
Phlpp	PH domain and leucine rich repeat protein phosphatase	98432	1.04	0.95	0.72	1.43	0.39	ns
Zc3h14	zinc finger CCCH type containing 14	75553	3.35	2.99	2.92	1.14	0.90	*
Plk2	polo-like kinase 2 (Drosophila)	20620	2.89	3.93	3.22	0.89	0.00	ns
Rapgef1	Rap guanine nucleotide exchange factor (GEF) 1	107746	0.49	0.40	0.35	1.41	0.72	ns
Lama5		16776	1.80	1.95	1.74	1.03	-0.42	ns
Lancl1	LanC (bacterial lantibiotic synthetase component C)-like 1	14768	1.16	1.16	0.91	1.28	0.92	**
4932438A13Rik		229227	1.19	1.21	1.17	1.01	-0.52	ns
Ddx42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	72047	0.68	0.69	0.65	1.06	0.71	ns
Gtf3a	general transcription factor III A	66596	2.38	2.32	2.78	0.85	-0.38	ns
Ccdc52	coiled-coil domain containing 52	212514	1.06	1.00	1.10	0.96	-0.62	ns
Herc4	hect domain and RLD 4	67345	1.32	1.34	1.21	1.08	0.14	ns
Dnmbp	dynamin binding protein	71972	1.72	1.81	1.37	1.25	0.81	ns
Slc39a14	solute carrier family 39 (zinc transporter), member 14	213053	1.15	1.28	1.71	0.67	-0.89	*
Eif4g1	eukaryotic translation initiation factor 4, gamma 1	208643	4.47	4.27	4.91	0.91	-0.78	ns
Epn1	epsin 1	13854	0.48	0.50	0.50	0.96	-0.51	ns
Mdfic	MyoD family inhibitor domain containing	16543	1.38	1.39	0.75	1.84	0.42	ns
Mal2	mal, T-cell differentiation protein 2	105853	5.93	6.39	6.95	0.85	-0.68	ns
Grhl2	grainyhead-like 2 (Drosophila)	252973	1.49	1.48	1.45	1.02	-0.29	ns
Nup188	nucleoporin 188	227699	0.53	0.59	0.47	1.12	0.03	ns
Smo	smoothened homolog (Drosophila)	319757	1.15	1.13	1.07	1.07	-0.24	ns
Tnks1bp1	tankyrase 1 binding protein 1	228140	0.52	0.29	0.27	1.88	0.35	ns
Eif4a1	eukaryotic translation initiation factor 4A1	13681	12.47	11.32	12.51	0.99	-0.45	ns
Mapk3	mitogen activated protein kinase 3	26417	1.83	1.52	2.11	0.86	-0.21	ns
Rbbp8	retinoblastoma binding protein 8	225182	1.20	1.33	1.34	0.89	0.21	ns
Scrib	scribbled homolog (Drosophila)	105782	1.22	1.22	1.44	0.84	-0.68	ns
Snx21	sorting nexin family member 21	101113	0.27	0.35	0.32	0.84	-0.64	ns
Lace1	lactation elevated 1	215951	0.38	0.40	0.23	1.64	0.56	ns
Pcmtd2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	245867	0.64	0.62	0.66	0.96	-0.51	ns
Snx19	sorting nexin 19	102607	0.40	0.46	0.29	1.37	0.74	ns
2610036D13Rik	RIKEN cDNA 2610036D13 gene	75425	1.40	1.28	1.77	0.79	-0.57	ns
Map4k5	mitogen-activated protein kinase kinase kinase kinase 5	399510	2.15	2.20	2.16	0.99	-0.50	ns
2810432D09Rik	RIKEN cDNA 2810432D09 gene	69961	0.55	0.50	0.45	1.21	0.42	ns
Zbed4	zinc finger, BED domain containing 4	223773	0.97	1.05	0.66	1.46	0.36	ns
Pole2	polymerase (DNA directed), epsilon 2 (p59 subunit)	18974	1.17	1.48	1.59	0.73	-0.47	ns
Cdcp1	CUB domain containing protein 1	109332	1.31	1.34	1.37	0.95	0.35	ns
Maz	MYC-associated zinc finger protein (purine-binding transcription factor)	17188	0.80	0.51	0.57	1.41	0.23	ns
Metrn	meteorin, glial cell differentiation regulator	70083	0.62	0.56	0.45	1.37	0.81	*
9530068E07Rik	RIKEN cDNA 9530068E07 gene	213673	3.32	2.91	3.42	0.97	0.00	ns
ORF61	open reading frame 61	216157	1.48	1.47	1.13	1.30	0.69	ns
Raver1	ribonucleoprotein, PTB-binding 1	71766	0.87	0.64	0.60	1.44	0.88	*
Ttl	tubulin tyrosine ligase	69737	0.28	0.42	0.32	0.88	0.19	ns
Setd1a	SET domain containing 1A	233904	0.55	0.66	0.65	0.84	-0.34	ns
Zfp26	zinc finger protein 26	22688	1.28	1.11	0.88	1.44	0.77	ns
Fbxo4	F-box protein 4	106052	0.27	0.28	0.38	0.71	-0.50	ns
Lrrc41	leucine rich repeat containing 41	230654	0.48	0.51	0.68	0.71	-0.87	*
Ptpn23	protein tyrosine phosphatase, non-receptor type 23	104831	0.62	0.64	0.65	0.95	0.44	ns
Lrrc58	leucine rich repeat containing 58	320184	3.40	3.32	3.75	0.90	-0.54	ns
Lrp2	low density lipoprotein receptor-related protein 2	14725	0.64	0.62	0.09	7.21	0.34	ns

Sfrs12	splicing factor, arginine/serine-rich 12	218543	0.91	1.16	1.20	0.75	-0.75	ns
Jarid1b	jumonji, AT rich interactive domain 1B (Rbp2 like)	75605	0.80	0.72	0.63	1.25	0.14	ns
F730047E07Rik	RIKEN cDNA F730047E07 gene	212377	0.48	0.56	0.59	0.81	-0.13	ns
Ascc2	activating signal cointegrator 1 complex subunit 2	75452	0.34	0.46	0.50	0.67	-0.85	*
Mrps30	mitochondrial ribosomal protein S30	59054	0.70	0.92	1.10	0.64	-0.68	ns
Pcf11	cleavage and polyadenylation factor subunit homolog (S. cerevisiae)	74737	0.59	0.80	0.71	0.82	-0.57	ns
Cenpf	centromere protein F	108000	3.49	3.65	3.03	1.15	0.73	ns
Elk4	ELK4, member of ETS oncogene family	13714	1.45	1.70	1.31	1.11	0.32	ns
Spg7	spastic paraplegia 7 homolog (human)	234847	0.52	0.50	0.45	1.15	0.72	ns
Rlf	rearranged L-myc fusion sequence	109263	0.58	0.59	0.85	0.68	-0.43	ns
Ofd1	oral-facial-digital syndrome 1 gene homolog (human)	237222	0.20	0.32	0.42	0.47	-0.52	ns
Mrps33	mitochondrial ribosomal protein S33	14548	1.04	1.16	1.46	0.71	-0.74	ns
OTTMUSG00000016327		665211	0.74	1.03	0.88	0.84	-0.31	ns
AI428936	expressed sequence AI428936	233066	0.54	0.42	0.74	0.73	-0.72	ns
Fyco1	FYVE and coiled-coil domain containing 1	17281	0.48	0.52	0.56	0.86	0.26	ns
Tmc4	transmembrane channel-like gene family 4	353499	1.63	1.51	1.79	0.90	-0.38	ns
Mef2a	myocyte enhancer factor 2A	17258	1.75	1.40	1.15	1.51	0.66	ns
Brd8	bromodomain containing 8	78656	1.04	1.00	1.20	0.86	-0.36	ns
Wnk4	WNK lysine deficient protein kinase 4	69847	0.97	1.04	0.90	1.07	-0.30	ns
Atr	ataxia telangiectasia and Rad3 related	245000	0.67	0.57	0.74	0.90	0.23	ns
Afg3l2	AFG3(ATPase family gene 3)-like 2 (yeast)	69597	0.43	0.49	0.62	0.69	-0.42	ns
Zfp451	zinc finger protein 451	98403	0.82	0.81	0.77	1.07	0.61	ns
Ifnz	interferon zeta	319146	0.22	0.33	0.39	0.57	-0.55	ns
Epn2	epsin 2	13855	1.04	0.86	0.86	1.20	0.76	ns
Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	15357	0.74	1.05	1.61	0.46	-0.87	*
Tshz1	teashirt zinc finger family member 1	110796	0.86	0.93	0.76	1.12	0.48	ns
Vangl1	vang-like 1 (van gogh, Drosophila)	229658	1.20	1.28	0.77	1.56	0.76	ns
Utx	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	22289	0.61	0.66	0.84	0.72	-0.69	ns
Papolg	poly(A) polymerase gamma	216578	0.46	0.40	0.37	1.24	0.62	ns
Ttc15	tetratricopeptide repeat domain 15	217449	0.55	0.46	0.82	0.66	-0.57	ns
Arfgap1	ADP-ribosylation factor GTPase activating protein 1	228998	0.86	0.79	0.80	1.06	0.00	ns
Whsc2	Wolf-Hirschhorn syndrome candidate 2 (human)	24116	0.89	0.74	0.84	1.05	0.01	ns
Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	11938	4.59	4.48	5.22	0.88	-0.77	ns
Trim24	tripartite motif protein 24	21848	0.76	0.71	0.73	1.03	-0.37	ns
Tpm3	tropomyosin 3, gamma	59069	7.52	9.23	7.78	0.96	-0.28	ns
Wwc1	WW, C2 and coiled-coil domain containing 1	211652	2.66	2.09	1.91	1.38	0.75	ns
Bsdc1	BSD domain containing 1	100383	0.60	0.55	0.56	1.07	0.19	ns
Zbtb44	zinc finger and BTB domain containing 44	235132	0.40	0.32	0.21	1.92	0.92	*
Fxn	frataxin	14297	0.63	0.65	0.57	1.09	0.63	ns
Mll1	myeloid/lymphoid or mixed-lineage leukemia 1	214162	1.14	0.93	0.86	1.32	0.87	*
Mrpl9	mitochondrial ribosomal protein L9	78523	2.05	2.21	1.64	1.24	0.08	ns
Rps6ka3	ribosomal protein S6 kinase polypeptide 3	110651	0.21	0.31	0.41	0.51	-0.20	ns
Piga	phosphatidylinositol glycan anchor biosynthesis, class A	18700	0.41	0.46	0.56	0.73	0.20	ns
Dysf		26903	1.34	1.36	1.22	1.10	0.30	ns
Fer1l3		226101	1.34	1.36	1.22	1.10	0.30	ns
Sfrs15		224432	0.46	0.49	0.53	0.87	-0.40	ns
Fastkd1	FAST kinase domains 1	320720	0.42	0.27	0.22	1.88	0.79	ns
Tubb2a		22151	1.09	1.46	1.30	0.83	0.30	ns
Tubb2b		73710	1.09	1.46	1.30	0.83	0.30	ns
Gtpbp6	GTP binding protein 6 (putative)	107999	0.36	0.43	0.50	0.71	-0.68	ns
Cda	cytidine deaminase	72269	0.23	0.28	0.42	0.54	-0.72	ns
Suv39h1	suppressor of variegation 3-9 homolog 1 (Drosophila)	20937	0.62	0.77	0.91	0.68	-0.01	ns
Chd6	chromodomain helicase DNA binding protein 6	71389	0.72	0.64	0.69	1.04	-0.36	ns
Arhgef16	Rho guanine nucleotide exchange factor (GEF) 16	230972	1.10	0.81	1.25	0.87	-0.41	ns
Itgb4	integrin beta 4	192897	0.81	0.85	0.74	1.09	0.39	ns
Csde1	cold shock domain containing E1, RNA binding	229663	10.52	9.59	8.55	1.22	0.50	ns
Trip11	thyroid hormone receptor interactor 11	109181	2.48	2.57	2.41	1.02	-0.03	ns
Hif1a	hypoxia inducible factor 1, alpha subunit	15251	6.10	6.18	6.15	0.99	-0.14	ns
Sfrs10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	20462	5.99	6.10	6.85	0.87	-0.69	ns
Prmt5	protein arginine N-methyltransferase 5	27374	1.02	1.08	1.21	0.84	-0.60	ns
App	amyloid beta (A4) precursor protein	11820	19.11	15.32	14.04	1.35	0.68	ns
Triobp	TRIO and F-actin binding protein	110253	1.78	1.78	1.73	1.02	0.59	ns
Rabep1	rabaptin, RAB GTPase binding effector protein 1	54189	0.46	0.28	0.30	1.53	0.55	ns
Myo1b	myosin IB	17912	0.19	0.37	0.35	0.56	-0.82	*
Pof1b	premature ovarian failure 1B	69693	0.07	0.38	1.05	0.06	-0.94	**
Cep152	centrosomal protein 152	99100	0.31	0.22	0.27	1.14	0.53	ns
Sfrs2	splicing factor, arginine/serine-rich 2 (SC-35)	20382	9.25	8.85	7.52	1.22	0.77	ns
Lama3		16774	0.35	0.39	0.41	0.85	0.01	ns
Eppk1	epiplakin 1	223650	2.48	2.51	2.75	0.90	-0.17	ns
Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	14874	0.58	0.65	0.65	0.89	-0.43	ns
Ift80	intraflagellar transport 80 homolog (Chlamydomonas)	68259	1.45	1.24	0.70	2.06	0.82	*
Atp9a	ATPase, class II, type 9A	11981	0.72	0.71	0.81	0.89	-0.04	ns
Tssc4	tumor-suppressing subchromosomal transferable fragment 4	56844	0.60	0.66	0.60	1.00	0.42	ns
Tcf12	transcription factor 12	21406	2.89	2.62	2.35	1.22	0.91	*
Nfib	nuclear factor I/B	18028	2.59	2.28	2.46	1.05	0.52	ns
Tnip1	TNFAIP3 interacting protein 1	57783	1.00	0.89	1.72	0.58	-0.32	ns
Nfkb1	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105	18033	1.12	1.10	0.93	1.21	0.81	*
Stil	Scl/Tal1 interrupting locus	20460	0.56	0.58	0.87	0.64	-0.60	ns
Rrp1	ribosomal RNA processing 1 homolog (S. cerevisiae)	18114	2.42	2.82	2.27	1.06	0.36	ns
1200011M11Rik	RIKEN cDNA 1200011M11 gene	74133	0.32	0.32	0.47	0.69	-0.64	ns
Trp53	transformation related protein 53	22059	1.47	1.29	1.29	1.13	0.37	ns
Lcn2	lipocalin 2	16819	1.58	3.20	4.36	0.36	-0.77	ns
Rabac1	Rab acceptor 1 (prenylated)	14470	1.64	1.87	2.54	0.64	-0.53	ns
Ctse		13034	0.33	0.30	0.23	1.46	-0.08	ns
Rpl34	ribosomal protein L34	68436	25.65	23.47	17.98	1.42	0.92	**
Zc3h15	zinc finger CCCH-type containing 15	69082	2.01	1.83	1.79	1.12	0.23	ns

0610010O12Rik	RIKEN cDNA 0610010O12 gene	66060	3.11	3.28	3.78	0.82	-0.26 ns
1810031K17Rik	RIKEN cDNA 1810031K17 gene	69171	1.11	1.29	0.87	1.27	0.08 ns
Dnttip2	deoxynucleotidyltransferase, terminal, interacting protein 2	99480	1.21	1.37	1.12	1.08	0.08 ns
Pold4	polymerase (DNA-directed), delta 4	69745	0.98	0.86	1.09	0.90	-0.17 ns
Pom121	nuclear pore membrane protein 121	107939	2.30	2.69	2.94	0.78	-0.41 ns
Spna2	spectrin alpha 2	20740	7.06	6.22	4.19	1.67	0.79 ns
Pmvk	phosphomevalonate kinase	68603	0.66	0.82	0.77	0.85	-0.53 ns
2310004N24Rik	RIKEN cDNA 2310004N24 gene	69535	0.64	0.74	0.71	0.90	0.00 ns
Suds3	suppressor of defective silencing 3 homolog (S. cerevisiae)	71954	1.72	1.62	1.70	1.01	0.19 ns
Rnf6	ring finger protein (C3H2C3 type) 6	74132	1.36	1.24	1.61	0.84	-0.57 ns
Mrps18c	mitochondrial ribosomal protein S18C	68735	2.19	2.12	2.22	0.98	0.31 ns
Phpt1	phosphohistidine phosphatase 1	75454	2.94	3.15	2.01	1.46	0.60 ns
2410091C18Rik	RIKEN cDNA 2410091C18 gene	73694	0.53	0.45	0.42	1.27	0.63 ns
1810063B07Rik	RIKEN cDNA 1810063B07 gene	67509	0.28	0.36	0.51	0.55	-0.64 ns
1110037F02Rik	RIKEN cDNA 1110037F02 gene	66185	0.61	0.60	0.71	0.86	-0.11 ns
Bnip1	BCL2/adenovirus E1B interacting protein 1, NIP1	224630	0.48	0.39	0.43	1.12	0.54 ns
2410015M20Rik	RIKEN cDNA 2410015M20 gene	224904	3.81	3.91	2.51	1.51	0.66 ns
Cbr3	carbonyl reductase 3	109857	0.40	0.71	0.55	0.72	-0.61 ns
Rwdd1	RWD domain containing 1	66521	2.35	2.47	2.67	0.87	-0.81 *
Tceb1	transcription elongation factor B (SIII), polypeptide 1	67923	4.03	3.99	3.72	1.08	-0.06 ns
St7l	suppression of tumorigenicity 7-like	229681	0.54	0.55	0.45	1.20	0.67 ns
Ssbp3	single-stranded DNA binding protein 3	72475	1.00	0.94	0.67	1.47	0.56 ns
Rhoq	ras homolog gene family, member Q	104215	1.19	1.13	0.63	1.88	0.27 ns
Zmpste24	zinc metallopeptidase, STE24 homolog (S. cerevisiae)	230709	1.62	1.41	1.38	1.17	0.66 ns
Hscb	HscB iron-sulfur cluster co-chaperone homolog (E. coli)	100900	0.59	0.52	0.52	1.13	-0.05 ns
Pdxk	pyridoxal (pyridoxine, vitamin B6) kinase	216134	2.08	1.22	0.83	2.49	0.46 ns
Zfp294	zinc finger protein 294	78913	1.00	1.04	1.25	0.80	-0.86 *
Deb1	differentially expressed in B16F10 1	26901	0.63	0.68	0.73	0.87	-0.03 ns
Abhd10	abhydrolase domain containing 10	213012	0.41	0.43	0.50	0.82	-0.90 *
Ccdc102a		234582	0.36	0.42	0.25	1.42	0.78 ns
Ssbp1	single-stranded DNA binding protein 1	381760	3.40	3.76	3.30	1.03	0.28 ns
Zfp654	zinc finger protein 654	72020	0.36	0.40	0.49	0.73	-0.78 ns
Cdc73	Vcell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	214498	1.32	1.53	0.89	1.48	0.51 ns
4933407C03Rik	RIKEN cDNA 4933407C03 gene	74440	0.34	0.37	0.37	0.90	0.01 ns
Csad	cysteine sulfinic acid decarboxylase	246277	0.38	0.31	0.26	1.49	0.37 ns
Syne2	synaptic nuclear envelope 2	319565	16.20	14.52	15.59	1.03	-0.37 ns
Safb2	scaffold attachment factor B2	224902	0.71	0.75	0.45	1.57	0.83 *
Usp45	ubiquitin specific petidase 45	77593	0.35	0.34	0.46	0.75	-0.34 ns
Rab12	RAB12, member RAS oncogene family	19328	0.82	0.65	0.36	2.23	0.92 *
1110007M04Rik	RIKEN cDNA 1110007M04 gene	68493	0.51	0.41	0.34	1.47	0.36 ns
Lsm12	LSM12 homolog (S. cerevisiae)	268490	0.39	0.34	0.45	0.86	0.15 ns
Tmem60	transmembrane protein 60	212090	1.10	1.06	1.19	0.92	-0.07 ns
3300001G02Rik	RIKEN cDNA 3300001G02 gene	78372	0.90	0.88	1.11	0.81	-0.05 ns
Erbb2ip	Erbb2 interacting protein	59079	2.58	3.43	4.03	0.64	-0.93 **
H2afv	H2A histone family, member V	77605	6.01	5.41	6.51	0.92	0.04 ns
Tmbim4	transmembrane BAX inhibitor motif containing 4	68212	0.81	0.69	0.90	0.89	-0.37 ns
Zmym1	zinc finger, MYM domain containing 1	68310	0.47	0.48	0.59	0.79	-0.33 ns
Hat1	histone aminotransferase 1	107435	3.00	2.59	2.59	1.15	0.25 ns
Ankrd46	ankyrin repeat domain 46	68839	1.01	0.80	1.00	1.01	0.07 ns
Ccdc120	coiled-coil domain containing 120	54648	0.32	0.53	1.01	0.31	-0.62 ns
Cdca7	cell division cycle associated 7	66953	0.84	0.92	0.59	1.41	0.34 ns
1110038D17Rik	RIKEN cDNA 1110038D17 gene	68778	0.45	0.45	0.40	1.11	0.00 ns
Nup88	nucleoporin 88	19069	1.69	1.58	2.04	0.83	-0.52 ns
Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	68194	3.46	3.37	3.94	0.87	-0.50 ns
Pgam5	phosphoglycerate mutase family member 5	72542	1.45	1.51	1.55	0.93	-0.55 ns
Klhl21	kelch-like 21 (Drosophila)	242785	0.27	0.28	0.37	0.74	-0.89 *
Acsl5	acyl-CoA synthetase long-chain family member 5	433256	4.18	4.94	4.26	0.98	0.04 ns
1110057K04Rik	RIKEN cDNA 1110057K04 gene	68832	1.35	1.40	1.45	0.93	-0.55 ns
Dnm1l	dynamin 1-like	74006	3.47	3.29	3.94	0.88	-0.80 ns
Ptcd3	Pentatricopeptide repeat domain 3	69956	0.67	0.87	0.81	0.83	-0.57 ns
Lamp2	lysosomal-associated membrane protein 2	16784	2.59	3.01	3.63	0.71	-0.71 ns
Ipo11	importin 11	76582	0.51	0.81	0.79	0.65	-0.54 ns
Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	110809	5.71	7.25	8.13	0.70	-0.95 **
Rnf38	ring finger protein 38	73469	1.35	1.22	1.48	0.91	-0.03 ns
Adam10	a disintegrin and metallopeptidase domain 10	11487	3.10	2.91	2.67	1.16	0.38 ns
Tpx2	TPX2, microtubule-associated protein homolog (Xenopus laevis)	72119	1.63	1.91	1.87	0.87	-0.13 ns
1300001I01Rik	RIKEN cDNA 1300001I01 gene	74148	0.43	0.49	0.56	0.76	-0.99 ***
Vps11	vacuolar protein sorting 11 (yeast)	71732	0.51	0.49	0.44	1.15	0.73 ns
Armet	arginine-rich, mutated in early stage tumors	74840	2.14	2.25	2.41	0.88	0.16 ns
Tmtc4	transmembrane and tetratricopeptide repeat containing 4	70551	2.46	2.00	1.89	1.30	0.73 ns
Dynlt1	dynein light chain Tctex-type 1	21648	10.51	9.46	8.04	1.30	0.96 **
Fbxw9	F-box and WD-40 domain protein 9	68628	0.55	0.55	0.60	0.90	-0.40 ns
Gtf2e1	general transcription factor II E, polypeptide 1 (alpha subunit)	74197	1.09	1.15	1.30	0.83	-0.74 ns
Cdc42se1	CDC42 small effector 1	57912	3.25	3.17	2.90	1.11	0.50 ns
Coq9	coenzyme Q9 homolog (yeast)	67914	0.66	0.61	0.64	1.03	0.49 ns
Arl8b	ADP-ribosylation factor-like 8B	67166	1.99	1.87	2.24	0.89	-0.47 ns
Pnpla2	patatin-like phospholipase domain containing 2	66853	0.52	0.61	0.80	0.65	-0.61 ns
Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	52538	2.21	2.49	1.77	1.24	0.53 ns
Rpl18a	Ribosomal protein L18A	76808	23.93	22.40	18.46	1.29	0.87 *
Mrps10	mitochondrial ribosomal protein S10	64657	1.47	1.47	1.12	1.31	0.88 *
Akt1s1	AKT1 substrate 1 (proline-rich)	67605	1.10	1.02	1.22	0.90	-0.61 ns
Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	70316	2.40	2.12	2.89	0.83	-0.60 ns
Chchd2	coiled-coil-helix-coiled-coil-helix domain containing 2	14004	18.29	16.61	15.52	1.17	0.50 ns
4933421E11Rik	RIKEN cDNA 4933421E11 gene	321000	0.78	0.99	0.87	0.90	-0.44 ns
Sar1b	SAR1 gene homolog B (S. cerevisiae)	66397	3.09	2.78	3.61	0.85	-0.37 ns

Nudt9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	74167	0.73	0.82	0.82	0.89	-0.30	ns
Vps24	vacuolar protein sorting 24 (yeast)	66700	0.48	0.53	0.72	0.66	-0.78	ns
Mpzl1	myelin protein zero-like 1	68481	1.23	1.25	0.72	1.69	0.37	ns
Atg16l1	autophagy-related 16-like 1 (yeast)	77040	0.47	0.38	0.36	1.31	0.82	*
Zfp180	zinc finger protein 180	210135	0.28	0.34	0.46	0.60	-0.60	ns
Prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	328110	1.20	1.01	1.32	0.90	-0.39	ns
Eml2	echinoderm microtubule associated protein like 2	72205	0.58	0.53	0.67	0.86	-0.23	ns
LOC433458		433458	1.65	1.55	1.68	0.98	0.04	ns
Trappc6b	trafficking protein particle complex 6B	78232	2.26	2.34	3.07	0.74	-0.67	ns
Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	72900	4.65	3.93	3.09	1.50	0.98	***
Etfb	electron transferring flavoprotein, beta polypeptide	110826	1.43	1.46	1.37	1.04	-0.17	ns
Prpsap1	phosphoribosyl pyrophosphate synthetase-associated protein 1	67763	2.63	2.56	2.21	1.18	0.85	*
Kctd6	potassium channel tetramerisation domain containing 6	71393	0.61	0.61	0.63	0.97	-0.47	ns
Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	16423	2.78	2.84	3.49	0.79	-0.82	*
Slc25a1	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	13358	2.14	1.78	2.72	0.78	-0.56	ns
Usp9x	ubiquitin specific peptidase 9, X chromosome	22284	0.82	0.85	1.44	0.56	-0.27	ns
1200015F23Rik	RIKEN cDNA 1200015F23 gene	67809	0.69	0.60	0.50	1.38	0.52	ns
Tspan9	tetraspanin 9	109246	0.98	1.05	0.78	1.25	0.84	*
2310036O22Rik	RIKEN cDNA 2310036O22 gene	68544	3.65	3.80	3.39	1.07	0.46	ns
1810037C20Rik	RIKEN cDNA 1810037C20 gene	66294	0.33	0.39	0.56	0.58	-0.80	ns
Bcl7a	B-cell CLL/lymphoma 7A	77045	0.74	0.80	0.71	1.04	-0.11	ns
Nsmce4a	non-SMC element 4 homolog A (S. cerevisiae)	67872	2.26	2.16	2.46	0.91	-0.06	ns
Tomm7	translocase of outer mitochondrial membrane 7 homolog (yeast)	66169	1.89	1.92	2.54	0.74	-0.76	ns
1600012H06Rik	RIKEN cDNA 1600012H06 gene	67912	0.92	0.81	0.64	1.44	0.93	**
EG628746		628746	3.01	3.19	3.70	0.81	-0.91	*
Rybp		56353	3.01	3.19	3.70	0.81	-0.91	*
5730419I09Rik	RIKEN cDNA 5730419I09 gene	74741	0.36	0.45	0.46	0.78	-0.87	*
Rest	RE1-silencing transcription factor	19712	0.79	0.88	1.00	0.79	-0.77	ns
Cpsf6	cleavage and polyadenylation specific factor 6	432508	2.25	2.00	2.25	1.00	-0.25	ns
Sdhd	succinate dehydrogenase complex, subunit D, integral membrane protein	66925	2.33	1.72	1.74	1.34	0.78	ns
Acbd5	acyl-Coenzyme A binding domain containing 5	74159	1.66	1.74	1.42	1.16	-0.13	ns
Ankrd16	ankyrin repeat domain 16	320816	0.48	0.45	0.41	1.16	0.46	ns
2310035K24Rik	RIKEN cDNA 2310035K24 gene	69596	0.27	0.20	0.37	0.72	-0.57	ns
1700021K19Rik	RIKEN cDNA 1700021K19 gene	224118	0.57	0.52	0.80	0.71	-0.52	ns
Larp1	La ribonucleoprotein domain family, member 1	73158	1.97	1.96	2.12	0.93	-0.64	ns
Vps26b	vacuolar protein sorting 26 homolog B (yeast)	69091	0.51	0.44	0.58	0.87	0.03	ns
Nfx1	nuclear transcription factor, X-box binding 1	74164	1.03	0.85	0.91	1.12	-0.15	ns
Pygo2	pygopus 2	68911	2.16	2.07	1.63	1.32	0.76	ns
Smchd1	SMC hinge domain containing 1	74355	2.60	2.74	2.51	1.03	0.60	ns
Chmp2b	chromatin modifying protein 2B	68942	2.53	2.93	3.32	0.76	-0.93	**
Purb	Purine rich element binding protein B	19291	2.63	2.64	3.55	0.74	-0.31	ns
Luc7l	Luc7 homolog (S. cerevisiae)-like	66978	1.07	0.97	0.74	1.44	0.88	*
Dynlrb1	dynein light chain roadblock-type 1	67068	3.88	3.87	4.79	0.81	-0.72	ns
2010107E04Rik	RIKEN cDNA 2010107E04 gene	70257	5.23	4.75	5.41	0.96	-0.08	ns
Pxdn	peroxidasin homolog (Drosophila)	69675	1.73	1.88	1.39	1.24	0.57	ns
EG668559		668559	6.78	7.03	5.77	1.17	0.36	ns
LOC545592		545592	6.78	7.03	5.77	1.17	0.36	ns
LOC630401		630401	6.78	7.03	5.77	1.17	0.36	ns
Tceb2	transcription elongation factor B (SIII), polypeptide 2	67673	7.51	6.46	4.77	1.57	0.99	***
Ppp2r1b	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	73699	0.93	0.85	0.91	1.01	0.47	ns
Dhx40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	67487	0.97	0.88	1.02	0.95	-0.28	ns
Glt8d1	glycosyltransferase 8 domain containing 1	76485	1.47	1.52	1.35	1.08	0.21	ns
Eif1b	eukaryotic translation initiation factor 1B	68969	0.93	0.89	0.94	0.98	0.49	ns
Abhd13	abhydrolase domain containing 13	68904	0.55	0.68	0.78	0.70	-0.54	ns
Otud6b	OTU domain containing 6B	72201	0.60	0.62	0.59	1.02	-0.05	ns
Fip1l1	FIP1 like 1 (S. cerevisiae)	66899	1.28	1.35	1.53	0.83	-0.65	ns
Trub1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	72133	0.44	0.61	0.49	0.89	-0.01	ns
Tbce	tubulin-specific chaperone e	70430	0.80	0.72	0.94	0.85	-0.73	ns
Cyp2s1	cytochrome P450, family 2, subfamily s, polypeptide 1	74134	0.84	0.67	1.00	0.83	-0.36	ns
8430427H17Rik	RIKEN cDNA 8430427H17 gene	329540	0.21	0.27	0.42	0.50	-0.54	ns
2900097C17Rik	RIKEN cDNA 2900097C17 gene	347740	6.05	6.46	6.17	0.98	-0.22	ns
Cul5	cullin 5	75717	0.43	0.31	0.26	1.67	0.96	**
Mipep	mitochondrial intermediate peptidase	70478	0.56	0.35	0.41	1.37	0.42	ns
Exosc8	exosome component 8	69639	2.95	2.73	2.42	1.21	0.89	*
2310022M17Rik	RIKEN cDNA 2310022M17 gene	69556	1.81	1.78	1.94	0.93	-0.22	ns
Polr2l	polymerase (RNA) II (DNA directed) polypeptide L	66491	1.43	1.41	1.60	0.89	-0.20	ns
Dyrk1a	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	13548	1.01	0.99	1.39	0.72	-0.86	*
Specc1l	SPECC1-like	74392	1.19	0.84	0.82	1.45	0.66	ns
B930046C15Rik		544998	0.25	0.35	0.17	1.51	0.44	ns
ENSMUSG00000068790		545007	0.25	0.35	0.17	1.51	0.44	ns
LOC544988		544988	0.25	0.35	0.17	1.51	0.44	ns
LOC666329		666329	0.25	0.35	0.17	1.51	0.44	ns
LOC666740		666740	0.25	0.35	0.17	1.51	0.44	ns
Mrpl48	mitochondrial ribosomal protein L48	52443	0.72	0.68	0.68	1.05	0.70	ns
Esco2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	71988	0.80	0.99	1.38	0.57	-0.47	ns
Ddit4	DNA-damage-inducible transcript 4	74747	2.40	1.86	2.26	1.06	-0.33	ns
Zdhhc13	zinc finger, DHHC domain containing 13	243983	0.95	0.85	1.42	0.66	-0.66	ns
Pdrg1	p53 and DNA damage regulated 1	68559	0.62	0.53	0.57	1.08	-0.21	ns
Ccdc6	coiled-coil domain containing 6	76551	1.56	1.23	1.17	1.33	0.67	ns
Pcnp	PEST proteolytic signal containing nuclear protein	76302	5.73	5.21	6.17	0.92	-0.51	ns
Ebna1bp2	EBNA1 binding protein 2	69072	0.68	0.84	0.88	0.77	-0.65	ns
Fundc2	FUN14 domain containing 2	67391	1.99	1.35	1.88	1.05	-0.31	ns
Pdlim7	PDZ and LIM domain 7	67399	2.22	2.32	1.94	1.14	0.23	ns
Jmjd1b	jumonji domain containing 1B	277250	0.75	0.77	0.90	0.83	-0.28	ns
Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	68342	3.11	2.76	2.28	1.36	0.70	ns

Hrsp12	heat-responsive protein 12	15473	0.85	1.08	1.04	0.81	-0.65	ns
Trak1	trafficking protein, kinesin binding 1	67095	0.59	0.60	0.55	1.07	0.70	ns
Nup50	nucleoporin 50	18141	1.05	1.06	1.27	0.82	-0.24	ns
Dopey2	dopey family member 2	70028	0.54	0.51	0.57	0.93	-0.62	ns
Ostm1	osteopetrosis associated transmembrane protein 1	14628	0.92	0.91	0.59	1.56	0.57	ns
Scfd1	sec1 family domain containing 1	76983	1.15	1.14	1.22	0.94	-0.49	ns
Zfp655	zinc finger protein 655	72611	0.74	0.81	0.92	0.80	-0.74	ns
Rcor3	REST corepressor 3	214742	0.88	0.96	0.61	1.43	0.55	ns
Ppapdc2	phosphatidic acid phosphatase type 2 domain containing 2	74411	0.60	0.61	0.58	1.03	0.67	ns
Trafd1	TRAF type zinc finger domain containing 1	231712	0.43	0.40	0.48	0.89	0.31	ns
Gzf1	GDNF-inducible zinc finger protein 1	74533	0.74	0.59	0.76	0.97	0.06	ns
Ppm1m	protein phosphatase 1M	67905	0.52	0.54	0.49	1.05	0.61	ns
Foxk2	forkhead box K2	68837	1.07	1.15	1.44	0.74	-0.29	ns
Scnm1	sodium channel modifier 1	69269	1.02	1.05	0.89	1.14	0.28	ns
Lonp1	lon peptidase 1, mitochondrial	74142	2.40	2.66	2.26	1.06	0.61	ns
1600027N09Rik	RIKEN cDNA 1600027N09 gene	73247	0.34	0.41	0.42	0.80	-0.74	ns
Arhgap21	Rho GTPase activating protein 21	71435	2.53	2.24	1.79	1.41	0.31	ns
St5	suppression of tumorigenicity 5	76954	0.39	0.37	0.49	0.79	-0.81	ns
Glce	glucuronyl C5-epimerase	93683	0.89	0.76	0.49	1.81	0.88	*
0610007C21Rik	RIKEN cDNA 0610007C21 gene	381629	1.13	1.09	1.41	0.80	-0.67	ns
2700038C09Rik	RIKEN cDNA 2700038C09 gene	66496	1.07	0.95	1.26	0.84	-0.77	ns
Smarcc2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	68094	0.81	0.73	0.71	1.14	0.59	ns
2310021P13Rik	RIKEN cDNA 2310021P13 gene	268721	0.48	0.51	0.46	1.04	0.08	ns
March8	membrane-associated ring finger (C3HC4) 8	71779	1.35	1.25	1.65	0.82	-0.81	ns
Tnks2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	74493	8.92	9.31	7.13	1.24	0.84	*
Wdr43	WD repeat domain 43	72515	1.10	1.11	0.72	1.51	0.76	ns
Smurf1		75788	0.33	0.35	0.63	0.53	-0.79	ns
Zcchc3	zinc finger, CCHC domain containing 3	67917	0.95	0.96	0.93	1.02	-0.14	ns
Hcfc1r1	host cell factor C1 regulator 1 (XPO1-dependent)	353502	4.31	4.68	3.38	1.27	0.60	ns
Hnrpa0	heterogeneous nuclear ribonucleoprotein A0	77134	4.10	4.01	3.52	1.16	0.88	*
D12Ertd551e	DNA segment, Chr 12, ERATO Doi 551, expressed	52635	1.19	1.37	1.58	0.75	-0.81	ns
Nat13	N-acetyltransferase 13	72117	4.75	4.17	5.55	0.85	-0.16	ns
1700020I14Rik	RIKEN cDNA 1700020I14 gene	66602	2.78	2.18	1.92	1.44	0.60	ns
Rnf113a2	ring finger protein 113A2	66381	0.29	0.35	0.53	0.55	-0.81	*
3110050N22Rik	RIKEN cDNA 3110050N22 gene	67306	1.14	1.14	0.81	1.40	0.33	ns
1200009I06Rik	RIKEN cDNA 1200009I06 gene	74190	0.25	0.35	0.62	0.40	-0.85	*
Glod4	glyoxalase domain containing 4	67201	2.08	2.40	1.88	1.10	0.38	ns
Pcgf3	polycomb group ring finger 3	69587	1.49	1.40	1.25	1.18	0.82	*
Tgfbrap1	transforming growth factor, beta receptor associated protein 1	73122	0.60	0.62	0.47	1.29	0.56	ns
Abhd11	abhydrolase domain containing 11	68758	0.95	0.97	1.06	0.89	-0.36	ns
Hipk2	homeodomain interacting protein kinase 2	15258	0.66	0.87	0.54	1.22	-0.19	ns
Lsm14a	LSM14 homolog A (SCD6, S. cerevisiae)	67070	3.57	2.61	2.75	1.29	0.71	ns
Slc25a12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	78830	0.85	0.79	0.69	1.22	-0.19	ns
Rap1gap	Rap1 GTPase-activating protein	110351	0.34	0.21	0.36	0.94	-0.41	ns
Yif1b	Yip1 interacting factor homolog B (S. cerevisiae)	77254	0.46	0.57	0.62	0.74	-0.20	ns
Dync2li1	dynein cytoplasmic 2 light intermediate chain 1	213575	0.96	0.77	0.44	2.15	0.52	ns
2610034B18Rik	RIKEN cDNA 2610034B18 gene	70420	0.46	0.54	0.56	0.82	-0.81	*
Lrrc47	leucine rich repeat containing 47	72946	0.81	1.01	1.01	0.80	-0.64	ns
Nat12	N-acetyltransferase 12	70646	0.92	0.99	1.05	0.88	-0.36	ns
Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	26932	2.31	2.30	1.94	1.18	0.43	ns
Tmem147	transmembrane protein 147	69804	1.75	1.80	1.97	0.88	-0.17	ns
Chd3	chromodomain helicase DNA binding protein 3	216848	0.87	0.93	0.54	1.60	0.60	ns
Exoc2	exocyst complex component 2	66482	0.60	0.61	0.63	0.95	0.27	ns
Sorbs1	sorbin and SH3 domain containing 1	20411	0.69	0.74	0.80	0.86	-0.62	ns
Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	19056	2.00	1.92	1.99	1.00	0.47	ns
Reep4	receptor accessory protein 4	72549	0.96	0.89	1.21	0.78	-0.11	ns
Osbpl3	oxysterol binding protein-like 3	71720	1.86	1.86	2.31	0.80	-0.52	ns
Pigk	phosphatidylinositol glycan anchor biosynthesis, class K	329777	0.59	0.50	0.44	1.32	0.35	ns
Zcrb1	zinc finger CCHC-type and RNA binding motif 1	67197	2.08	2.37	2.34	0.88	-0.11	ns
C1galt1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	94192	0.54	0.75	1.09	0.49	-0.73	ns
Commd10	COMM domain containing 10	69456	0.55	0.56	0.69	0.80	-0.05	ns
Sipa1l3		74206	0.80	1.22	0.86	0.92	0.04	ns
Polr2i	polymerase (RNA) II (DNA directed) polypeptide I	69920	1.37	1.51	1.44	0.95	-0.64	ns
Secisbp2	SECIS binding protein 2	75420	0.48	0.32	0.51	0.93	-0.18	ns
1110051M20Rik	RIKEN cDNA 1110051M20 gene	228356	0.40	0.25	0.34	1.16	-0.36	ns
Actr6	ARP6 actin-related protein 6 homolog (yeast)	67019	0.53	0.54	0.54	0.99	-0.47	ns
Ccdc90b	coiled-coil domain containing 90B	66365	1.00	1.06	1.22	0.81	-0.50	ns
Atic	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	108147	2.45	2.52	1.66	1.47	0.45	ns
Hdhd2	haloacid dehalogenase-like hydrolase domain containing 2	76987	0.42	0.47	0.44	0.94	0.34	ns
Tbc1d2b	TBC1 domain family, member 2B	67016	0.39	0.43	0.29	1.36	0.76	ns
Myo1e	myosin IE	71602	0.76	0.45	0.50	1.52	0.72	ns
Lphn1	latrophilin 1	330814	0.28	0.34	0.55	0.51	-0.09	ns
Phkg2	phosphorylase kinase, gamma 2 (testis)	68961	0.79	0.68	0.58	1.36	0.57	ns
Calcoco1	calcium binding and coiled coil domain 1	67488	0.78	0.66	0.65	1.19	-0.01	ns
Alkbh7	alkB, alkylation repair homolog 7 (E. coli)	66400	0.90	0.71	0.34	2.65	0.91	*
Wdfy3	WD repeat and FYVE domain containing 3	72145	1.86	1.48	1.31	1.41	0.87	*
Mlf1ip	myeloid leukemia factor 1 interacting protein	71876	0.46	0.55	0.74	0.62	-0.28	ns
2610528E23Rik	RIKEN cDNA 2610528E23 gene	66497	0.95	1.13	1.03	0.92	0.39	ns
1110032A13Rik	RIKEN cDNA 1110032A13 gene	68731	0.53	0.57	0.56	0.95	0.31	ns
Ttf2	transcription termination factor, RNA polymerase II	74044	0.97	1.01	1.04	0.93	0.02	ns
Lsmd1	LSM domain containing 1	78304	1.77	2.29	2.59	0.68	-0.75	ns
Snx7	sorting nexin 7	76561	0.46	0.56	0.55	0.83	0.09	ns
2810026P18Rik	RIKEN cDNA 2810026P18 gene	72655	0.89	1.45	0.70	1.27	0.31	ns
EG629116		629116	16.98	17.78	15.30	1.10	0.27	ns

LOC677113		677113	16.98	17.78	15.30	1.10	0.27	ns
Ints7	integrator complex subunit 7	77065	1.72	1.51	1.34	1.27	0.19	ns
D1Bwg0212e	DNA segment, Chr 1, Brigham & Women's Genetics 0212 expressed	52846	0.92	0.87	0.67	1.36	0.54	ns
2610207I05Rik	RIKEN cDNA 2610207I05 gene	233789	0.93	0.86	1.14	0.81	-0.36	ns
Pak4	p21 (CDKN1A)-activated kinase 4	70584	0.91	0.97	0.96	0.94	-0.58	ns
Trmt11	tRNA methyltransferase 11 homolog (S. cerevisiae)	73681	0.57	0.47	0.41	1.37	0.63	ns
Glrx5	glutaredoxin 5 homolog (S. cerevisiae)	73046	2.80	3.02	2.95	0.94	-0.02	ns
1810035L17Rik	RIKEN cDNA 1810035L17 gene	380773	2.23	2.54	3.14	0.71	-0.62	ns
Setd2	SET domain containing 2	235626	1.04	0.96	0.91	1.14	0.47	ns
Pigy	phosphatidylinositol glycan anchor biosynthesis, class Y	66459	0.61	0.75	0.65	0.93	-0.40	ns
Xpo5	exportin 5	72322	0.71	0.70	0.54	1.31	0.74	ns
Zfp579	zinc finger protein 579	68490	0.54	0.41	0.37	1.45	0.16	ns
Unkl	unkempt-like (Drosophila)	74154	0.59	0.44	0.45	1.31	0.48	ns
Basp1	brain abundant, membrane attached signal protein 1	70350	8.26	9.33	14.38	0.57	-0.35	ns
Chn2	chimerin (chimaerin) 2	69993	0.51	0.42	0.45	1.12	0.30	ns
Hif1an	hypoxia-inducible factor 1, alpha subunit inhibitor	319594	0.89	1.01	0.78	1.13	0.60	ns
Fmnl2	formin-like 2	71409	2.60	1.78	0.86	3.01	0.51	ns
Blvra	biliverdin reductase A	109778	1.09	0.99	0.91	1.19	0.16	ns
Haghl	hydroxyacylglutathione hydrolase-like	68977	1.51	1.07	0.63	2.39	0.89	*
Actn1	actinin, alpha 1	109711	6.58	5.61	6.03	1.09	0.61	ns
Tmem41b	transmembrane protein 41B	233724	0.66	0.65	0.75	0.88	-0.51	ns
Mrpl41	mitochondrial ribosomal protein L41	107733	1.06	1.08	0.74	1.43	0.69	ns
Usp38	ubiquitin specific peptidase 38	74841	0.39	0.38	0.38	1.01	0.37	ns
1700029F09Rik	RIKEN cDNA 1700029F09 gene	75623	1.22	1.33	1.17	1.04	0.50	ns
Garnl1	GTPase activating RANGAP domain-like 1	56784	1.18	1.07	1.16	1.01	0.11	ns
Tbc1d9b	TBC1 domain family, member 9B	76795	0.88	0.80	0.92	0.95	-0.33	ns
Nin	ninein	18080	0.29	0.38	0.43	0.66	-0.79	ns
LOC100036521	hypothetical gene LOC100036521	#######	0.53	0.71	0.81	0.64	-0.40	ns
Mylc2b	myosin light chain, regulatory B	67938	9.23	8.47	6.22	1.48	0.63	ns
P2ry5	purinergic receptor P2Y, G-protein coupled, 5	67168	0.68	0.58	0.79	0.86	-0.66	ns
Zfp131	zinc finger protein 131	72465	0.79	1.27	1.30	0.61	-0.58	ns
Hcfc2	host cell factor C2	67933	0.90	0.74	0.73	1.22	0.56	ns
2310005N03Rik	RIKEN cDNA 2310005N03 gene	66359	1.39	1.33	1.09	1.27	0.88	*
Ensa	endosulfine alpha	56205	1.91	1.86	1.61	1.18	0.80	ns
Vps25	vacuolar protein sorting 25 (yeast)	28084	1.86	1.51	2.16	0.86	-0.27	ns
Plxna1	plexin A1	18844	0.56	0.50	0.64	0.86	-0.63	ns
Zfp518	zinc finger protein 518	72672	0.58	0.79	0.51	1.13	-0.19	ns
Uqcrc2	ubiquinol cytochrome c reductase core protein 2	67003	3.25	3.00	3.20	1.01	0.04	ns
Steap2	six transmembrane epithelial antigen of prostate 2	74051	1.49	1.55	1.81	0.82	-0.86	*
Dyrk2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	69181	0.49	0.55	0.34	1.42	0.37	ns
Lin9	lin-9 homolog (C. elegans)	72568	0.43	0.39	0.48	0.89	-0.73	ns
Gnai3	guanine nucleotide binding protein, alpha inhibiting 3	14679	5.00	5.01	3.93	1.26	0.66	ns
LOC676870	region containing RIKEN cDNA 2310056B04 gene; pre B-cell leukemia transcription factor 1	676870	1.44	1.45	1.13	1.27	-0.03	ns
Cand1	cullin associated and neddylation disassociated 1	71902	1.84	1.74	1.74	1.06	-0.06	ns
Tns1	tensin 1	21961	2.28	0.99	0.58	3.92	0.84	*
0610010F05Rik	RIKEN cDNA 0610010F05 gene	71675	0.79	0.77	0.76	1.03	0.22	ns
1200016B10Rik	RIKEN cDNA 1200016B10 gene	66875	0.42	0.39	0.32	1.33	0.62	ns
Rreb1	ras responsive element binding protein 1	68750	0.47	0.45	0.68	0.69	-0.82	*
EG628161		628161	0.67	0.62	0.99	0.67	-0.41	ns
LOC635999		635999	0.67	0.62	0.99	0.67	-0.41	ns
Pin4		69713	0.67	0.62	0.99	0.67	-0.41	ns
Nfkbil2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2	72749	0.80	0.87	1.01	0.79	-0.32	ns
Maoa	monoamine oxidase A	17161	0.59	0.61	0.03	17.44	0.71	ns
Acbd3	acyl-Coenzyme A binding domain containing 3	170760	0.81	0.73	0.79	1.03	0.04	ns
2200002D01Rik	RIKEN cDNA 2200002D01 gene	72275	0.48	0.44	0.50	0.96	-0.06	ns
Snrpf	small nuclear ribonucleoprotein polypeptide F	69878	1.70	2.01	2.69	0.63	-0.93	**
Sympk	symplekin	68188	0.68	0.80	1.38	0.49	-0.71	ns
1110049F12Rik	RIKEN cDNA 1110049F12 gene	66193	0.69	0.78	0.87	0.79	-0.76	ns
Wdr73	WD repeat domain 73	71968	0.40	0.48	0.56	0.70	-0.83	*
0610010K14Rik	RIKEN cDNA 0610010K14 gene	104457	0.61	0.69	1.17	0.52	-0.72	ns
Gm608	gene model 608, (NCBI)	207806	1.39	1.23	1.67	0.83	-0.52	ns
Zc3h6	zinc finger CCCH type containing 6	78751	0.22	0.20	0.48	0.45	-0.55	ns
1500001M20Rik	RIKEN cDNA 1500001M20 gene	68971	0.64	0.64	0.66	0.97	-0.21	ns
Zfp687	zinc finger protein 687	78266	0.86	0.84	0.61	1.40	0.83	*
Pdcd11	programmed cell death protein 11	18572	0.83	1.00	0.80	1.03	0.52	ns
Tysnd1	trypsin domain containing 1	71767	0.32	0.39	0.37	0.85	-0.44	ns
Chd2	chromodomain helicase DNA binding protein 2	244059	1.15	0.98	1.08	1.05	0.49	ns
Hddc3	HD domain containing 3	68695	0.25	0.26	0.39	0.62	-0.73	ns
2310014G06Rik	RIKEN cDNA 2310014G06 gene	654795	0.66	0.56	0.48	1.37	0.89	*
Dpp8	dipeptidylpeptidase 8	74388	0.53	0.45	0.37	1.43	0.96	**
Prr6	proline-rich polypeptide 6	73139	0.09	0.14	0.39	0.24	-0.62	ns
Ptms	parathymosin	69202	4.96	4.13	4.61	1.07	0.48	ns
Mrpl24	mitochondrial ribosomal protein L24	67707	3.43	3.92	3.12	1.10	0.04	ns
Pgrmc2	progesterone receptor membrane component 2	70804	1.84	1.77	1.35	1.36	0.79	ns
Pex1	peroxisome biogenesis factor 1	71382	0.45	0.34	0.47	0.95	-0.28	ns
Klhl28	kelch-like 28 (Drosophila)	66689	0.46	0.57	0.48	0.94	0.29	ns
Pias2	protein inhibitor of activated STAT 2	17344	0.65	0.64	0.56	1.16	0.63	ns
Ddx51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	69663	0.47	0.35	0.35	1.34	0.32	ns
Usp54	ubiquitin specific peptidase 54	78787	0.55	0.43	0.56	0.96	-0.27	ns
Gramd3	GRAM domain containing 3	107022	0.57	0.46	0.32	1.80	0.02	ns
D14Ertd449e	DNA segment, Chr 14, ERATO Doi 449, expressed	66039	2.55	2.77	2.24	1.13	-0.17	ns
Bri3bp	Bri3 binding protein	76809	0.84	0.72	0.80	1.05	0.17	ns
Trspap1	tRNA selenocysteine associated protein 1	71787	0.88	0.96	1.15	0.76	-0.63	ns
Dmxl2	Dmx-like 2	235380	0.27	0.23	0.20	1.35	0.50	ns
Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2	104252	0.71	0.61	0.46	1.54	0.62	ns

Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	67618	0.66	0.68	0.27	2.44	0.79 ns
Tmem86a	transmembrane protein 86A	67893	0.35	0.28	0.23	1.52	-0.04 ns
Ccdc49	coiled-coil domain containing 49	67480	0.47	0.38	0.50	0.94	-0.02 ns
Map3k7ip3	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	66724	0.76	0.71	1.03	0.73	-0.78 ns
Smug1	single-strand selective monofunctional uracil DNA glycosylase	71726	0.67	0.73	0.74	0.89	0.25 ns
Bcor	Bcl6 interacting corepressor	71458	0.30	0.25	0.38	0.79	-0.46 ns
1110008L16Rik	RIKEN cDNA 1110008L16 gene	66132	0.43	0.61	0.58	0.74	-0.72 ns
Zbtb41	zinc finger and BTB domain containing 41 homolog	226470	1.53	1.26	1.11	1.37	0.59 ns
Uqcrc1	ubiquinol-cytochrome c reductase core protein 1	22273	3.74	3.37	3.54	1.05	0.61 ns
Amotl1	angiomotin-like 1	75723	1.76	1.30	0.65	2.72	0.86 *
Ralgps2	Ral GEF with PH domain and SH3 binding motif 2	78255	0.34	0.36	0.35	0.96	-0.61 ns
Specc1	sperm antigen with calponin homology and coiled-coil domains 1	432572	0.98	0.99	1.19	0.82	-0.25 ns
1110021L09Rik	RIKEN cDNA 1110021L09 gene	76306	0.39	0.34	0.29	1.34	-0.20 ns
Setd6	SET domain containing 6	66083	0.50	0.54	0.62	0.81	-0.71 ns
Pus7l	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	78895	0.48	0.44	0.36	1.35	0.32 ns
Mfap3l	microfibrillar-associated protein 3-like	71306	1.92	1.53	1.43	1.34	0.61 ns
Slc35e3	solute carrier family 35, member E3	215436	0.43	0.52	0.39	1.11	0.04 ns
Csnk1g1	casein kinase 1, gamma 1	214897	0.88	0.74	0.81	1.09	0.65 ns
Mon2	MON2 homolog (yeast)	67074	1.14	1.08	1.05	1.09	-0.09 ns
Agpat2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	67512	1.43	1.51	1.11	1.28	0.23 ns
Snx24	sorting nexing 24	69226	1.17	1.36	1.02	1.14	0.49 ns
Hddc2	HD domain containing 2	69692	1.04	0.83	0.74	1.39	0.25 ns
2310003C23Rik	RIKEN cDNA 2310003C23 gene	76425	0.52	0.52	0.68	0.76	-0.60 ns
Nr6a1	nuclear receptor subfamily 6, group A, member 1	14536	0.47	0.45	0.26	1.80	0.62 ns
Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)	107823	0.90	0.99	1.33	0.68	-0.21 ns
Rpain	RPA interacting protein	69723	0.56	0.53	0.64	0.86	-0.04 ns
1600002H07Rik	RIKEN cDNA 1600002H07 gene	72016	0.42	0.38	0.33	1.27	0.85 *
Dusp4	dual specificity phosphatase 4	319520	0.54	0.77	1.37	0.40	-0.91 *
Myh14		71960	0.36	0.68	1.26	0.28	-0.88 *
Klhl14	kelch-like 14 (Drosophila)	225266	0.33	0.22	0.23	1.44	0.13 ns
Wdr53	WD repeat domain 53	68980	0.36	0.44	0.52	0.70	-0.82 *
Ngfrap1	nerve growth factor receptor (TNFRSF16) associated protein 1	12070	5.60	5.73	6.98	0.80	0.24 ns
March5	membrane-associated ring finger (C3HC4) 5	69104	3.63	3.82	3.41	1.06	0.42 ns
Bclaf1	BCL2-associated transcription factor 1	72567	2.35	2.29	1.63	1.43	0.15 ns
Macf1	microtubule-actin crosslinking factor 1	11426	1.50	1.41	1.59	0.94	-0.74 ns
Cd99	CD99 antigen	673094	0.75	1.07	1.61	0.46	-0.17 ns
1300014I06Rik	RIKEN cDNA 1300014I06 gene	66895	0.31	0.37	0.45	0.68	-0.20 ns
Ptch1	patched homolog 1	19206	1.22	1.15	1.46	0.83	-0.57 ns
Tmed8	transmembrane emp24 domain containing 8	382620	0.87	0.83	0.80	1.07	0.37 ns
Sap130	Sin3A associated protein, 130kDa	269003	0.43	0.46	0.54	0.80	-0.47 ns
Wdr70	WD repeat domain 70	545085	0.45	0.39	0.40	1.12	0.26 ns
Nolc1	nucleolar and coiled-body phosphoprotein 1	70769	1.20	1.87	1.19	1.00	0.26 ns
4121402D02Rik	RIKEN cDNA 4121402D02 gene	74026	1.56	1.30	1.55	1.01	0.00 ns
1110019N10Rik	RIKEN cDNA 1110019N10 gene	68523	2.07	2.07	2.52	0.82	0.08 ns
Srp72	signal recognition particle 72	66661	2.25	2.13	2.32	0.96	-0.47 ns
0610038F07Rik	RIKEN cDNA 0610038F07 gene	66072	0.92	0.95	0.70	1.30	0.70 ns
Klc1	kinesin light chain 1	16593	0.55	0.62	0.59	0.93	0.27 ns
Tmem57	transmembrane protein 57	66146	1.39	1.34	1.46	0.94	-0.27 ns
Rbbp5	retinoblastoma binding protein 5	213464	0.93	0.77	0.70	1.32	0.85 *
Alkbh3	alkB, alkylation repair homolog 3 (E. coli)	69113	1.13	0.96	1.06	1.06	-0.04 ns
Fem1c	fem-1 homolog c (C.elegans)	240263	0.90	1.09	0.95	0.95	0.30 ns
9130213B05Rik	RIKEN cDNA 9130213B05 gene	231440	0.40	0.48	0.70	0.57	-0.79 ns
Ppil1	peptidylprolyl isomerase (cyclophilin)-like 1	68816	1.58	1.57	1.10	1.43	0.86 *
1300018J18Rik	RIKEN cDNA 1300018J18 gene	223776	0.34	0.38	0.45	0.75	-0.56 ns
Mett5d1	methyltransferase 5 domain containing 1	76894	0.52	0.53	0.46	1.12	0.68 ns
Rraga	Ras-related GTP binding A	68441	0.98	0.81	0.97	1.00	-0.08 ns
Gtf2h5	general transcription factor IIH, polypeptide 5	66467	1.58	1.53	1.20	1.31	0.95 **
Rbm25	RNA binding motif protein 25	67039	3.01	3.38	3.31	0.90	-0.40 ns
2310022B05Rik	RIKEN cDNA 2310022B05 gene	69551	1.50	1.39	1.01	1.47	0.90 *
Ttll4	tubulin tyrosine ligase-like family, member 4	67534	0.54	0.45	0.46	1.16	0.31 ns
Sirt5	sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	68346	0.46	0.43	0.44	1.02	0.23 ns
Fgfr1op	Fgfr1 oncogene partner	75296	0.96	0.88	0.64	1.50	0.89 *
Mocs3	molybdenum cofactor synthesis 3	69372	0.41	0.36	0.39	1.05	-0.41 ns
Parp6	poly (ADP-ribose) polymerase family, member 6	67287	0.41	0.24	0.26	1.57	0.72 ns
Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	67972	1.36	1.35	1.17	1.16	-0.31 ns
Mt2	metallothionein 2	17750	7.58	5.62	3.69	2.04	0.17 ns
Xpot	exportin, tRNA (nuclear export receptor for tRNAs)	73192	2.27	2.54	1.86	1.22	0.01 ns
Otud7b	OTU domain containing 7B	229603	0.58	0.87	0.69	0.84	-0.08 ns
Sfrs16	splicing factor, arginine/serine-rich 16 (suppressor-of-white-apricot homolog, Drosophila)	53609	0.30	0.31	0.45	0.67	-0.63 ns
2610204K14Rik	RIKEN cDNA 2610204K14 gene	67148	1.18	0.99	1.34	0.88	-0.46 ns
Cep57	centrosomal protein 57	74360	1.20	1.05	0.44	2.72	0.95 **
D030074E01Rik	RIKEN cDNA D030074E01 gene	75964	1.46	1.37	1.75	0.83	-0.05 ns
Ccny	cyclin Y	67974	0.81	0.81	0.89	0.90	0.23 ns
Atad2b	ATPase family, AAA domain containing 2B	320817	2.55	2.61	3.02	0.84	-0.44 ns
Ints12	integrator complex subunit 12	71793	0.75	0.72	0.48	1.55	0.61 ns
Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	76408	0.23	0.34	2.58	0.09	-0.67 ns
Unc13d	unc-13 homolog D (C. elegans)	70450	0.23	0.28	0.41	0.56	-0.31 ns
Phf23	PHD finger protein 23	78246	1.43	1.54	1.58	0.90	-0.63 ns
Phf3	PHD finger protein 3	213109	2.02	1.76	1.53	1.31	0.30 ns
Snw1	SNW domain containing 1	66354	2.54	2.59	2.69	0.94	-0.72 ns
Phip	pleckstrin homology domain interacting protein	83946	2.08	2.11	1.62	1.28	0.82 *
Mfhas1	malignant fibrous histiocytoma amplified sequence 1	52065	2.22	2.24	1.63	1.35	0.88 *
1810074P20Rik	RIKEN cDNA 1810074P20 gene	67490	0.23	0.23	0.40	0.56	-0.77 *

Smcr8	Smith-Magenis syndrome chromosome region, candidate 8 homolog (human)	237782	0.41	0.37	0.42	0.97	-0.07	ns
Pon2	paraoxonase 2	330260	0.95	1.06	0.87	1.08	-0.10	ns
Gcc1	golgi coiled coil 1	74375	0.30	0.38	0.38	0.78	-0.74	ns
Camsap1l1	calmodulin regulated spectrin-associated protein 1-like 1	67886	1.05	1.11	1.01	1.03	-0.03	ns
Rtf1	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	76246	0.88	0.86	0.73	1.21	0.71	ns
Bloc1s2	biogenesis of lysosome-related organelles complex-1, subunit 2	73689	1.76	1.95	1.51	1.16	0.68	ns
Nuak2	NUAK family, SNF1-like kinase, 2	74137	2.43	2.28	1.29	1.87	0.63	ns
Mrpl47	mitochondrial ribosomal protein L47	74600	1.69	1.46	1.14	1.48	0.65	ns
4930506M07Rik	RIKEN cDNA 4930506M07 gene	71653	2.13	2.40	2.27	0.93	0.00	ns
Narg1l	NMDA receptor regulated 1-like	66897	0.51	0.46	0.64	0.79	-0.43	ns
Tmem107	transmembrane protein 107	66910	3.40	4.17	4.89	0.69	-0.38	ns
Kif16b	kinesin family member 16B	16558	0.77	0.85	0.92	0.83	-0.63	ns
Dip2c	DIP2 disco-interacting protein 2 homolog C (Drosophila)	208440	0.32	0.45	0.40	0.79	-0.16	ns
EG433125		433125	19.00	18.76	17.27	1.09	0.52	ns
LOC545423		545423	19.00	18.76	17.27	1.09	0.52	ns
LOC636855		636855	19.00	18.76	17.27	1.09	0.52	ns
LOC675278		675278	19.00	18.76	17.27	1.09	0.52	ns
LOC676253		676253	19.00	18.76	17.27	1.09	0.52	ns
LOC676590		676590	19.00	18.76	17.27	1.09	0.52	ns
Rpl21		19933	19.00	18.76	17.27	1.09	0.52	ns
Mphosph10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	67973	0.43	0.55	0.58	0.74	-0.63	ns
Gcc2	GRIP and coiled-coil domain containing 2	70297	1.86	1.68	1.28	1.44	0.47	ns
Vezf1	vascular endothelial zinc finger 1	22344	3.01	2.60	2.50	1.20	0.82	*
2900026A02Rik	RIKEN cDNA 2900026A02 gene	243219	2.20	2.15	1.93	1.13	-0.12	ns
Vkorc1l1	vitamin K epoxide reductase complex, subunit 1-like 1	69568	0.44	0.45	0.64	0.68	-0.79	ns
Ddi2	DNA-damage inducible protein 2	68817	0.65	0.62	0.74	0.88	-0.52	ns
Tomm22	translocase of outer mitochondrial membrane 22 homolog (yeast)	223696	2.69	2.43	2.91	0.92	0.10	ns
Msl2l1	male-specific lethal 2-like 1 (Drosophila)	77853	0.76	0.61	0.55	1.36	0.81	ns
Tln2		70549	0.26	0.37	0.13	1.99	0.40	ns
Iah1	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	67732	0.97	0.94	1.03	0.93	-0.30	ns
1700040I03Rik	RIKEN cDNA 1700040I03 gene	73327	0.44	0.43	0.54	0.80	-0.41	ns
Rab27a	RAB27A, member RAS oncogene family	11891	0.34	0.35	0.24	1.42	0.85	*
Rexo1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	66932	0.98	0.71	0.52	1.87	0.88	*
Prei4	preimplantation protein 4	74182	0.60	0.46	0.48	1.23	-0.06	ns
Nhlrc2	NHL repeat containing 2	66866	1.18	1.23	0.98	1.20	0.65	ns
Gins3	GINS complex subunit 3 (Psf3 homolog)	78833	0.23	0.32	0.28	0.82	0.22	ns
Ccdc77	coiled-coil domain containing 77	67200	0.29	0.37	0.46	0.64	-0.14	ns
Wdr68	WD repeat domain 68	71833	3.00	2.38	2.66	1.12	0.56	ns
Slc35f2	solute carrier family 35, member F2	72022	0.38	0.30	0.16	2.30	0.74	ns
4933411K20Rik	RIKEN cDNA 4933411K20 gene	66756	1.21	1.31	1.18	1.02	0.41	ns
2610036L11Rik	RIKEN cDNA 2610036L11 gene	66311	0.61	0.58	0.70	0.86	-0.50	ns
Clmn	calmin	94040	1.41	1.24	2.30	0.61	-0.41	ns
Ccdc112	coiled-coil domain containing 112	240261	0.32	0.36	0.32	0.99	0.51	ns
Ncapg	on-SMC condensin I complex, subunit G	54392	0.81	1.20	1.40	0.57	-0.25	ns
Dnase1l1	deoxyribonuclease 1-like 1	69537	0.27	0.31	0.50	0.53	-0.84	*
Wdr34	WD repeat domain 34	71820	0.57	0.52	0.38	1.47	0.28	ns
Cox11	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	69802	0.62	0.47	0.68	0.91	-0.39	ns
Arsb	arylsulfatase B	11881	0.99	1.62	1.65	0.60	-0.86	*
Dhx33	DEAH (Asp-Glu-Ala-His) box polypeptide 33	216877	0.44	0.48	0.50	0.87	-0.92	**
Ankib1	ankyrin repeat and IBR domain containing 1	70797	1.07	1.03	1.09	0.98	0.28	ns
Tigd2	tigger transposable element derived 2	68140	0.40	0.37	0.40	1.00	-0.55	ns
Saal1	serum amyloid A-like 1	78935	0.43	0.50	0.61	0.70	-0.76	ns
Camk2n2	calcium/calmodulin-dependent protein kinase II inhibitor 2	73047	1.03	0.94	0.81	1.27	0.85	*
Mllt3	myeloid/lymphoid or mixed lineage-leukemia translocation to 3 homolog (Drosophila)	70122	0.42	0.39	0.27	1.58	0.22	ns
1200009F10Rik	RIKEN cDNA 1200009F10 gene	67454	0.38	0.42	0.29	1.29	0.44	ns
Sept11	septin 11	52398	3.94	3.47	2.98	1.32	0.97	**
Stx16	syntaxin 16	228960	2.21	2.07	2.57	0.86	-0.67	ns
Stard4	StAR-related lipid transfer (START) domain containing 4	170459	1.77	1.72	1.52	1.16	0.58	ns
2610524H06Rik	RIKEN cDNA 2610524H06 gene	330173	0.35	0.64	1.00	0.34	-0.65	ns
2810002N01Rik	RIKEN cDNA 2810002N01 gene	68020	1.00	0.94	1.09	0.91	0.01	ns
Dync2h1	dynein cytoplasmic 2 heavy chain 1	110350	0.40	0.30	0.16	2.48	0.98	***
Prdm2	PR domain containing 2, with ZNF domain	110593	0.50	0.46	0.48	1.04	-0.23	ns
Zmym4	zinc finger, MYM-type 4	67785	0.39	0.34	0.37	1.05	0.52	ns
1190007I07Rik		544717	0.96	0.88	0.64	1.47	0.85	*
2210411K11Rik		664968	0.64	0.61	0.66	0.96	-0.35	ns
Rassf6	Ras association (RalGDS/AF-6) domain family 6	73246	1.75	1.95	3.01	0.58	-0.79	ns
C030044B11Rik	RIKEN cDNA C030044B11 gene	68128	1.04	0.84	0.68	1.52	0.63	ns
Rnf130	ring finger protein 130	59044	0.76	0.96	1.72	0.44	-0.57	ns
Syce2	synaptonemal complex central element protein 2	71846	1.34	2.17	2.36	0.57	-0.24	ns
Nubpl	nucleotide binding protein-like	76826	0.70	0.84	1.00	0.70	-0.57	ns
Mobkl2b	MOB1, Mps One Binder kinase activator-like 2B (yeast)	214944	0.72	0.58	0.72	0.99	-0.44	ns
Psmd1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	70247	2.86	2.64	2.32	1.23	0.46	ns
Trip13	thyroid hormone receptor interactor 13	69716	1.04	1.49	1.81	0.57	-0.53	ns
Ddah1	dimethylarginine dimethylaminohydrolase 1	69219	1.13	1.15	0.91	1.23	-0.20	ns
Ube2q1	ubiquitin-conjugating enzyme E2Q (putative) 1	70093	1.74	1.83	1.69	1.02	-0.07	ns
Qk	quaking	19317	3.65	3.61	2.43	1.50	0.70	ns
Rnf149	ring finger protein 149	67702	2.90	2.89	2.46	1.17	-0.04	ns
Cenpl	centromere protein L	70454	0.28	0.32	0.37	0.74	-0.37	ns
Nsfl1c	NSFL1 (p97) cofactor (p47)	386649	3.54	4.02	3.46	1.02	0.42	ns
Snapc1	small nuclear RNA activating complex, polypeptide 1	75627	0.20	0.22	0.25	0.79	-0.59	ns
Sema3c	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	20348	10.40	10.97	11.22	0.92	-0.68	ns
Klhl24	kelch-like 24 (Drosophila)	75785	1.19	0.94	0.88	1.34	0.04	ns
4930579G24Rik	RIKEN cDNA 4930579G24 gene	75939	1.04	1.44	1.11	0.93	0.11	ns
Wipi2	WD repeat domain, phosphoinositide interacting 2	74781	1.14	0.91	0.90	1.26	0.79	ns

Crtc2	CREB regulated transcription coactivator 2	74343	0.34	0.40	0.27	1.24	0.47	ns
Anapc10	anaphase promoting complex subunit 10	68999	1.30	1.10	1.22	1.06	0.32	ns
Tomm40l	translocase of outer mitochondrial membrane 40 homolog-like (yeast)	641376	0.33	0.41	0.35	0.95	0.19	ns
Csnk1g3	casein kinase 1, gamma 3	70425	0.83	0.97	0.91	0.91	0.27	ns
Gstcd	glutathione S-transferase, C-terminal domain containing	67553	1.07	1.20	0.86	1.24	0.44	ns
Eny2	enhancer of yellow 2 homolog (Drosophila)	223527	1.13	0.93	0.85	1.32	0.36	ns
Cpm	carboxypeptidase M	70574	0.20	0.29	0.26	0.77	-0.65	ns
Cdc14b	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	218294	0.52	0.66	0.71	0.73	-0.76	ns
Rnf139	ring finger protein 139	75841	2.28	1.69	1.46	1.55	0.92	**
Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box	21416	1.11	1.25	0.80	1.38	0.20	ns
Ikzf5	IKAROS family zinc finger 5	67143	0.93	0.84	0.90	1.02	-0.44	ns
Bat2d	BAT2 domain containing 1	226562	1.94	2.32	1.18	1.63	0.39	ns
Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	56194	0.94	0.89	0.73	1.28	0.21	ns
Rasl11a	RAS-like, family 11, member A	68895	0.30	0.35	0.74	0.40	-0.52	ns
Sdccag1	serologically defined colon cancer antigen 1	66244	2.63	2.91	3.56	0.74	-0.72	ns
Mrpl55	mitochondrial ribosomal protein L55	67212	0.75	0.79	1.04	0.72	-0.62	ns
Gapvd1	GTPase activating protein and VPS9 domains 1	66691	3.02	2.89	1.95	1.54	0.74	ns
2410127L17Rik		67383	3.34	3.56	3.56	0.93	-0.61	ns
Ints2	integrator complex subunit 2	70422	1.08	1.02	1.18	0.91	-0.60	ns
1200003I07Rik	RIKEN cDNA 1200003I07 gene	66869	0.49	0.62	0.65	0.74	-0.44	ns
Dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2	56445	7.26	6.84	7.34	0.98	0.43	ns
Utp11l	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	67205	0.99	1.20	1.31	0.75	-0.52	ns
Zdhhc21	zinc finger, DHHC domain containing 21	68268	0.61	0.72	0.67	0.90	0.04	ns
Rif1		51869	1.83	1.74	1.52	1.20	0.32	ns
Snx6	sorting nexin 6	72183	2.19	2.31	2.42	0.90	-0.60	ns
Fbxo5	F-box protein 5	67141	1.60	1.67	1.56	1.02	0.47	ns
2900024C23Rik	RIKEN cDNA 2900024C23 gene	67266	0.65	0.61	0.39	1.68	0.19	ns
2310057M21Rik	RIKEN cDNA 2310057M21 gene	68277	0.35	0.39	0.46	0.75	-0.75	ns
Ubr2	ubiquitin protein ligase E3 component n-recognin 2	224826	1.08	1.17	0.67	1.59	0.84	*
Fpgt	fucose-1-phosphate guanylyltransferase	75540	0.52	0.61	0.72	0.73	-0.92	*
Alkbh8	alkB, alkylation repair homolog 8 (E. coli)	67667	0.37	0.39	0.17	2.15	0.64	ns
Rae1	RAE1 RNA export 1 homolog (S. pombe)	66679	2.19	2.10	2.19	1.00	-0.13	ns
Tsen54	tRNA splicing endonuclease 54 homolog (SEN54, S. cerevisiae)	76265	0.38	0.36	0.37	1.00	0.34	ns
Morc2a	microrchidia 2A	74522	1.33	1.35	1.33	0.99	-0.51	ns
Armc8	armadillo repeat containing 8	74125	0.57	0.57	0.57	1.00	0.48	ns
5730406M06Rik	RIKEN cDNA 5730406M06 gene	66625	0.67	0.65	0.84	0.79	-0.28	ns
Bcl2l13	BCL2-like 13 (apoptosis facilitator)	94044	0.57	0.59	0.57	0.98	0.41	ns
Zfp777	zinc finger protein 777	72306	0.18	0.21	0.21	0.87	-0.43	ns
Sdccag3	serologically defined colon cancer antigen 3	68112	1.22	1.01	1.07	1.13	0.40	ns
Mcm8	minichromosome maintenance deficient 8 (S. cerevisiae)	66634	0.35	0.44	0.57	0.61	-0.36	ns
Larp7	La ribonucleoprotein domain family, member 7	28036	1.91	2.30	1.48	1.28	0.56	ns
Pcgf5	polycomb group ring finger 5	76073	1.65	1.57	1.58	1.04	0.63	ns
Mlkl	mixed lineage kinase domain-like	74568	0.20	0.28	0.33	0.60	-0.09	ns
Rbm34	RNA binding motif protein 34	52202	0.48	0.59	0.34	1.38	0.50	ns
2810474O19Rik	RIKEN cDNA 2810474O19 gene	67246	1.37	1.56	1.18	1.15	0.55	ns
2700049A03Rik	RIKEN cDNA 2700049A03 gene	76967	0.54	0.55	0.70	0.77	-0.53	ns
Eml4	echinoderm microtubule associated protein like 4	78798	1.24	1.06	0.87	1.42	0.60	ns
Prpf18	PRP18 pre-mRNA processing factor 18 homolog (yeast)	67229	0.63	0.63	0.50	1.25	0.58	ns
Zfp91	zinc finger protein 91	109910	5.14	5.01	3.47	1.47	0.64	ns
Cyld	cylindromatosis (turban tumor syndrome)	74256	0.76	0.89	1.00	0.75	-0.45	ns
8430406I07Rik	RIKEN cDNA 8430406I07 gene	74528	0.37	0.29	0.39	0.95	0.21	ns
Ppil3	peptidylprolyl isomerase (cyclophilin)-like 3	70225	1.10	1.06	0.80	1.37	0.42	ns
Anubl1	AN1, ubiquitin-like, homolog (Xenopus laevis)	67492	0.50	0.49	0.50	1.00	0.40	ns
Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	229782	3.12	3.13	2.98	1.04	-0.33	ns
Prrc1	proline-rich coiled-coil 1	73137	0.61	0.70	0.67	0.91	0.30	ns
Gpsn2	glycoprotein, synaptic 2	106529	6.07	4.60	5.64	1.07	0.32	ns
1300003B13Rik	RIKEN cDNA 1300003B13 gene	74149	0.92	0.85	0.53	1.72	0.69	ns
Plaa	phospholipase A2, activating protein	18786	0.90	0.95	1.07	0.83	-0.28	ns
Ndufa11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	69875	3.19	3.04	1.84	1.73	0.77	ns
Pmpcb	peptidase (mitochondrial processing) beta	73078	2.33	2.94	2.32	1.00	0.44	ns
Foxp4	forkhead box P4	74123	0.42	0.45	0.29	1.42	0.07	ns
Zbtb4	zinc finger and BTB domain containing 4	75580	0.91	0.86	0.90	1.00	0.31	ns
6330409N04Rik	RIKEN cDNA 6330409N04 gene	66674	0.60	0.53	0.41	1.44	0.37	ns
Prpf4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	70052	0.40	0.37	0.41	0.97	0.22	ns
4632434I11Rik	RIKEN cDNA 4632434I11 gene	74041	0.32	0.38	0.34	0.95	-0.38	ns
Patz1	POZ (BTB) and AT hook containing zinc finger 1	56218	0.80	0.72	0.67	1.18	-0.31	ns
Bbs5	Bardet-Biedl syndrome 5 (human)	72569	0.33	0.38	0.33	0.99	-0.48	ns
Cnih4	cornichon homolog 4 (Drosophila)	98417	3.64	3.89	2.95	1.23	0.76	ns
Tmtc2	transmembrane and tetratricopeptide repeat containing 2	278279	0.84	0.56	0.68	1.23	-0.11	ns
2610002D18Rik	RIKEN cDNA 2610002D18 gene	69885	0.22	0.23	0.42	0.52	-0.36	ns
Yaf2	YY1 associated factor 2	67057	1.47	1.52	1.76	0.83	0.00	ns
2310043J07Rik	RIKEN cDNA 2310043J07 gene	69665	0.61	0.61	0.79	0.78	-0.51	ns
Supt7l	suppressor of Ty 7 (S. cerevisiae)-like	72195	0.50	0.37	0.38	1.33	0.80	ns
1700094D03Rik	RIKEN cDNA 1700094D03 gene	73545	0.27	0.23	0.21	1.29	-0.20	ns
Mcph1	microcephaly, primary autosomal recessive 1	244329	0.30	0.37	0.43	0.68	0.00	ns
2210011C24Rik	RIKEN cDNA 2210011C24 gene	70134	0.61	0.69	0.45	1.35	0.75	ns
5330426P16Rik	RIKEN cDNA 5330426P16 gene	68190	1.08	1.16	1.49	0.72	-0.24	ns
Ttc19	tetratricopeptide repeat domain 19	72795	0.46	0.49	0.43	1.07	0.02	ns
Akr1a4	aldo-keto reductase family 1, member A4 (aldehyde reductase)	58810	12.63	13.43	14.16	0.89	-0.55	ns
Pqlc1	PQ loop repeat containing 1	66943	0.41	0.56	0.27	1.50	0.24	ns
Reep6	receptor accessory protein 6	70335	2.65	2.19	2.06	1.28	0.06	ns
Commd8	COMM domain containing 8	27784	0.85	0.80	0.85	1.00	-0.41	ns
Tbc1d8b	TBC1 domain family, member 8B	245638	0.58	0.69	0.98	0.59	-0.09	ns
Yars2	tyrosyl-tRNA synthetase 2 (mitochondrial)	70120	0.33	0.29	0.46	0.70	-0.74	ns
Dnase2a	deoxyribonuclease II alpha	13423	0.40	0.35	0.44	0.91	-0.41	ns
Casc5		76464	0.18	0.26	0.22	0.80	0.11	ns

Stard3nl	STARD3 N-terminal like	76205	0.74	0.68	0.76	0.97	0.09	ns
Dock5	dedicator of cytokinesis 5	68813	0.29	0.32	0.45	0.64	-0.35	ns
LOC677317		677317	0.62	0.67	1.01	0.61	-0.72	ns
Uqcrq	ubiquinol-cytochrome c reductase, complex III subunit VII	22272	2.15	2.06	2.78	0.77	-0.39	ns
Glis3	GLIS family zinc finger 3	226075	2.25	2.63	1.77	1.26	0.24	ns
0610025P10Rik	RIKEN cDNA 0610025P10 gene	216860	0.51	0.51	0.52	0.98	-0.01	ns
Mtch2	mitochondrial carrier homolog 2 (C. elegans)	56428	2.61	2.01	2.12	1.23	0.16	ns
Tmem79	transmembrane protein 79	71913	0.51	0.53	0.35	1.46	0.74	ns
Mtx2	metaxin 2	53375	1.95	1.76	1.39	1.39	0.48	ns
Rnf167	ring finger protein 167	70510	2.03	1.59	2.15	0.94	-0.27	ns
Nmral1	NmrA-like family domain containing 1	67824	0.37	0.39	0.25	1.47	0.56	ns
Tsc22d2	TSC22 domain family 2	72033	1.54	1.42	0.98	1.56	0.78	ns
Erh	enhancer of rudimentary homolog (Drosophila)	13877	8.12	7.61	8.88	0.91	-0.46	ns
2210013O21Rik	RIKEN cDNA 2210013O21 gene	70123	0.65	0.67	0.52	1.24	0.65	ns
EG433923		433923	5.22	5.32	7.85	0.66	-0.64	ns
Zfp318	zinc finger protein 318	57908	0.56	0.58	0.39	1.43	0.74	ns
Cdkn3	cyclin-dependent kinase inhibitor 3	72391	0.50	0.64	0.74	0.67	-0.19	ns
Vgll3	vestigial like 3 (Drosophila)	73569	0.82	0.86	0.48	1.70	0.80	ns
4632415K11Rik	RIKEN cDNA 4632415K11 gene	74347	0.30	0.27	0.24	1.25	0.01	ns
9030605I04Rik		74548	2.29	2.28	0.58	3.95	-0.16	ns
Asnsd1	asparagine synthetase domain containing 1	70396	1.98	1.91	1.46	1.35	0.56	ns
Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	27226	2.02	1.70	0.98	2.05	0.92	**
5830427D03Rik	RIKEN cDNA 5830427D03 gene	76061	1.03	1.01	1.03	0.99	-0.43	ns
Ndufa13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	67184	5.83	5.40	3.80	1.53	0.88	*
Ankrd24	ankyrin repeat domain 24	70615	0.29	0.33	0.30	0.98	-0.44	ns
Rmi1	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	74386	0.82	0.85	1.10	0.74	-0.64	ns
Nuf2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	66977	1.23	1.21	1.21	1.01	0.37	ns
Bbx	bobby sox homolog (Drosophila)	70508	0.68	0.71	0.72	0.94	-0.27	ns
Slc9a8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	77031	0.44	0.40	0.33	1.35	0.12	ns
1810027O10Rik	RIKEN cDNA 1810027O10 gene	69186	1.89	1.91	2.34	0.81	-0.34	ns
9030025P20Rik	RIKEN cDNA 9030025P20 gene	#######	0.46	0.57	0.40	1.15	0.39	ns
Peci	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	23986	1.02	1.06	1.35	0.75	-0.78	ns
Agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	77559	0.56	0.57	0.75	0.75	-0.69	ns
Lsm6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	78651	2.03	1.55	1.73	1.17	0.41	ns
Ccdc50	coiled-coil domain containing 50	67501	0.28	0.32	0.42	0.66	-0.79	ns
Eif4enif1	eukaryotic translation initiation factor 4E nuclear import factor 1	74203	1.39	1.42	1.50	0.92	-0.22	ns
Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	18537	1.71	1.48	1.86	0.92	-0.25	ns
Spc24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	67629	1.24	1.22	1.11	1.11	0.64	ns
Hoxd8	homeo box D8	15437	3.64	3.41	1.92	1.89	0.46	ns
Tars2	threonyl-tRNA synthetase 2, mitochondrial (putative)	71807	0.84	0.80	0.76	1.10	0.79	ns
0610011F06Rik	RIKEN cDNA 0610011F06 gene	68347	1.33	1.11	1.02	1.30	0.47	ns
Cuedc2	CUE domain containing 2	67116	1.58	1.57	1.00	1.57	0.93	**
Cpne8	copine VIII	66871	0.99	1.13	0.35	2.83	0.41	ns
Chmp4c	chromatin modifying protein 4C	66371	0.73	0.71	0.48	1.50	0.71	ns
Rpl10a	ribosomal protein L10A	19896	20.43	17.99	14.61	1.39	0.74	ns
Sox11	SRY-box containing gene 11	20666	0.71	0.69	1.60	0.44	-0.82	*
Btbd9	BTB (POZ) domain containing 9	224671	0.44	0.43	0.35	1.23	0.54	ns
Cldnd1	claudin domain containing 1	224250	2.19	2.43	2.56	0.85	-0.71	ns
2310014H01Rik	RIKEN cDNA 2310014H01 gene	76448	0.76	0.77	0.68	1.11	0.61	ns
5830417I10Rik	RIKEN cDNA 5830417I10 gene	76022	0.74	0.81	0.57	1.30	0.33	ns
1810055E12Rik	RIKEN cDNA 1810055E12 gene	67894	0.58	0.69	0.51	1.13	0.41	ns
Efhd2	EF hand domain containing 2	27984	0.74	0.99	1.23	0.60	-0.98	***
Fars2	phenylalanine-tRNA synthetase 2 (mitochondrial)	69955	0.68	0.57	0.57	1.18	0.23	ns
1110007C09Rik	RIKEN cDNA 1110007C09 gene	68480	0.45	0.49	0.65	0.70	-0.18	ns
Parva	parvin, alpha	57342	1.52	1.28	1.37	1.10	-0.02	ns
Grinl1a	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	28015	3.96	3.11	2.70	1.46	0.94	**
Rai12	retinoic acid induced 12	54351	1.34	1.56	1.73	0.77	-0.57	ns
Dusp14	dual specificity phosphatase 14	56405	0.61	0.57	0.53	1.15	0.61	ns
Med8	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)	80509	0.91	1.12	1.41	0.64	-0.74	ns
Trim59		66949	0.70	0.62	0.53	1.32	0.50	ns
Hoxa10	homeo box A10	15395	0.63	0.58	0.64	0.97	-0.17	ns
EG665989		665989	1.03	0.90	1.13	0.91	-0.01	ns
LOC433064		433064	1.03	0.90	1.13	0.91	-0.01	ns
LOC629952		629952	1.03	0.90	1.13	0.91	-0.01	ns
LOC666411		666411	1.03	0.90	1.13	0.91	-0.01	ns
Ppih		66101	1.03	0.90	1.13	0.91	-0.01	ns
1810020G14Rik		66272	1.20	0.89	0.99	1.21	0.49	ns
Anxa9	annexin A9	71790	2.14	1.92	1.13	1.89	0.97	**
Tsen34	tRNA splicing endonuclease 34 homolog (SEN34, S. cerevisiae)	66078	2.62	2.42	3.02	0.86	-0.62	ns
Dtnbp1	dystrobrevin binding protein 1	94245	0.93	1.01	0.96	0.96	0.00	ns
Timm8b	translocase of inner mitochondrial membrane 8 homolog b (yeast)	30057	1.43	1.12	1.41	1.01	0.25	ns
EG243642		243642	23.74	20.88	15.63	1.51	0.92	**
EG666668		666668	23.74	20.88	15.63	1.51	0.92	**
LOC639606		639606	23.74	20.88	15.63	1.51	0.92	**
LOC676958		676958	23.74	20.88	15.63	1.51	0.92	**
Irak1bp1	interleukin-1 receptor-associated kinase 1 binding protein 1	65099	0.36	0.48	0.27	1.32	0.59	ns
Bxdc5	brix domain containing 5	70285	1.15	1.03	0.95	1.20	-0.02	ns
Stk11ip	serine/threonine kinase 11 interacting protein	71728	0.48	0.49	0.31	1.55	0.79	ns
Syde1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	71709	0.38	0.36	0.15	2.47	0.62	ns
D5Wsu178e	DNA segment, Chr 5, Wayne State University 178, expressed	28042	0.93	0.99	0.83	1.11	-0.20	ns
Sp3	trans-acting transcription factor 3	20687	2.42	2.33	1.81	1.33	0.51	ns
Fbxo34	F-box protein 34	78938	0.35	0.44	0.49	0.71	-0.58	ns
Eps8l1	EPS8-like 1	67425	0.38	0.44	0.32	1.20	-0.40	ns
Azi2	5-azacytidine induced gene 2	27215	1.16	1.05	0.89	1.29	0.71	ns
Tlk2	tousled-like kinase 2 (Arabidopsis)	24086	1.09	0.90	0.78	1.40	0.89	*
Rgl3	ral guanine nucleotide dissociation stimulator-like 3	71746	3.20	2.58	1.73	1.84	0.79	ns

Odf2l	outer dense fiber of sperm tails 2-like	52184	0.28	0.38	0.37	0.75	-0.52 ns
E2f1	E2F transcription factor 1	13555	0.85	0.85	1.03	0.82	0.03 ns
Mus81	MUS81 endonuclease homolog (yeast)	71711	0.33	0.29	0.35	0.95	-0.62 ns
Plcd3	phospholipase C, delta 3	72469	0.28	0.29	0.41	0.69	-0.27 ns
Stag1	stromal antigen 1	20842	0.95	0.89	0.93	1.02	0.39 ns
Crls1	cardiolipin synthase 1	66586	1.11	1.19	1.03	1.07	0.12 ns
Rabl2a	RAB, member of RAS oncogene family-like 2A	68708	0.88	0.79	0.61	1.43	0.50 ns
Pmm2	phosphomannomutase 2	54128	0.66	0.56	0.80	0.82	-0.67 ns
Pank2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	74450	0.90	0.74	0.95	0.94	0.24 ns
Usp16	ubiquitin specific peptidase 16	74112	0.76	0.70	0.87	0.87	-0.75 ns
Stambp	Stam binding protein	70527	0.62	0.61	0.76	0.81	-0.74 ns
Rnf41	ring finger protein 41	67588	0.43	0.35	0.38	1.11	0.12 ns
Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	67834	2.06	1.88	1.92	1.07	0.60 ns
Artn	artemin	11876	0.17	0.26	0.24	0.67	-0.49 ns
Veph1	ventricular zone expressed PH domain homolog 1 (zebrafish)	72789	0.51	0.68	0.19	2.68	0.09 ns
Ccdc132	coiled-coil domain containing 132	73288	0.85	0.82	0.86	0.99	-0.32 ns
Zdhhc4	zinc finger, DHHC domain containing 4	72881	0.95	0.98	0.82	1.15	-0.14 ns
Rchy1	ring finger and CHY zinc finger domain containing 1	68098	1.34	1.30	1.34	1.00	-0.48 ns
Trappc2	trafficking protein particle complex 2	66226	0.34	0.52	0.63	0.53	0.04 ns
Gcsh		68133	1.26	1.49	0.75	1.67	0.02 ns
LOC674321		674321	1.26	1.49	0.75	1.67	0.02 ns
Mnat1	menage a trois 1	17420	1.11	1.06	1.17	0.94	-0.26 ns
Nup43	nucleoporin 43	69912	0.77	0.74	0.66	1.16	0.54 ns
Ccnl2	cyclin L2	56036	1.57	1.54	1.73	0.90	-0.37 ns
Chmp5	chromatin modifying protein 5	76959	4.64	4.27	5.68	0.81	-0.47 ns
Dcun1d5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	76863	1.35	1.13	0.61	2.21	0.96 **
Cenpp	centromere protein P	66336	0.46	0.55	0.47	0.99	0.45 ns
Spr	sepiapterin reductase	20751	0.40	0.58	0.52	0.78	-0.37 ns
Ccdc21	coiled-coil domain containing 21	70012	0.32	0.51	0.16	1.94	0.55 ns
Eapp	E2F-associated phosphoprotein	66266	1.21	1.38	1.74	0.70	-0.68 ns
2310005N01Rik	RIKEN cDNA 2310005N01 gene	70088	0.47	0.51	0.53	0.88	-0.21 ns
2310057J16Rik	RIKEN cDNA 2310057J16 gene	69697	1.35	1.30	1.28	1.05	0.09 ns
Krtcap3	keratinocyte associated protein 3	69815	0.61	0.60	0.86	0.70	-0.69 ns
1700019E19Rik	RIKEN cDNA 1700019E19 gene	76411	1.87	2.00	2.20	0.85	-0.87 *
Snf8	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	27681	1.89	1.65	2.20	0.86	-0.30 ns
Rfc3	replication factor C (activator 1) 3	69263	1.45	1.55	1.68	0.86	-0.29 ns
Ubc	ubiquitin C	22190	25.01	21.32	19.77	1.26	0.85 *
Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	22630	11.73	12.19	13.71	0.85	-0.92 **
Fgd3	FYVE, RhoGEF and PH domain containing 3	30938	0.76	0.79	0.43	1.77	0.21 ns
Mcm10	minichromosome maintenance deficient 10 (S. cerevisiae)	70024	0.71	0.71	0.76	0.93	0.42 ns
Tgm2	transglutaminase 2, C polypeptide	21817	0.06	0.04	0.47	0.12	-0.75 ns
Pigs	phosphatidylinositol glycan anchor biosynthesis, class S	276846	0.87	0.70	0.76	1.14	-0.28 ns
Cdc23	CDC23 (cell division cycle 23, yeast, homolog)	52563	0.31	0.45	0.45	0.69	-0.35 ns
LOC672959		672959	24.93	22.75	19.14	1.30	0.72 ns
Rps12		20042	24.93	22.75	19.14	1.30	0.72 ns
Myst2	MYST histone acetyltransferase 2	217127	1.61	1.40	1.54	1.04	0.31 ns
Thtpa		105663	0.61	0.68	0.45	1.35	0.56 ns
Cpne1	copine I	266692	2.06	1.89	3.13	0.65	-0.42 ns
Fbxl5	F-box and leucine-rich repeat protein 5	242960	1.26	1.22	1.87	0.67	-0.79 ns
Klhl9	kelch-like 9 (Drosophila)	242521	2.26	2.25	2.54	0.89	-0.75 ns
Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	208715	7.39	8.89	10.22	0.72	-0.88 *
Cct4	chaperonin subunit 4 (delta)	12464	7.89	8.90	9.29	0.85	-0.71 ns
Slc25a44	solute carrier family 25, member 44	229517	0.50	0.51	0.38	1.28	0.54 ns
Sh2b3	SH2B adaptor protein 3	16923	0.48	0.37	0.48	1.00	-0.01 ns
Ttc7b	tetratricopeptide repeat domain 7B	104718	0.33	0.37	0.52	0.62	-0.67 ns
0610010K06Rik	RIKEN cDNA 0610010K06 gene	71678	2.05	1.90	1.66	1.23	0.93 **
Ipo13	importin 13	230673	0.28	0.41	0.37	0.76	-0.20 ns
AI467606	expressed sequence AI467606	101602	0.48	0.12	0.05	9.03	0.74 ns
Slc7a6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	330836	0.73	0.90	0.65	1.11	0.50 ns
Immt	inner membrane protein, mitochondrial	76614	1.53	1.73	2.34	0.65	-0.77 ns
EG664868		664868	30.46	27.77	22.74	1.33	0.96 **
LOC625646		625646	30.46	27.77	22.74	1.33	0.96 **
LOC638514		638514	30.46	27.77	22.74	1.33	0.96 **
Rpl38		67671	30.46	27.77	22.74	1.33	0.96 **
C78339	expressed sequence C78339	97863	3.98	3.52	4.23	0.94	-0.02 ns
Parl	presenilin associated, rhomboid-like	381038	1.94	1.82	1.95	0.99	-0.46 ns
2900010J23Rik	RIKEN cDNA 2900010J23 gene	72931	3.16	3.11	3.15	1.00	0.44 ns
Gpr56	G protein-coupled receptor 56	14766	2.63	2.48	2.05	1.28	0.77 ns
Gns	glucosamine (N-acetyl)-6-sulfatase	75612	2.39	2.41	2.30	1.03	-0.49 ns
Fgfr2	fibroblast growth factor receptor 2	14183	1.28	1.03	0.49	2.61	0.57 ns
Epb4.1l2	erythrocyte protein band 4.1-like 2	13822	2.16	1.81	1.46	1.47	0.82 *
Glt25d1	glycosyltransferase 25 domain containing 1	234407	1.00	1.49	1.12	0.90	0.34 ns
Aqr	aquarius	11834	1.47	1.08	1.07	1.37	0.50 ns
2010005J08Rik	RIKEN cDNA 2010005J08 gene	72046	0.63	0.82	0.69	0.91	-0.13 ns
Pygb	brain glycogen phosphorylase	110078	2.28	2.11	1.97	1.15	0.38 ns
Lrrc8d	leucine rich repeat containing 8D	231549	1.59	1.11	0.68	2.31	0.61 ns
Hmgn2	high mobility group nucleosomal binding domain 2	15331	10.96	10.67	11.69	0.93	-0.14 ns
Klf6	Kruppel-like factor 6	23849	3.81	3.98	3.32	1.14	0.49 ns
Ndufa12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	66414	5.28	4.66	4.79	1.10	-0.16 ns
Etnk1	ethanolamine kinase 1	75320	1.73	1.53	1.65	1.05	-0.30 ns
Myeov2	myeloma overexpressed 2	66915	4.05	3.90	3.29	1.23	0.27 ns
Lcmt2	leucine carboxyl methyltransferase 2	329504	0.42	0.37	0.38	1.10	-0.21 ns
Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	98415	13.01	12.36	9.80	1.32	0.67 ns
Scap	SREBF chaperone	235623	1.16	1.11	1.17	0.99	0.50 ns
Ankrd13c	ankyrin repeat domain 13c	433667	2.62	2.45	1.61	1.62	0.51 ns

Pskh1	protein serine kinase H1	244631	0.38	0.34	0.38	0.98	0.09	ns
AU042671	expressed sequence AU042671	269700	0.42	0.35	0.37	1.14	0.15	ns
Ireb2	iron responsive element binding protein 2	64602	1.41	1.07	1.17	1.20	0.75	ns
Gtf2a2	general transcription factor II A, 2	235459	1.53	1.35	1.57	0.97	0.33	ns
Acsl4	acyl-CoA synthetase long-chain family member 4	50790	0.70	1.05	2.65	0.27	-0.75	ns
Cct2	chaperonin subunit 2 (beta)	12461	11.55	9.32	9.60	1.20	0.06	ns
Commd3	COMM domain containing 3	12238	1.96	1.70	1.62	1.20	-0.04	ns
Ubap2l	ubiquitin associated protein 2-like	74383	2.19	2.16	2.11	1.03	-0.38	ns
Inpp5f	inositol polyphosphate-5-phosphatase F	101490	0.76	0.72	0.73	1.04	0.65	ns
Anln	anillin, actin binding protein (scraps homolog, Drosophila)	68743	5.66	4.95	4.92	1.15	0.69	ns
Nudcd1	NudC domain containing 1	67429	1.01	1.13	1.22	0.83	-0.60	ns
Mare	alpha globin regulatory element containing gene	17168	0.41	0.29	0.45	0.90	-0.12	ns
Chfr	checkpoint with forkhead and ring finger domains	231600	1.17	1.16	1.79	0.65	-0.82	*
Polr2b	polymerase (RNA) II (DNA directed) polypeptide B	231329	4.01	3.48	3.48	1.15	0.80	ns
AU022870	expressed sequence AU022870	231874	2.29	2.27	2.60	0.88	-0.41	ns
Eaf1	ELL associated factor 1	74427	0.77	0.67	0.95	0.80	-0.43	ns
Cbx7	chromobox homolog 7	52609	0.45	0.40	0.41	1.09	0.41	ns
Dab2ip	disabled homolog 2 (Drosophila) interacting protein	69601	0.93	0.89	0.57	1.62	0.75	ns
Slc45a4	solute carrier family 45, member 4	106068	1.88	1.42	1.43	1.30	0.43	ns
Atp5f1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	11950	10.74	11.75	9.00	1.19	0.34	ns
Prpf38a	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	230596	1.13	1.28	1.25	0.90	0.16	ns
Gmps	guanine monphosphate synthetase	229363	3.05	3.26	3.48	0.87	-0.89	*
Ran		19384	11.43	11.92	12.19	0.93	-0.62	ns
Cdc37l1	cell division cycle 37 homolog (S. cerevisiae)-like 1	67072	1.56	1.55	0.99	1.57	0.79	ns
Tmem30b	transmembrane protein 30B	238257	1.19	2.59	1.90	0.62	-0.64	ns
1190002N15Rik	RIKEN cDNA 1190002N15 gene	68861	0.22	0.32	0.22	1.01	0.34	ns
Tnpo1	transportin 1	238799	1.72	2.08	2.64	0.65	-0.93	**
Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	19058	1.68	1.59	1.81	0.92	-0.42	ns
Commd2	COMM domain containing 2	52245	1.36	1.40	1.14	1.19	0.68	ns
Baz1a	bromodomain adjacent to zinc finger domain 1A	217578	2.04	2.18	3.47	0.59	-0.75	ns
Ndufs6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	407785	1.83	2.78	3.19	0.57	-0.79	ns
Inpp5a	inositol polyphosphate-5-phosphatase A	212111	0.35	0.29	0.62	0.56	-0.38	ns
Dcp1a	decapping enzyme	75901	0.58	0.63	0.57	1.01	0.26	ns
AA986860	expressed sequence AA986860	212439	0.34	0.28	0.21	1.61	-0.17	ns
Ap2s1	adaptor-related protein complex 2, sigma 1 subunit	232910	1.94	1.99	2.35	0.82	-0.20	ns
Pank3	pantothenate kinase 3	211347	2.44	2.42	3.61	0.67	-0.74	ns
Snx27	sorting nexin family member 27	76742	0.70	0.72	0.56	1.23	0.75	ns
B4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	56336	0.45	0.40	0.59	0.76	-0.68	ns
C330006A16Rik	RIKEN cDNA C330006A16 gene	109299	0.52	0.57	0.44	1.18	0.26	ns
Wdr41	WD repeat domain 41	218460	0.17	0.31	0.37	0.45	-0.86	*
Gemin4	gem (nuclear organelle) associated protein 4	276919	0.30	0.39	0.31	0.97	-0.30	ns
Zfp367	zinc finger protein 367	238673	0.96	1.71	2.28	0.42	-0.66	ns
5830434P21Rik	RIKEN cDNA 5830434P21 gene	227723	1.96	1.79	1.42	1.37	0.80	ns
Sec23ip	Sec23 interacting protein	207352	0.72	0.76	0.89	0.80	-0.63	ns
Irf2bp2		270110	1.18	1.06	0.50	2.36	0.12	ns
Wdr18	WD repeat domain 18	216156	0.56	0.53	0.41	1.36	0.57	ns
Smad5	MAD homolog 5 (Drosophila)	17129	0.81	0.84	0.97	0.83	-0.28	ns
Pomt2	protein-O-mannosyltransferase 2	217734	0.22	0.30	0.37	0.59	-0.89	*
Slc44a1	solute carrier family 44, member 1	100434	4.19	4.67	4.20	0.99	0.28	ns
Mrps27	mitochondrial ribosomal protein S27	218506	0.32	0.50	0.55	0.58	-0.53	ns
Rhobtb3	Rho-related BTB domain containing 3	73296	1.18	1.42	1.57	0.75	-0.58	ns
Spag9	sperm associated antigen 9	70834	3.66	2.82	3.73	0.98	0.06	ns
Aof1	amine oxidase, flavin containing 1	218214	0.56	0.51	0.57	0.99	-0.32	ns
Wtip	WT1-interacting protein	101543	0.37	0.46	0.81	0.45	-0.74	ns
Mgea5	meningioma expressed antigen 5 (hyaluronidase)	76055	4.50	4.25	4.32	1.04	0.36	ns
Rnf141	ring finger protein 141	67150	0.45	0.54	0.66	0.69	-0.25	ns
Gnl3	guanine nucleotide binding protein-like 3 (nucleolar)	30877	1.81	2.03	1.61	1.12	0.05	ns
Pcbp4	poly(rC) binding protein 4	59092	1.05	0.95	0.80	1.30	0.89	*
AU014645	expressed sequence AU014645	433702	0.86	0.83	1.03	0.83	-0.61	ns
Ube2q2	ubiquitin-conjugating enzyme E2Q (putative) 2	109161	1.40	1.32	1.20	1.16	0.79	ns
Vps41	vacuolar protein sorting 41 (yeast)	218035	1.14	1.32	1.17	0.97	0.14	ns
Pnrc1	proline-rich nuclear receptor coactivator 1	108767	2.22	2.18	2.87	0.77	-0.74	ns
Emp2	epithelial membrane protein 2	13731	6.60	6.43	11.04	0.59	-0.61	ns
Wnk1	WNK lysine deficient protein kinase 1	232341	6.70	6.21	5.32	1.25	0.92	**
Sfrs8	splicing factor, arginine/serine-rich 8	231769	0.78	0.81	0.86	0.90	-0.33	ns
Fubp3	far upstream element (FUSE) binding protein 3	320267	1.15	1.62	1.48	0.77	-0.67	ns
Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	207212	0.65	0.63	0.58	1.11	-0.10	ns
Rbm35b	RNA binding motif protein 35b	77411	1.71	1.55	1.72	0.99	-0.43	ns
Chmp6	chromatin modifying protein 6	208092	1.40	1.44	1.49	0.93	0.15	ns
6430706D22Rik		381280	4.15	3.98	3.80	1.09	0.62	ns
Cabin1	calcineurin binding protein 1	104248	0.43	0.48	0.37	1.16	0.63	ns
Rps9	ribosomal protein S9	76846	15.77	14.08	12.51	1.25	0.56	ns
2210016L21Rik	RIKEN cDNA 2210016L21 gene	72357	0.41	0.43	0.45	0.89	0.03	ns
Nat10	N-acetyltransferase 10	98956	0.44	0.35	0.28	1.55	0.56	ns
Hn1l	hematological and neurological expressed 1-like	52009	4.23	3.19	2.22	1.90	0.88	*
4933433P14Rik	RIKEN cDNA 4933433P14 gene	66787	0.91	0.79	0.99	0.91	0.02	ns
Bahd1	bromo adjacent homology domain containing 1	228536	0.69	0.58	0.77	0.88	-0.23	ns
Ptplad1	protein tyrosine phosphatase-like A domain containing 1	57874	2.19	1.98	1.51	1.44	0.94	**
Srp68	signal recognition particle 68	217337	2.36	2.08	3.13	0.75	-0.28	ns
Cant1	calcium activated nucleotidase 1	76025	0.74	0.75	0.74	0.99	0.14	ns
Edc3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	353190	0.51	0.50	0.49	1.04	0.61	ns
Sesn1	sestrin 1	140742	0.54	0.50	0.37	1.46	0.30	ns
AW555464	expressed sequence AW555464	217882	3.23	3.27	3.92	0.82	-0.62	ns
Gcn1l1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	231659	1.29	1.23	1.26	1.01	0.18	ns
D19Wsu162e	DNA segment, Chr 19, Wayne State University 162, expressed	226178	1.20	1.31	0.80	1.49	0.72	ns

Cbx1	chromobox homolog 1 (Drosophila HP1 beta)	12412	2.23	2.42	3.18	0.70	-0.81	ns
Rps21	ribosomal protein S21	66481	16.70	16.03	14.01	1.19	0.14	ns
Akap13	A kinase (PRKA) anchor protein 13	75547	0.62	0.57	0.93	0.66	-0.75	ns
Acvr1b	activin A receptor, type 1B	11479	1.57	1.34	1.79	0.87	-0.16	ns
2310035C23Rik	RIKEN cDNA 2310035C23 gene	227446	1.50	1.35	1.00	1.50	0.47	ns
Elmod2	ELMO domain containing 2	244548	0.87	1.11	1.11	0.78	-0.39	ns
Cry1	cryptochrome 1 (photolyase-like)	12952	0.35	0.60	0.53	0.66	-0.56	ns
Hcfc1	host cell factor C1	15161	2.24	2.11	2.36	0.94	-0.17	ns
LOC677213	similar to U2AF homology motif (UHM) kinase 1	677213	1.31	1.17	1.18	1.10	-0.19	ns
Papd5	PAP associated domain containing 5	214627	1.07	1.07	1.49	0.71	-0.22	ns
Tmem87b	transmembrane protein 87B	72477	0.50	0.59	0.58	0.86	-0.55	ns
Trio	triple functional domain (PTPRF interacting)	223435	2.13	2.07	2.10	1.01	-0.53	ns
Wdr3	WD repeat domain 3	269470	1.52	1.98	1.42	1.07	0.24	ns
Lnpep	leucyl/cystinyl aminopeptidase	240028	3.67	2.88	1.98	1.84	0.79	ns
Zdhhc18	zinc finger, DHHC domain containing 18	503610	0.46	0.47	0.52	0.88	-0.78	ns
Gna13	guanine nucleotide binding protein, alpha 13	14674	2.47	2.50	2.33	1.06	0.75	ns
Slc31a1	solute carrier family 31, member 1	20529	0.51	0.45	0.73	0.69	-0.80	ns
Slc39a10	solute carrier family 39 (zinc transporter), member 10	227059	1.28	1.38	1.26	1.02	-0.38	ns
D030016E14Rik	RIKEN cDNA D030016E14 gene	320714	1.04	1.06	1.19	0.87	-0.39	ns
Mbnl2	muscleblind-like 2	105559	2.62	2.46	2.69	0.97	-0.55	ns
Mier1	mesoderm induction early response 1 homolog (Xenopus laevis	71148	0.84	0.81	0.96	0.87	-0.57	ns
S100pbp	S100P binding protein	74648	0.62	0.69	0.71	0.87	-0.52	ns
Dpy19l1	dpy-19-like 1 (C. elegans)	244745	0.32	0.42	0.25	1.28	0.63	ns
Rhbdd3	rhomboid domain containing 3	279766	0.35	0.37	0.32	1.10	0.07	ns
Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	83679	0.62	0.75	0.71	0.87	-0.63	ns
1110018G07Rik	RIKEN cDNA 1110018G07 gene	68497	0.96	0.87	0.96	0.99	0.24	ns
Palld	palladin, cytoskeletal associated protein	72333	0.59	0.41	0.34	1.75	-0.02	ns
Als2cl	ALS2 C-terminal like	235633	1.01	0.94	1.08	0.93	0.13	ns
Dpysl2	dihydropyrimidinase-like 2	12934	7.68	6.85	6.79	1.12	0.75	ns
Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	382985	0.58	0.53	0.68	0.85	-0.61	ns
C77080	expressed sequence C77080	97130	1.19	1.28	1.05	1.13	0.73	ns
Lhfp	lipoma HMGIC fusion partner	108927	1.72	1.52	1.59	1.08	-0.28	ns
L3mbtl2	l(3)mbt-like 2 (Drosophila)	214669	0.38	0.50	0.57	0.67	-0.54	ns
Tnks	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	21951	1.62	1.92	2.87	0.56	-0.67	ns
Casc4	cancer susceptibility candidate 4	319996	1.48	1.27	0.93	1.59	0.49	ns
Cldn12	claudin 12	64945	2.68	3.13	3.40	0.78	-0.60	ns
9030612M13Rik	RIKEN cDNA 9030612M13 gene	208292	2.98	2.57	1.85	1.60	0.76	ns
Serf2	small EDRK-rich factor 2	378702	6.84	5.22	4.35	1.56	0.89	*
Setx	senataxin	269254	2.95	2.90	2.61	1.12	0.66	ns
Tgfbr3	transforming growth factor, beta receptor III	21814	1.65	1.32	0.52	3.14	-0.13	ns
E130309D02Rik	RIKEN cDNA E130309D02 gene	231868	0.79	0.71	0.60	1.31	0.61	ns
Rdh13	retinol dehydrogenase 13 (all-trans and 9-cis)	108841	0.34	0.30	0.24	1.42	0.25	ns
Jak1	Janus kinase 1	16451	2.00	1.77	1.94	1.03	-0.11	ns
6720463M24Rik	RIKEN cDNA 6720463M24 gene	77744	0.47	0.45	0.58	0.81	-0.42	ns
Mllt6		246198	1.69	1.48	1.65	1.02	0.22	ns
Tmem48	transmembrane protein 48	72787	0.45	0.44	0.55	0.83	-0.29	ns
Mcart1	mitochondrial carrier triple repeat 1	230125	1.30	1.25	1.44	0.90	-0.64	ns
1110012D08Rik	RIKEN cDNA 1110012D08 gene	73827	0.37	0.31	0.26	1.42	0.67	ns
Anapc5	anaphase-promoting complex subunit 5	59008	8.82	7.54	8.23	1.07	0.52	ns
4833418A01Rik	RIKEN cDNA 4833418A01 gene	75763	0.54	0.44	0.35	1.54	0.46	ns
Unc84b	unc-84 homolog B (C. elegans)	223697	2.19	2.13	2.10	1.04	0.61	ns
Fndc3b	fibronectin type III domain containing 3B	72007	4.64	3.81	2.58	1.79	0.88	*
March6	membrane-associated ring finger (C3HC4) 6	223455	3.19	2.97	3.19	0.99	0.12	ns
8430408G22Rik	RIKEN cDNA 8430408G22 gene	213393	0.36	0.29	1.05	0.34	-0.62	ns
Dars2	aspartyl-tRNA synthetase 2 (mitochondrial)	226539	0.36	0.38	0.46	0.79	-0.71	ns
C330006K01Rik	RIKEN cDNA C330006K01 gene	231855	0.38	0.35	0.33	1.15	0.29	ns
Lrrfip1	leucine rich repeat (in FLII) interacting protein 1	16978	3.55	4.06	2.46	1.44	0.18	ns
Hs1bp3	HCLS1 binding protein 3	58240	0.41	0.45	0.54	0.75	-0.81	ns
LOC627908		627908	5.13	5.53	5.65	0.90	-0.62	ns
Ppp4r2		232314	5.13	5.53	5.65	0.90	-0.62	ns
C330002I19Rik	RIKEN cDNA C330002I19 gene	77480	4.45	4.18	3.57	1.24	0.19	ns
Hisppd1	histidine acid phosphatase domain containing 1	227399	0.98	0.96	0.61	1.60	0.21	ns
Fat1		14107	5.68	4.73	3.20	1.76	0.80	ns
6030458C11Rik	RIKEN cDNA 6030458C11 gene	77877	0.98	0.93	1.09	0.89	-0.64	ns
Cc2d1b	coiled-coil and C2 domain containing 1B	319965	0.44	0.56	0.66	0.67	-0.83	*
Espl1	extra spindle poles-like 1 (S. cerevisiae)	105988	1.04	0.99	1.07	0.97	0.46	ns
1810030O07Rik	RIKEN cDNA 1810030O07 gene	69155	0.27	0.39	0.48	0.57	-0.18	ns
Btbd3	BTB (POZ) domain containing 3	228662	0.76	0.73	0.80	0.95	-0.01	ns
Zxdc	ZXD family zinc finger C	80292	0.68	0.94	0.85	0.79	-0.74	ns
Atad4	ATPase family, AAA domain containing 4	217138	0.85	0.71	0.68	1.24	-0.16	ns
R3hdm1	R3H domain 1 (binds single-stranded nucleic acids)	226412	2.31	1.95	1.94	1.19	0.45	ns
2410042D21Rik	RIKEN cDNA 2410042D21 gene	72425	0.70	0.46	0.52	1.33	0.61	ns
Pcnt	pericentrin (kendrin)	18541	0.69	0.72	0.72	0.96	-0.58	ns
4732418C07Rik	RIKEN cDNA 4732418C07 gene	230648	0.86	0.81	0.98	0.87	0.04	ns
Mrps26	mitochondrial ribosomal protein S26	99045	1.06	1.17	1.29	0.81	-0.55	ns
Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11	230935	0.31	0.32	0.35	0.87	-0.03	ns
Cnot10	CCR4-NOT transcription complex, subunit 10	78893	0.64	0.65	0.61	1.05	0.58	ns
Tpm4	tropomyosin 4	326618	6.53	6.98	8.42	0.77	-0.08	ns
Eif2b5	eukaryotic translation initiation factor 2B, subunit 5 epsilon	224045	1.65	1.59	1.94	0.84	-0.29	ns
Bat3	HLA-B-associated transcript 3	224727	1.81	1.49	1.31	1.37	0.63	ns
Lgr4	leucine-rich repeat-containing G protein-coupled receptor 4	107515	4.92	3.05	2.51	1.95	0.31	ns
Spag5	sperm associated antigen 5	54141	0.83	0.90	0.68	1.20	0.76	ns
Tmem127	transmembrane protein 127	69470	0.87	0.86	0.69	1.26	0.26	ns
AI597468	expressed sequence AI597468	103266	1.79	1.70	1.65	1.08	0.65	ns
0610007L01Rik	RIKEN cDNA 0610007L01 gene	71667	1.66	1.46	1.70	0.97	-0.49	ns
AU021838	expressed sequence AU021838	328099	2.35	2.49	2.63	0.89	-0.86	*
Cttn	cortactin	13043	6.70	6.87	6.34	1.05	0.20	ns

Zcchc6	zinc finger, CCHC domain containing 6	214290	1.44	1.40	1.48	0.97	0.25	ns
Smg6	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	103677	0.45	0.28	0.26	1.73	0.85	*
Atg4d	autophagy-related 4D (yeast)	235040	0.64	0.56	0.62	1.03	0.48	ns
Asb4	ankyrin repeat and SOCS box-containing protein 4	65255	0.29	0.27	0.05	5.89	0.51	ns
Dph3	DPH3 homolog (KTI11, S. cerevisiae)	105638	0.59	0.59	0.70	0.83	-0.46	ns
Rab35	RAB35, member RAS oncogene family	77407	1.03	0.99	0.98	1.05	0.31	ns
Dync1li2	dynein, cytoplasmic 1 light intermediate chain 2	234663	1.41	1.40	1.40	1.00	0.43	ns
Uspl1	ubiquitin specific peptidase like 1	231915	0.96	1.01	1.04	0.92	-0.08	ns
C030046I01Rik	RIKEN cDNA C030046I01 gene	109284	1.92	1.77	2.06	0.93	-0.41	ns
Sec24a	SEC24 related gene family, member A (S. cerevisiae)	77371	0.71	0.81	1.04	0.68	-0.75	ns
0610010E21Rik	RIKEN cDNA 0610010E21 gene	68332	0.36	0.48	0.74	0.48	-0.63	ns
Trp53bp2	transformation related protein 53 binding protein 2	209456	0.78	0.78	0.54	1.44	0.13	ns
Spag7	sperm associated antigen 7	216873	1.23	1.25	1.71	0.72	-0.89	*
Myo6	myosin VI	17920	1.83	1.73	1.34	1.36	0.54	ns
Arl5a	ADP-ribosylation factor-like 5A	75423	3.83	2.51	2.05	1.86	0.80	ns
Zfp277	zinc finger protein 277	246196	1.43	1.37	1.71	0.83	-0.56	ns
C030048B08Rik	RIKEN cDNA C030048B08 gene	269623	0.50	0.50	0.56	0.88	-0.81	*
Cntrob	centrobin, centrosomal BRCA2 interacting protein	216846	0.35	0.39	0.44	0.80	-0.11	ns
Isg20l2	interferon stimulated exonuclease gene 20-like 2	229504	1.90	2.06	1.69	1.12	0.04	ns
6720458F09Rik	RIKEN cDNA 6720458F09 gene	328162	0.25	0.38	0.26	0.97	0.19	ns
Bola3	bolA-like 3 (E. coli)	78653	0.85	0.96	0.92	0.92	-0.27	ns
Cdk10	cyclin-dependent kinase (CDC2-like) 10	234854	0.53	0.60	0.46	1.16	0.30	ns
Rbms2	RNA binding motif, single stranded interacting protein 2	56516	1.33	1.17	0.86	1.54	0.60	ns
Cnksr3	Cnksr family member 3	215748	1.55	1.60	1.08	1.43	0.48	ns
Mdh2	malate dehydrogenase 2, NAD (mitochondrial)	17448	9.50	8.13	8.70	1.09	-0.01	ns
BC024659	cDNA sequence BC024659	108934	0.45	0.48	0.46	0.96	0.43	ns
Shroom2		110380	0.97	0.90	1.16	0.83	0.14	ns
4931406P16Rik	RIKEN cDNA 4931406P16 gene	233103	0.67	0.70	0.81	0.83	-0.24	ns
4933427D14Rik	RIKEN cDNA 4933427D14 gene	74477	0.51	0.50	0.50	1.01	0.13	ns
Slk	STE20-like kinase (yeast)	20874	2.51	2.81	2.09	1.19	0.64	ns
Ttc9c	tetratricopeptide repeat domain 9C	70387	1.47	1.66	1.25	1.18	0.59	ns
Dhps	deoxyhypusine synthase	330817	0.67	0.71	0.65	1.02	0.24	ns
Rbms1	RNA binding motif, single stranded interacting protein 1	56878	5.90	5.32	4.26	1.38	0.91	*
BC051227	cDNA sequence BC051227	234384	0.87	0.84	1.01	0.86	-0.35	ns
Gyltl1b	glycosyltransferase-like 1B	228366	0.94	0.63	0.55	1.69	0.18	ns
Grlf1	glucocorticoid receptor DNA binding factor 1	232906	0.79	0.73	0.71	1.10	0.35	ns
Als2cr13	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (human)	72750	0.58	0.61	0.61	0.95	-0.28	ns
Ints5	integrator complex subunit 5	109077	7.00	8.01	6.18	1.13	0.54	ns
Znrf2	zinc and ring finger 2	387524	0.38	0.40	0.47	0.79	-0.13	ns
BC043098	cDNA sequence BC043098	214469	1.79	1.59	1.34	1.33	0.66	ns
Pdap1	PDGFA associated protein 1	231887	2.38	2.59	2.66	0.89	-0.19	ns
C230096C10Rik	RIKEN cDNA C230096C10 gene	230866	0.88	0.90	0.86	1.01	-0.20	ns
Zbtb33	zinc finger and BTB domain containing 33	56805	0.92	0.96	1.41	0.65	-0.70	ns
Atp8b2	Atpase, class I, type 8B, member 2	54667	0.86	0.88	0.51	1.67	0.86	*
Gtpbp10	GTP-binding protein 10 (putative)	207704	0.50	0.52	0.68	0.73	-0.82	*
Zfp692	zinc finger protein 692	103836	0.48	0.39	0.50	0.94	-0.54	ns
Mtss1	metastasis suppressor 1	211401	0.71	1.37	2.00	0.35	-0.96	**
Dnajc13	DnaJ (Hsp40) homolog, subfamily C, member 13	235567	0.90	0.98	0.89	1.00	0.47	ns
Mtmr3	myotubularin related protein 3	74302	1.70	1.46	1.48	1.14	0.22	ns
Repin1	replication initiator 1	58887	0.70	0.85	0.85	0.82	-0.15	ns
Cdkn1b	cyclin-dependent kinase inhibitor 1B	12576	3.35	3.58	3.72	0.89	-0.62	ns
Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	230075	1.82	2.14	2.79	0.65	-0.67	ns
Mtmr12	myotubularin related protein 12	268783	0.79	0.67	0.86	0.92	0.00	ns
Herc1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	235439	0.73	0.59	0.64	1.14	0.50	ns
Rp2h	retinitis pigmentosa 2 homolog (human)	19889	0.58	0.54	1.08	0.53	-0.71	ns
Rabgap1l	RAB GTPase activating protein 1-like	29809	0.44	0.46	0.35	1.24	0.54	ns
Zfp664	zinc finger protein 664	269704	1.67	1.65	1.71	0.97	-0.58	ns
Cwf19l1	CWF19-like 1, cell cycle control (S. pombe)	72502	0.44	0.50	0.29	1.52	0.64	ns
Gtf3c1	general transcription factor III C 1	233863	0.61	0.65	0.75	0.82	-0.80	ns
Jag1	jagged 1	16449	1.00	1.38	1.04	0.96	-0.25	ns
Pelo	pelota homolog (Drosophila)	105083	0.21	0.26	0.41	0.51	-0.82	*
BC030336	cDNA sequence BC030336	233812	0.87	0.80	0.82	1.04	0.35	ns
Wdr37	WD repeat domain 37	207615	0.44	0.37	0.55	0.79	-0.10	ns
Ubfd1	ubiquitin family domain containing 1	28018	0.66	0.58	0.65	1.02	-0.16	ns
Aebp2	AE binding protein 2	11569	1.98	1.97	2.36	0.84	-0.39	ns
Ap1g1	adaptor protein complex AP-1, gamma 1 subunit	11765	0.94	0.89	0.83	1.14	0.39	ns
Pctk2	PCTAIRE-motif protein kinase 2	237459	1.20	0.89	0.79	1.51	0.44	ns
5730601F06Rik	RIKEN cDNA 5730601F06 gene	77519	2.04	1.52	1.32	1.54	0.93	**
Zfp523	zinc finger protein 523	224656	0.61	0.53	0.47	1.29	0.82	*
Gpr107	G protein-coupled receptor 107	277463	0.36	0.38	0.39	0.92	-0.15	ns
Zkscan17	zinc finger with KRAB and SCAN domains 17	268417	1.30	1.26	1.17	1.10	0.48	ns
Synpo	synaptopodin	104027	0.47	0.43	0.44	1.06	0.52	ns
Atg9b	ATG9 autophagy related 9 homolog B (S. cerevisiae)	213948	0.73	0.62	1.27	0.57	-0.79	ns
Slc4a4	solute carrier family 4 (anion exchanger), member 4	54403	0.39	0.57	0.84	0.46	-0.68	ns
D10627	cDNA sequence D10627	234358	0.33	0.54	0.40	0.82	-0.08	ns
Slc35e1	solute carrier family 35, member E1	270066	0.65	0.73	0.64	1.00	0.47	ns
Epm2aip1	EPM2A (laforin) interacting protein 1	77781	0.84	0.78	0.77	1.09	0.73	ns
Spata2	spermatogenesis associated 2	263876	0.77	0.65	0.70	1.10	-0.22	ns
Fbxo11	F-box protein 11	225055	1.03	0.99	0.88	1.16	0.46	ns
Sh3bgrl2	SH3 domain binding glutamic acid-rich protein like 2	212531	1.18	1.04	0.87	1.36	0.67	ns
Lphn2	latrophilin 2	99633	2.92	3.09	3.83	0.76	-0.79	ns
Rexo4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	227656	0.66	0.98	0.69	0.96	-0.38	ns
Cdh13	cadherin 13	12554	0.38	0.47	0.30	1.25	0.61	ns
Cbx2	chromobox homolog 2 (Drosophila Pc class)	12416	0.49	0.41	0.58	0.83	-0.10	ns
Tceb3	transcription elongation factor B (SIII), polypeptide 3	27224	0.35	0.32	0.41	0.85	-0.15	ns

Metap2	methionine aminopeptidase 2	56307	6.31	5.99	5.29	1.19	0.77	ns
Fut11	fucosyltransferase 11	73068	0.43	0.44	0.56	0.77	-0.80	ns
Utp15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (yeast)	105372	0.46	0.67	0.83	0.55	-0.68	ns
EG544973		544973	15.31	15.93	13.90	1.10	0.10	ns
H3f3a		15078	15.31	15.93	13.90	1.10	0.10	ns
LOC625328		625328	15.31	15.93	13.90	1.10	0.10	ns
Zfp574	zinc finger protein 574	232976	0.80	0.65	0.67	1.19	0.41	ns
Lhfpl2	lipoma HMGIC fusion partner-like 2	218454	0.29	0.48	0.30	0.94	-0.47	ns
Rufy1	RUN and FYVE domain containing 1	216724	0.35	0.39	0.51	0.68	-0.81	ns
E430025E21Rik	RIKEN cDNA E430025E21 gene	223593	3.30	3.11	3.43	0.96	-0.05	ns
Wdr42a	WD repeat domain 42A	98193	1.19	1.07	0.70	1.69	0.39	ns
B3galnt2	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2	97884	0.51	0.46	0.54	0.93	-0.08	ns
Prune	prune homolog (Drosophila)	229589	0.94	0.86	0.63	1.49	0.87	*
Ppm1d	protein phosphatase 1D magnesium-dependent, delta isoform	53892	0.87	0.84	0.75	1.16	0.86	*
2410187C16Rik	RIKEN cDNA 2410187C16 gene	76773	0.39	0.34	0.62	0.63	-0.31	ns
Shb	src homology 2 domain-containing transforming protein B	230126	0.77	0.77	0.70	1.10	-0.21	ns
2310061I04Rik	RIKEN cDNA 2310061I04 gene	69662	0.86	0.67	0.66	1.30	0.08	ns
Rab11fip4	RAB11 family interacting protein 4 (class II)	268451	1.21	1.03	0.66	1.82	0.94	**
Gmds	GDP-mannose 4, 6-dehydratase	218138	1.09	1.10	1.05	1.03	-0.21	ns
Lin52	lin-52 homolog (C. elegans)	217708	0.53	0.51	0.55	0.97	0.25	ns
2700078E11Rik	RIKEN cDNA 2700078E11 gene	78832	1.73	1.92	1.27	1.35	0.42	ns
Peo1	progressive external ophthalmoplegia 1 (human)	226153	0.65	0.80	0.35	1.83	0.55	ns
D19Bwg1357e	DNA segment, Chr 19, Brigham & Women's Genetics 1357 expressed	52874	2.88	3.71	2.69	1.07	0.37	ns
Lysmd3	LysM, putative peptidoglycan-binding, domain containing 3	80289	0.42	0.62	0.79	0.53	-0.71	ns
Mll3	myeloid/lymphoid or mixed-lineage leukemia 3	231051	0.74	0.83	1.15	0.64	-0.53	ns
LOC546078		546078	1.19	1.22	1.35	0.88	0.23	ns
Samd1		666704	1.19	1.22	1.35	0.88	0.23	ns
Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	26921	0.90	0.98	0.87	1.02	0.02	ns
Acaca	acetyl-Coenzyme A carboxylase alpha	107476	0.67	0.62	0.82	0.81	-0.72	ns
Mtap2	microtubule-associated protein 2	17756	1.16	0.53	0.18	6.42	0.83	*
Atrn	attractin	11990	0.44	0.49	0.51	0.87	-0.66	ns
0910001L09Rik	RIKEN cDNA 0910001L09 gene	66096	0.84	0.72	0.86	0.97	-0.10	ns
Nudt19	nudix (nucleoside diphosphate linked moiety X)-type motif 19	110959	0.31	0.33	0.42	0.74	-0.77	ns
C330019G07Rik	RIKEN cDNA C330019G07 gene	215476	0.83	0.76	0.85	0.97	-0.52	ns
Stim2	stromal interaction molecule 2	116873	1.22	1.36	1.45	0.84	-0.80	ns
Nup98	nucleoporin 98	269966	1.03	1.15	1.07	0.95	0.16	ns
BC030863	cDNA sequence BC030863	194404	0.55	0.64	0.67	0.82	-0.47	ns
Sipa1l1	signal-induced proliferation-associated 1 like 1	217692	0.74	0.77	0.96	0.76	-0.61	ns
Tbl2	transducin (beta)-like 2	27368	0.61	0.67	0.85	0.71	-0.40	ns
Polb	polymerase (DNA directed), beta	18970	1.42	1.69	1.91	0.74	-0.53	ns
Rpl35	ribosomal protein L35	66489	24.42	22.00	15.73	1.54	0.86	*
2610030H06Rik	RIKEN cDNA 2610030H06 gene	67048	0.56	0.53	1.00	0.56	-0.57	ns
Slc20a2	solute carrier family 20, member 2	20516	0.96	0.88	1.08	0.89	-0.42	ns
Taf2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor	319944	1.09	1.04	1.18	0.93	-0.23	ns
Wdr67	WD repeat domain 67	210544	0.98	1.03	1.22	0.80	0.04	ns
Usp37	ubiquitin specific peptidase 37	319651	1.25	1.15	1.26	0.99	-0.58	ns
Cybasc3	cytochrome b, ascorbate dependent 3	225912	0.71	0.86	0.75	0.94	0.18	ns
Prkch	protein kinase C, eta	18755	0.21	0.25	0.44	0.47	-0.89	*
Cnot1	CCR4-NOT transcription complex, subunit 1	234594	3.54	3.57	3.85	0.91	0.17	ns
Phactr4	phosphatase and actin regulator 4	100169	0.62	0.46	0.50	1.23	0.06	ns
F630110N24Rik	RIKEN cDNA F630110N24 gene	73822	0.43	0.46	0.47	0.92	-0.58	ns
Nek1	NIMA (never in mitosis gene a)-related expressed kinase 1	18004	0.67	0.67	0.71	0.94	0.30	ns
Adar	adenosine deaminase, RNA-specific	56417	0.68	0.95	1.00	0.67	-0.71	ns
Npcd		504193	0.26	0.40	0.45	0.58	-0.21	ns
Nptxr		73340	0.26	0.40	0.45	0.58	-0.21	ns
Ypel2	yippee-like 2 (Drosophila)	77864	0.44	0.38	0.37	1.20	-0.33	ns
Mtm1	X-linked myotubular myopathy gene 1	17772	4.97	4.56	3.20	1.55	0.70	ns
Wiz	Widely-interspaced zinc finger motifs	22404	3.16	3.17	1.58	1.99	0.91	*
Arid5b	AT rich interactive domain 5B (Mrf1 like)	71371	1.06	0.94	1.15	0.92	-0.65	ns
Bdp1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	544971	1.06	1.60	1.92	0.55	-0.81	ns
Frmd4a	FERM domain containing 4A	209630	0.29	0.29	0.13	2.25	0.60	ns
Bivm	basic, immunoglobulin-like variable motif containing	246229	0.64	0.48	0.40	1.59	0.75	ns
Gtdc1	glycosyltransferase-like domain containing 1	227835	0.53	0.46	0.35	1.50	0.88	*
Serf1	small EDRK-rich factor 1	20365	0.33	0.63	0.80	0.42	-0.72	ns
Rabl4	RAB, member of RAS oncogene family-like 4	67042	0.96	1.14	1.13	0.84	-0.42	ns
Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	77300	1.17	1.04	1.08	1.08	0.37	ns
U2af1l4	U2 small nuclear RNA auxiliary factor 1-like 4	233073	0.73	0.81	0.76	0.96	0.10	ns
Rab3ip	RAB3A interacting protein	216363	2.16	1.97	1.46	1.48	0.31	ns
Fntb	farnesyltransferase, CAAX box, beta	110606	0.71	0.66	0.93	0.76	-0.14	ns
Bmpr2	bone morphogenic protein receptor, type II (serine/threonine kinase)	12168	3.22	2.98	2.25	1.42	0.75	ns
Rab11fip5	RAB11 family interacting protein 5 (class I)	52055	1.85	2.33	2.99	0.62	-0.90	*
Chsy1	carbohydrate (chondroitin) synthase 1	269941	0.34	0.39	0.27	1.29	0.74	ns
Tcfe3	transcription factor E3	209446	0.56	0.62	0.85	0.66	-0.02	ns
Gtf3c4	general transcription factor IIIC, polypeptide 4	269252	0.91	0.83	0.90	1.01	-0.18	ns
Micall2	MICAL-like 2	231830	0.39	0.43	0.61	0.63	-0.58	ns
Adipor2	adiponectin receptor 2	68465	1.75	1.65	2.40	0.72	-0.46	ns
Eif2c1	eukaryotic translation initiation factor 2C, 1	236511	0.89	0.76	0.99	0.89	-0.29	ns
Zzz3	zinc finger, ZZ domain containing 3	108946	2.24	2.08	1.56	1.43	0.18	ns
Dip2b	DIP2 disco-interacting protein 2 homolog B (Drosophila)	239667	1.00	1.03	1.28	0.77	-0.91	*
Rcor1	REST corepressor 1	217864	2.67	2.47	3.30	0.81	-0.60	ns
Fnbp1l	formin binding protein 1-like	214459	5.73	6.37	5.10	1.12	-0.02	ns
Gpkow	G patch domain and KOW motifs	209416	1.03	1.22	1.77	0.58	-0.13	ns
Fez2	fasciculation and elongation protein zeta 2 (zygin II)	225020	0.65	0.53	0.43	1.51	0.74	ns
Nup214	nucleoporin 214	227720	0.94	0.87	0.81	1.15	0.41	ns

Psma5	proteasome (prosome, macropain) subunit, alpha type 5	26442	6.11	7.19	6.09	1.00	-0.29	ns
BC055324	cDNA sequence BC055324	381306	0.64	0.67	0.67	0.94	-0.15	ns
Nutf2	nuclear transport factor 2	68051	11.29	11.92	12.10	0.93	0.15	ns
Cryab	crystallin, alpha B	12955	3.34	2.86	2.88	1.15	-0.15	ns
B930006L02Rik	RIKEN cDNA B930006L02 gene	319604	0.78	0.77	0.96	0.81	-0.52	ns
Cd44	CD44 antigen	12505	0.36	0.69	1.21	0.30	-0.71	ns
Mxd4	Max dimerization protein 4	17122	0.53	0.55	0.40	1.32	0.57	ns
Serinc2	serine incorporator 2	230779	0.81	0.91	1.19	0.68	-0.57	ns
Pja2	praja 2, RING-H2 motif containing	224938	2.11	1.67	1.31	1.60	0.88	*
Nrip1	nuclear receptor interacting protein 1	268903	2.01	1.82	1.28	1.56	0.51	ns
Tom1l2	target of myb1-like 2 (chicken)	216810	0.82	0.65	0.81	1.00	0.00	ns
Itfg3	integrin alpha FG-GAP repeat containing 3	106581	2.22	2.06	1.22	1.81	0.62	ns
Mobkl2a	MOB1, Mps One Binder kinase activator-like 2A (yeast)	208228	0.36	0.32	0.27	1.34	0.29	ns
Sos1	Son of sevenless homolog 1 (Drosophila)	20662	1.41	1.42	1.12	1.25	0.82	*
Man1a2	mannosidase, alpha, class 1A, member 2	17156	1.42	1.51	1.28	1.11	0.45	ns
EG433297		433297	13.28	13.74	10.87	1.22	0.71	ns
EG667952		667952	13.28	13.74	10.87	1.22	0.71	ns
Myl6		17904	13.28	13.74	10.87	1.22	0.71	ns
Zdhhc17	zinc finger, DHHC domain containing 17	320150	0.40	0.25	0.13	3.04	0.72	ns
Nkrf	NF-kappaB repressing factor	77286	0.22	0.27	0.39	0.55	-0.71	ns
Tgif2	TGFB-induced factor 2	228839	0.68	0.65	0.81	0.84	-0.34	ns
Zcchc2	zinc finger, CCHC domain containing 2	227449	0.71	0.70	0.71	0.99	-0.51	ns
Samd8	sterile alpha motif domain containing 8	67630	0.64	0.65	0.73	0.87	-0.93	**
Spred2	sprouty-related, EVH1 domain containing 2	114716	0.89	0.92	1.11	0.79	-0.59	ns
C030011O14Rik	RIKEN cDNA C030011O14 gene	215708	0.30	0.47	0.69	0.43	-0.88	*
Srgap2	SLIT-ROBO Rho GTPase activating protein 2	14270	0.62	0.63	0.48	1.29	0.49	ns
Atxn3	ataxin 3	110616	0.59	0.68	0.70	0.85	-0.60	ns
Solh	Small optic lobes homolog (Drosophila)	50817	2.42	1.76	1.21	1.99	0.80	ns
Rffl	ring finger and FYVE like domain containing protein	67338	0.52	0.56	0.60	0.86	-0.70	ns
Tcerg1	transcription elongation regulator 1 (CA150)	56070	1.99	2.41	2.59	0.76	-0.18	ns
Cox17	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)	12856	2.72	2.92	5.08	0.53	-0.70	ns
Morc4	microrchidia 4	75746	0.59	0.72	1.12	0.53	0.04	ns
Rrm2	ribonucleotide reductase M2	20135	6.02	6.28	9.66	0.62	-0.39	ns
Samhd1	SAM domain and HD domain, 1	56045	0.57	0.51	0.50	1.14	0.40	ns
1110018J18Rik	RIKEN cDNA 1110018J18 gene	66129	0.69	0.95	1.23	0.56	-0.71	ns
Zfp715	zinc finger protein 715	69930	0.58	0.50	0.60	0.96	0.34	ns
BC088983	cDNA sequence BC088983	382010	0.55	0.59	0.60	0.91	0.32	ns
Vldlr	very low density lipoprotein receptor	22359	3.50	4.23	4.04	0.86	-0.63	ns
Otud4	OTU domain containing 4	73945	1.91	2.53	2.61	0.73	-0.79	ns
Dusp3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	72349	0.70	0.76	0.81	0.86	-0.10	ns
Slc16a5	solute carrier family 16 (monocarboxylic acid transporters), member 5	217316	0.61	0.50	0.36	1.68	0.64	ns
Crtc1	CREB regulated transcription coactivator 1	382056	0.39	0.29	0.28	1.39	0.62	ns
Heca	headcase homolog (Drosophila)	380629	0.93	1.01	1.26	0.73	-0.79	ns
Usp12	ubiquitin specific peptidase 12	22217	0.51	0.42	0.47	1.08	-0.21	ns
Mef2d	myocyte enhancer factor 2D	17261	1.13	1.02	0.85	1.33	0.52	ns
Elmo3	engulfment and cell motility 3, ced-12 homolog (C. elegans)	234683	0.65	0.72	0.93	0.69	-0.94	**
Npepl1	aminopeptidase-like 1	228961	0.87	1.05	1.04	0.83	-0.65	ns
Rapgef6	Rap guanine nucleotide exchange factor (GEF) 6	192786	1.79	1.74	1.73	1.03	0.00	ns
Phkb	phosphorylase kinase beta	102093	0.85	0.95	0.63	1.35	0.33	ns
EG632248		632248	4.16	4.12	3.01	1.38	0.88	*
Atp13a3	ATPase type 13A3	224088	3.12	2.75	3.37	0.92	-0.62	ns
Rbm15	RNA binding motif protein 15	229700	0.76	0.96	0.95	0.80	-0.26	ns
Phka2	phosphorylase kinase alpha 2	110094	0.38	0.43	0.61	0.63	-0.08	ns
Eif2b3	eukaryotic translation initiation factor 2B, subunit 3	108067	0.37	0.34	0.51	0.71	-0.33	ns
Eif2b2	eukaryotic translation initiation factor 2B, subunit 2 beta	217715	2.70	2.62	2.86	0.94	-0.08	ns
Khdrbs1	KH domain containing, RNA binding, signal transduction associated 1	20218	3.91	4.09	4.30	0.91	-0.79	ns
Bola2	bolA-like 2 (E. coli)	66162	0.63	0.85	0.95	0.66	-0.53	ns
Smg5	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	229512	0.96	1.03	0.79	1.20	0.13	ns
Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	11737	1.68	1.65	1.08	1.55	0.90	*
Hip1	huntingtin interacting protein 1	215114	0.35	0.48	0.40	0.87	0.02	ns
Wdr47	WD repeat domain 47	99512	0.62	0.63	0.59	1.06	-0.40	ns
Asxl1	additional sex combs like 1 (Drosophila)	228790	1.04	1.25	1.42	0.73	-0.27	ns
E2f3	E2F transcription factor 3	13557	0.59	0.58	0.57	1.02	-0.43	ns
Cgrrf1	cell growth regulator with ring finger domain 1	68755	0.61	0.54	0.56	1.08	0.56	ns
4732496O08Rik	RIKEN cDNA 4732496O08 gene	242736	0.39	0.41	0.44	0.88	-0.23	ns
Vps13b	vacuolar protein sorting 13B (yeast)	666173	1.15	1.27	1.11	1.04	0.56	ns
Epb4.1l1	erythrocyte protein band 4.1-like 1	13821	0.92	0.91	0.99	0.93	-0.22	ns
BC052040	cDNA sequence BC052040	399568	0.78	0.66	0.60	1.30	0.17	ns
Enpp4	ectonucleotide pyrophosphatase/phosphodiesterase 4	224794	0.98	0.76	0.78	1.25	0.47	ns
Ptdss2	phosphatidylserine synthase 2	27388	1.78	1.46	1.80	0.99	-0.35	ns
Eif5a2	eukaryotic translation initiation factor 5A2	208691	0.40	0.47	0.44	0.89	-0.63	ns
Larp5	La ribonucleoprotein domain family, member 5	217980	4.26	4.54	5.02	0.84	-0.32	ns
Eif5b	eukaryotic translation initiation factor 5B	226982	1.45	1.54	1.26	1.15	0.67	ns
Erbb3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	13867	4.09	3.72	3.84	1.06	-0.34	ns
Ddx52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	78394	0.98	1.03	1.24	0.79	-0.74	ns
Ddx52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	78394	0.72	0.63	0.78	0.91	-0.58	ns
Vprbp	Vpr (HIV-1) binding protein	321006	1.07	0.93	1.12	0.95	0.35	ns
1810013L24Rik	RIKEN cDNA 1810013L24 gene	69053	3.33	2.78	2.29	1.45	0.44	ns
4932417H02Rik	RIKEN cDNA 4932417H02 gene	74370	0.43	0.47	0.54	0.79	-0.05	ns
Iqce	IQ motif containing E	74239	0.36	0.48	0.29	1.24	0.24	ns
4930432O21Rik	RIKEN cDNA 4930432O21 gene	74670	1.30	1.15	0.72	1.79	0.85	*
Nrf1	Nuclear respiratory factor 1	18181	0.57	0.55	0.57	0.99	0.34	ns
Rhpn2	rhophilin, Rho GTPase binding protein 2	52428	1.94	2.58	1.87	1.03	-0.49	ns
Ankrd28	ankyrin repeat domain 28	105522	0.64	0.64	0.69	0.92	-0.44	ns
Sin3b	transcriptional regulator, SIN3B (yeast)	20467	1.61	1.49	1.67	0.96	0.43	ns
Hsd17b11	hydroxysteroid (17-beta) dehydrogenase 11	114664	4.93	5.54	4.50	1.09	-0.02	ns
Sap18	Sin3-associated polypeptide 18	20220	3.69	3.31	3.65	1.00	0.25	ns

Ccm2	cerebral cavernous malformation 2 homolog (human)	216527	1.64	1.98	2.27	0.72	-0.47	ns
Cdc42bpb	Cdc42 binding protein kinase beta	217866	1.42	1.39	1.62	0.87	-0.83	*
Cog3	component of oligomeric golgi complex 3	338337	1.01	0.96	1.12	0.90	-0.47	ns
Foxk1	forkhead box K1	17425	0.61	0.51	0.67	0.90	-0.43	ns
B230339M05Rik	RIKEN cDNA B230339M05 gene	228850	1.11	1.10	1.36	0.81	-0.33	ns

3110056O03Rik	RIKEN cDNA 3110056O03 gene	73218	0.60	0.40	0.33	1.80	0.65	ns
5830411G16Rik	RIKEN cDNA 5830411G16 gene	78937	0.87	0.74	1.05	0.83	-0.72	ns
Alkbh1	alkB, alkylation repair homolog 1 (E. coli)	211064	0.59	0.52	0.58	1.02	-0.19	ns
Atg4a	autophagy-related 4A (yeast)	666468	0.25	0.32	0.50	0.50	-0.34	ns
Aga	aspartylglucosaminidase	11593	0.50	0.57	0.60	0.83	-0.63	ns
Lyst	lysosomal trafficking regulator	17101	0.51	0.49	0.52	0.99	-0.17	ns
Mtmr9	myotubularin related protein 9	210376	0.96	0.85	0.92	1.04	0.55	ns
Mbnl3	muscleblind-like 3 (Drosophila)	171170	1.44	1.27	1.51	0.95	0.35	ns
Plekhg3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	263406	1.50	1.42	1.26	1.18	0.89	*
Zfp770	zinc finger protein 770	228491	0.59	0.39	0.31	1.86	0.86	*
Rin3	Ras and Rab interactor 3	217835	0.52	0.47	0.67	0.77	-0.42	ns
D3Ertd300e	DNA segment, Chr 3, ERATO Doi 300, expressed	56790	0.59	0.55	0.46	1.28	0.43	ns
Zfp637	zinc finger protein 637	232337	0.53	0.67	0.63	0.83	-0.72	ns
Lycat	lysocardiolipin acyltransferase	225010	0.67	0.81	0.55	1.21	0.38	ns
1110034B05Rik	RIKEN cDNA 1110034B05 gene	68736	0.46	0.47	0.35	1.32	0.51	ns
Lrrc8a	leucine rich repeat containing 8A	241296	1.10	1.10	0.98	1.12	0.43	ns
Dtl	denticleless homolog (Drosophila)	76843	1.54	1.84	1.41	1.09	0.40	ns
Ift52	intraflagellar transport 52 homolog (Chlamydomonas)	245866	1.02	1.02	1.08	0.94	-0.02	ns
6030408C04Rik	RIKEN cDNA 6030408C04 gene	217558	1.08	0.95	1.45	0.74	-0.13	ns
Extl3	exostoses (multiple)-like 3	54616	0.46	0.64	0.52	0.88	-0.10	ns
Ctbp2	C-terminal binding protein 2	13017	2.30	2.28	2.16	1.06	0.03	ns
Sbf1	SET binding factor 1	77980	0.90	0.88	1.06	0.84	-0.30	ns
BC030867	cDNA sequence BC030867	217216	0.39	0.36	0.58	0.67	-0.31	ns
Smcr7l	Smith-Magenis syndrome chromosome region, candidate 7-like (human)	239555	0.91	0.88	1.03	0.89	-0.16	ns
Obfc1	oligonucleotide/oligosaccharide-binding fold containing 1	108689	0.72	0.94	0.77	0.93	-0.19	ns
Yrdc	yrdC domain containing (E.coli)	230734	0.51	0.53	0.71	0.72	-0.68	ns
Mga	MAX gene associated	29808	0.62	0.39	0.40	1.54	-0.10	ns
Ckap2	cytoskeleton associated protein 2	80986	1.88	2.22	2.72	0.69	-0.27	ns
Exoc3	exocyst complex component 3	211446	0.53	0.82	0.97	0.54	-0.69	ns
Nfrkb	nuclear factor related to kappa B binding protein	235134	0.81	0.72	0.61	1.32	0.81	*
Garnl4	GTPase activating RANGAP domain-like 4	380711	0.65	0.47	0.56	1.16	-0.05	ns
Cbfa2t2	core-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human)	12396	1.24	1.04	1.33	0.93	-0.59	ns

Akap11	A kinase (PRKA) anchor protein 11	219181	2.50	1.83	1.73	1.43	0.30	ns
Ep300	E1A binding protein p300	328572	3.22	2.16	2.00	1.60	0.83	*
C79407	expressed sequence C79407	217653	1.12	1.33	1.54	0.72	-0.41	ns
Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	20525	3.31	4.04	6.52	0.51	-0.71	ns
Pard3	par-3 (partitioning defective 3) homolog (C. elegans)	93742	0.99	0.87	0.55	1.78	0.89	*
Wapal	Wings apart-like homolog (Drosophila)	218914	2.16	1.91	1.92	1.12	0.32	ns
Usp42	ubiquitin specific peptidase 42	76800	0.78	0.87	1.07	0.73	-0.71	ns
Tmem106c	transmembrane protein 106C	380967	2.05	1.84	2.16	0.94	-0.48	ns
Lta4h	leukotriene A4 hydrolase	16993	2.38	2.13	2.16	1.09	0.25	ns
Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit A2	21871	0.59	0.45	0.44	1.32	0.39	ns
Exoc6b	exocyst complex component 6B	75914	0.51	0.52	0.51	1.00	0.21	ns
Mllt1	myeloid/lymphoid or mixed lineage-leukemia translocation to 1 homolog (Drosophila)	64144	0.68	0.67	0.47	1.45	0.78	ns
Palb2	partner and localizer of BRCA2	233826	0.37	0.30	0.40	0.90	-0.12	ns
Dok7	docking protein 7	231134	0.45	0.36	0.24	1.91	0.83	*
Wars	tryptophanyl-tRNA synthetase	22375	0.94	1.16	1.08	0.87	-0.05	ns
Gpi1	glucose phosphate isomerase 1	14751	10.28	10.19	13.34	0.77	-0.30	ns
Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	102626	0.50	0.63	0.34	1.48	0.60	ns
Vps33a	vacuolar protein sorting 33A (yeast)	77573	0.61	0.62	0.52	1.16	0.56	ns
Pkig	protein kinase inhibitor, gamma	18769	1.27	1.40	1.59	0.79	-0.35	ns
Brd1	bromodomain containing 1	223770	1.22	1.20	1.19	1.02	-0.41	ns
Pphln1	periphilin 1	223828	1.16	1.06	1.12	1.02	0.20	ns
Baz1b	bromodomain adjacent to zinc finger domain, 1B	22385	3.18	3.07	3.04	1.04	0.30	ns
Tnrc18	trinucleotide repeat containing 18	231861	1.48	1.18	0.83	1.78	0.91	*
Thoc6	THO complex 6 homolog (Drosophila)	386612	0.68	0.60	0.44	1.54	0.77	ns
B430201A12Rik	RIKEN cDNA B430201A12 gene	329739	2.03	1.20	0.84	2.39	0.56	ns
Cbl	Casitas B-lineage lymphoma	12402	1.19	0.92	0.89	1.33	0.81	ns
Nfatc2ip	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	18020	0.55	0.66	0.82	0.67	-0.34	ns
Mdc1	mediator of DNA damage checkpoint 1	240087	1.01	1.01	0.90	1.12	0.42	ns
Tbl1xr1	transducin (beta)-like 1X-linked receptor 1	81004	1.34	1.66	1.35	0.99	-0.29	ns
Upf3b	UPF3 regulator of nonsense transcripts homolog B (yeast)	68134	1.28	1.43	1.46	0.87	-0.21	ns
A430041B07Rik	RIKEN cDNA A430041B07 gene	328108	2.79	2.77	2.87	0.97	-0.37	ns
Dennd4c	DENN/MADD domain containing 4C	329877	0.75	0.71	1.05	0.71	-0.85	*
Iqgap3	IQ motif containing GTPase activating protein 3	404710	1.37	1.57	1.88	0.73	-0.27	ns
Crb3	crumbs homolog 3 (Drosophila)	224912	1.22	1.09	0.90	1.34	0.95	**
Mkrn1	makorin, ring finger protein, 1	54484	2.27	2.74	2.76	0.82	-0.14	ns
Amdhd2	amidohydrolase domain containing 2	245847	0.40	0.40	0.36	1.10	-0.42	ns
Ankrd44	ankyrin repeat domain 44	329154	0.81	0.70	0.48	1.68	0.63	ns
Umps	uridine monophosphate synthetase	22247	1.00	1.00	0.67	1.50	0.75	ns
Exoc7	exocyst complex component 7	53413	0.85	0.81	1.12	0.75	0.02	ns
Slc4a11	solute carrier family 4, sodium bicarbonate transporter-like, member 11	269356	0.92	1.34	1.97	0.47	-0.79	ns
Rpl37		67281	22.45	23.07	19.79	1.13	0.75	ns
Centb1	centaurin, beta 1	216859	0.48	0.66	1.50	0.32	-0.43	ns
Hmgn3	high mobility group nucleosomal binding domain 3	94353	3.21	2.57	1.12	2.87	0.97	**
Glt8d3	glycosyltransferase 8 domain containing 3	223827	1.13	1.07	1.21	0.93	0.15	ns
Cdc34	cell division cycle 34 homolog (S. cerevisiae)	216150	1.32	1.18	1.54	0.86	-0.64	ns

Etv6	ets variant gene 6 (TEL oncogene)	14011	0.75	0.79	0.74	1.01	-0.21	ns
Opa3	optic atrophy 3 (human)	403187	0.36	0.41	0.58	0.61	-0.53	ns
Plekha7	pleckstrin homology domain containing, family A member 7	233765	0.38	0.40	0.33	1.16	0.66	ns
Opa1	optic atrophy 1 homolog (human)	74143	2.35	2.32	2.20	1.06	0.83	*
Ptgfrn	prostaglandin F2 receptor negative regulator	19221	2.19	2.80	2.56	0.85	0.02	ns
Rbbp4	retinoblastoma binding protein 4	19646	8.21	8.02	9.08	0.90	-0.50	ns
Zc3h13	zinc finger CCCH type containing 13	67302	0.44	0.57	0.54	0.81	0.11	ns
Ppp1r13b	protein phosphatase 1, regulatory (inhibitor) subunit 13B	21981	0.97	0.93	1.36	0.71	-0.81	ns
Zfp422-rs1	zinc finger protein 422, related sequence 1	77652	0.74	0.83	0.61	1.20	0.61	ns
Slc25a4	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4	11739	5.40	5.37	5.39	1.00	0.02	ns
Mkl1	MKL (megakaryoblastic leukemia)/myocardin-like 1	223701	1.34	1.45	1.51	0.88	-0.81	ns
Zbtb2	zinc finger and BTB domain containing 2	381990	0.71	0.66	0.47	1.49	0.82	*
Tbpl1	TATA box binding protein-like 1	237336	0.71	0.57	0.57	1.25	0.40	ns
A830080D01Rik	RIKEN cDNA A830080D01 gene	382252	0.79	0.81	0.95	0.83	0.26	ns
Arhgap19	Rho GTPase activating protein 19	71085	0.79	0.81	0.71	1.10	0.71	ns
Cobl	cordon-bleu	12808	1.07	1.02	1.03	1.03	0.07	ns
Evl	Ena-vasodilator stimulated phosphoprotein	14026	0.92	1.56	1.76	0.52	-0.79	ns
Phf12	PHD finger protein 12	268448	0.32	0.31	0.25	1.29	0.17	ns
Cox19	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	68033	0.95	0.96	1.03	0.92	-0.38	ns
Phf2	PHD finger protein 2	18676	1.01	0.87	0.93	1.08	0.23	ns
Arhgef11		213498	0.58	0.59	0.61	0.95	-0.66	ns
Gas2l1	growth arrest-specific 2 like 1	78926	1.28	1.19	1.37	0.93	-0.41	ns
Tpcn1	two pore channel 1	252972	0.43	0.35	0.31	1.39	0.49	ns
Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1	230649	0.35	0.33	0.63	0.56	-0.67	ns
Aak1	AP2 associated kinase 1	269774	2.40	2.44	2.28	1.05	0.54	ns
Hirip3	HIRA interacting protein 3	233876	0.99	1.07	1.38	0.71	-0.56	ns
Esf1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	66580	0.93	1.34	1.24	0.74	-0.36	ns
Ccdc93	coiled-coil domain containing 93	70829	0.85	0.75	0.43	1.95	0.65	ns
Mpp5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	56217	1.17	1.07	1.18	0.98	-0.39	ns
Rnf170	ring finger protein 170	77733	0.44	0.56	0.69	0.64	-0.61	ns
Cdon	cell adhesion molecule-related/down-regulated by oncogenes	57810	1.00	0.57	0.62	1.59	0.42	ns
Supt3h	suppressor of Ty 3 homolog (S. cerevisiae)	109115	0.43	0.38	0.24	1.77	0.90	*
Zswim6	zinc finger, SWIM domain containing 6	67263	0.36	0.52	0.76	0.47	-0.83	*
Actr3	ARP3 actin-related protein 3 homolog (yeast)	74117	4.86	5.06	4.25	1.14	0.00	ns
Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1	13685	3.00	3.95	4.85	0.61	-0.65	ns
E130303B06Rik	RIKEN cDNA E130303B06 gene	102124	0.72	0.60	0.73	0.98	0.25	ns
Fbxw17	F-box and WD-40 domain protein 17	109082	0.52	0.50	0.76	0.68	-0.32	ns
Dedd	death effector domain-containing	21945	0.46	0.66	0.62	0.74	-0.77	ns
Slc25a16	solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16	73132	0.65	0.61	0.75	0.87	-0.44	ns
Cdc2l6	cell division cycle 2-like 6 (CDK8-like)	78334	0.88	0.66	0.57	1.54	0.76	ns
Suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	225888	0.76	0.73	0.61	1.24	0.65	ns
zfp507	zinc finger protein 507	668501	0.83	0.81	0.85	0.98	0.18	ns
Pank4	pantothenate kinase 4	269614	0.47	0.47	0.45	1.03	0.12	ns
Cenpe	centromere protein E	229841	1.87	2.03	1.83	1.01	0.57	ns
Abcb7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	11306	1.00	0.87	1.06	0.94	-0.35	ns
Slc9a6	solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	236794	0.79	0.76	0.84	0.94	-0.50	ns
Asb7	ankyrin repeat and SOCS box-containing protein 7	117589	0.69	0.63	0.68	1.01	0.08	ns
Heatr2	HEAT repeat containing 2	433956	0.60	0.49	0.73	0.82	-0.67	ns
Trak2	trafficking protein, kinesin binding 2	70827	0.71	0.49	0.53	1.33	0.35	ns
5930434B04Rik	RIKEN cDNA 5930434B04 gene	381356	0.80	0.78	0.82	0.98	-0.50	ns
Atxn7l3	ataxin 7-like 3	217218	1.34	1.34	1.56	0.86	-0.24	ns
Itsn2	intersectin 2	20403	1.18	1.30	1.36	0.86	0.01	ns
Ogfod1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	270086	0.20	0.30	0.30	0.66	-0.12	ns
Golga1	golgi autoantigen, golgin subfamily a, 1	76899	0.48	0.41	0.50	0.96	0.28	ns
Wdr7	WD repeat domain 7	104082	0.42	0.41	0.41	1.02	0.53	ns
Upf2	UPF2 regulator of nonsense transcripts homolog (yeast)	326622	1.52	1.36	1.06	1.42	0.91	*
Golgb1	golgi autoantigen, golgin subfamily b, macrogolgin 1	224139	1.34	1.27	1.42	0.94	-0.41	ns
Arhgef4	Rho guanine nucleotide exchange factor (GEF) 4	226970	0.18	0.36	0.18	1.01	0.29	ns
Rg9mtd2	RNA (guanine-9-) methyltransferase domain containing 2	108943	0.85	0.82	0.46	1.83	0.26	ns
D10Bwg1379e	DNA segment, Chr 10, Brigham & Women's Genetics 1379 expressed	215821	0.67	0.68	0.18	3.62	0.75	ns
Wdr44	WD repeat domain 44	72404	0.28	0.25	0.43	0.64	-0.39	ns
Eme1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	268465	0.40	0.33	0.45	0.88	0.02	ns
EG545878		545878	1.19	1.07	0.99	1.20	0.74	ns
Tom1		21968	1.19	1.07	0.99	1.20	0.74	ns
B230208H17Rik	RIKEN cDNA B230208H17 gene	227624	1.05	1.03	0.90	1.16	0.26	ns
Zfyve1	zinc finger, FYVE domain containing 1	217695	0.50	0.51	0.62	0.80	-0.69	ns
Tmem106b	transmembrane protein 106B	71900	4.78	3.90	5.50	0.87	-0.46	ns
2310047D13Rik	RIKEN cDNA 2310047D13 gene	116972	0.63	0.59	0.49	1.27	0.59	ns
Ctxn1	cortexin 1	330695	1.74	1.57	1.55	1.12	0.72	ns
Klhdc2	kelch domain containing 2	69554	2.02	2.19	2.85	0.70	-0.57	ns
Zfp568	zinc finger protein 568	243905	0.36	0.39	0.40	0.88	0.09	ns
Zfyve20	zinc finger, FYVE domain containing 20	78287	0.56	0.62	0.58	0.95	0.20	ns
Ric8b	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	237422	0.65	0.43	0.47	1.39	0.39	ns
Utp14a	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	72554	0.36	0.41	0.62	0.58	-0.38	ns
Farsb	phenylalanyl-tRNA synthetase, beta subunit	23874	1.80	2.06	1.76	1.02	-0.23	ns
Atp5h	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	71679	9.81	9.95	10.13	0.96	-0.11	ns
Wdhd1	WD repeat and HMG-box DNA binding protein 1	218973	1.03	1.06	1.08	0.95	-0.14	ns
Tsen2	tRNA splicing endonuclease 2 homolog (SEN2, S. cerevisiae)	381802	0.34	0.45	0.34	0.99	0.18	ns
Osgepl1	O-sialoglycoprotein endopeptidase-like 1	72085	0.42	0.31	0.26	1.60	0.86	*
Ptp4a2	Protein tyrosine phosphatase 4a2	19244	9.50	9.32	11.47	0.82	-0.44	ns
Ugcg	UDP-glucose ceramide glucosyltransferase	22234	0.36	0.33	0.45	0.79	-0.60	ns
1200016E24Rik		319202	0.65	0.85	1.15	0.56	-0.74	ns
Ide	insulin degrading enzyme	15925	1.85	2.15	1.35	1.36	0.60	ns
Sft2d2	SFT2 domain containing 2	108735	1.37	1.53	1.20	1.13	-0.07	ns
Pctk2	PCTAIRE-motif protein kinase 2	237459	0.39	0.38	0.24	1.61	0.19	ns

Plcg1	phospholipase C, gamma 1	18803	0.71	0.81	1.00	0.71	-0.70	ns
Rps3	ribosomal protein S3	27050	13.96	14.91	12.89	1.08	0.14	ns
Leng8	leukocyte receptor cluster (LRC) member 8	232798	0.31	0.24	0.20	1.51	-0.04	ns
Btbd6	BTB (POZ) domain containing 6	399566	0.49	0.46	0.45	1.09	-0.19	ns
Cgn	cingulin	70737	1.63	1.89	1.22	1.34	0.45	ns
BC046331	cDNA sequence BC046331	230967	0.33	0.34	0.40	0.82	-0.54	ns
Ahsa2	AHA1, activator of heat shock protein ATPase homolog 2 (yeast)	268390	0.54	0.54	0.53	1.02	-0.30	ns
Ranbp6	RAN binding protein 6	240614	0.49	0.52	0.41	1.19	0.78	ns
Eomes	eomesodermin homolog (Xenopus laevis)	13813	0.28	0.23	0.29	0.95	0.11	ns
Ate1	arginine-tRNA-protein transferase 1	11907	0.60	0.53	0.63	0.96	-0.15	ns
Rsbn1	rosbin, round spermatid basic protein 1	229675	0.94	1.08	1.32	0.70	-0.95	**
BC034090	cDNA sequence BC034090	207792	0.45	0.55	0.22	1.99	0.49	ns
Id2	inhibitor of DNA binding 2	15902	1.97	3.21	3.09	0.63	-0.26	ns
Lin54	lin-54 homolog (C. elegans)	231506	0.83	0.89	1.24	0.66	-0.76	ns
Lrrcc1	leucine rich repeat and coiled-coil domain containing 1	71710	0.55	0.54	0.41	1.34	0.79	ns
Vash1	vasohibin 1	238328	1.18	1.36	5.32	0.22	-0.37	ns
Pou3f3	POU domain, class 3, transcription factor 3	18993	0.37	0.48	0.15	2.53	0.68	ns
Man2a2	mannosidase 2, alpha 2	140481	0.41	0.60	0.68	0.60	-0.86	*
Dtx3l	deltex 3-like (Drosophila)	209200	0.38	0.52	1.04	0.37	-0.78	ns
Cdc42se2	CDC42 small effector 2	72729	0.94	1.01	1.20	0.78	-0.97	**
Foxp1	forkhead box P1	108655	1.04	1.09	0.97	1.06	-0.46	ns
Erlin2	ER lipid raft associated 2	244373	1.21	1.36	1.47	0.82	-0.38	ns
Crebbp	CREB binding protein	12914	2.65	2.41	2.60	1.02	-0.19	ns
Ibrdc3	IBR domain containing 3	75234	0.30	0.36	0.52	0.57	-0.45	ns
BC023829	cDNA sequence BC023829	236848	0.69	0.56	0.78	0.88	-0.09	ns
Coq4	coenzyme Q4 homolog (yeast)	227683	0.41	0.35	0.31	1.35	0.06	ns
Ncoa2	nuclear receptor coactivator 2	17978	1.51	1.34	1.10	1.37	0.50	ns
Baz2b	bromodomain adjacent to zinc finger domain, 2B	407823	0.91	0.77	0.62	1.47	0.15	ns
Heatr5a	HEAT repeat containing 5A	320487	1.29	1.50	1.16	1.11	0.46	ns
Zfp746	zinc finger protein 746	69228	0.40	0.35	0.45	0.90	-0.43	ns
Vav2	vav 2 oncogene	22325	0.45	0.47	0.35	1.29	0.18	ns
Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae)	107182	2.69	2.77	1.88	1.42	0.76	ns
Ints8	integrator complex subunit 8	72656	0.42	0.39	0.43	0.97	-0.34	ns
Snx13	sorting nexin 13	217463	2.10	1.75	1.83	1.14	0.00	ns
Plxnb1	plexin B1	235611	0.89	0.85	0.96	0.92	-0.04	ns
Tmem141	transmembrane protein 141	51875	0.31	0.40	0.27	1.17	0.05	ns
A930041I02Rik	RIKEN cDNA A930041I02 gene	320271	0.63	0.52	0.38	1.64	0.30	ns
Itpkb	inositol 1,4,5-trisphosphate 3-kinase B	320404	0.35	0.29	0.18	1.91	0.14	ns
Lemd3	LEM domain containing 3	380664	0.87	0.87	0.82	1.06	-0.27	ns
Tbc1d4	TBC1 domain family, member 4	210789	1.53	0.96	0.83	1.82	0.27	ns
Taf4b	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor	72504	0.23	0.33	0.23	1.00	0.36	ns
Kif11	kinesin family member 11	16551	1.83	1.99	1.62	1.13	0.66	ns
Ihpk2	inositol hexaphosphate kinase 2	76500	0.37	0.42	0.40	0.91	0.34	ns
Ankrd40	ankyrin repeat domain 40	71452	0.85	0.63	0.76	1.11	0.54	ns
Mboat1	membrane bound O-acyltransferase domain containing 1	218121	1.37	1.22	1.44	0.95	-0.10	ns
Hmgb1	high mobility group box 1	15289	11.01	10.23	9.93	1.10	0.59	ns
Usp46	ubiquitin specific peptidase 46	69727	0.51	0.45	0.46	1.09	-0.17	ns
Cyhr1	cysteine and histidine rich 1	54151	0.90	0.88	0.88	1.03	0.47	ns
Ttc7	tetratricopeptide repeat domain 7	225049	0.39	0.34	0.36	1.06	0.09	ns
Gnptab	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	432486	0.39	0.39	0.27	1.43	-0.06	ns
Celsr2	cadherin EGF LAG seven-pass G-type receptor 2	53883	1.18	1.35	1.00	1.18	-0.06	ns
Cdk6	cyclin-dependent kinase 6	12571	1.01	1.22	0.79	1.27	0.58	ns
Kctd15	potassium channel tetramerisation domain containing 15	233107	0.50	0.70	0.86	0.57	-0.81	*
Jmjd2a	jumonji domain containing 2A	230674	0.38	0.34	0.43	0.89	-0.41	ns
Ppig	peptidyl-prolyl isomerase G (cyclophilin G)	228005	1.99	2.07	1.48	1.33	0.53	ns
Tfdp2	transcription factor Dp 2	211586	0.91	0.71	0.56	1.62	0.64	ns
Ccdc82	coiled-coil domain containing 82	66396	0.62	0.48	0.26	2.35	0.78	ns
Nrp2	neuropilin 2	18187	0.51	0.42	0.37	1.37	0.21	ns
Fbxo42	F-box protein 42	213499	0.72	0.35	0.75	0.95	-0.04	ns
D4Wsu53e	DNA segment, Chr 4, Wayne State University 53, expressed	27981	0.39	0.40	0.44	0.88	-0.40	ns
Foxj3	forkhead box J3	230700	1.96	1.77	1.99	0.98	0.12	ns
Fastkd5	FAST kinase domains 5	380601	0.76	0.77	0.77	0.98	-0.02	ns
2410002O22Rik	RIKEN cDNA 2410002O22 gene	66975	0.68	0.83	0.89	0.76	-0.93	**
Cox10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)	70383	0.33	0.35	0.38	0.86	-0.64	ns
Rhoc	ras homolog gene family, member C	11853	2.58	2.72	3.02	0.85	-0.25	ns
Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	57423	8.79	8.66	7.50	1.17	0.45	ns
Stxbp6	syntaxin binding protein 6 (amisyn)	217517	0.79	0.85	0.63	1.25	0.55	ns
Stxbp5	syntaxin binding protein 5 (tomosyn)	78808	0.46	0.49	0.46	0.99	0.32	ns
Ttc26	tetratricopeptide repeat domain 26	264134	0.31	0.38	0.27	1.16	-0.04	ns
Cchcr1	coiled-coil alpha-helical rod protein 1	240084	0.63	0.69	0.51	1.22	0.79	ns
Dctn1	dynactin 1	13191	2.74	2.66	2.54	1.07	0.71	ns
Rps27l	ribosomal protein S27-like	67941	5.67	5.47	6.29	0.90	-0.13	ns
Epas1	Endothelial PAS domain protein 1	13819	0.09	0.25	0.53	0.18	-0.75	ns
Setd7	SET domain containing (lysine methyltransferase) 7	73251	1.10	1.10	1.26	0.87	-0.26	ns
Pdzd8	PDZ domain containing 8	107368	2.04	1.91	1.06	1.91	0.88	*
Wdsof1	WD repeats and SOF domain containing 1	223499	2.37	2.24	2.55	0.93	0.10	ns
Atf6	activating transcription factor 6	226641	0.83	0.63	0.52	1.61	0.75	ns
Chpt1	choline phosphotransferase 1	212862	2.15	1.88	1.72	1.24	-0.08	ns
Cpne3	copine III	70568	1.90	1.64	1.72	1.10	-0.11	ns
Hel308	helicase, mus308-like (Drosophila)	191578	0.37	0.36	0.40	0.91	-0.14	ns
Tmem20	transmembrane protein 20	240660	1.72	1.63	1.01	1.70	0.38	ns
BC006779	cDNA sequence BC006779	229003	0.25	0.27	0.53	0.47	-0.68	ns
Pim1	proviral integration site 1	18712	0.75	0.73	0.57	1.31	0.43	ns

Prkg2	protein kinase, cGMP-dependent, type II	19092	0.23	0.36	1.01	0.23	-0.60	ns
Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	99470	1.91	2.16	1.27	1.50	0.15	ns
Myo1d	myosin ID	338367	0.44	0.56	0.51	0.85	-0.32	ns
Kbtbd11	kelch repeat and BTB (POZ) domain containing 11	74901	0.19	0.09	0.53	0.36	-0.52	ns
Kremen1	kringle containing transmembrane protein 1	84035	0.38	0.30	0.45	0.85	-0.54	ns
Taf5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor	226182	0.45	0.46	0.42	1.06	0.68	ns
Lman2l	lectin, mannose-binding 2-like	214895	0.89	0.85	0.86	1.03	-0.34	ns
Braf	Braf transforming gene	109880	0.68	0.73	0.72	0.95	0.24	ns
Dsp	desmoplakin	109620	8.05	8.10	6.49	1.24	0.71	ns
Adora1	adenosine A1 receptor	11539	0.44	0.45	0.30	1.48	0.32	ns
5730590G19Rik	RIKEN cDNA 5730590G19 gene	77011	0.67	0.71	0.63	1.07	-0.15	ns
Dmwd	dystrophia myotonica-containing WD repeat motif	13401	0.56	0.51	0.44	1.28	0.66	ns
Ralb	v-ral simian leukemia viral oncogene homolog B (ras related)	64143	1.52	1.88	1.68	0.90	0.05	ns
Rap1b	RAS related protein 1b	215449	5.70	5.14	4.54	1.25	0.65	ns
2310016E02Rik	RIKEN cDNA 2310016E02 gene	67695	4.00	3.62	4.21	0.95	-0.32	ns
Tor1aip2	torsin A interacting protein 2	240832	1.97	1.66	1.96	1.00	-0.27	ns
Nfic	nuclear factor I/C	18029	0.80	1.00	0.87	0.91	0.08	ns
D2Bwg1335e	DNA segment, Chr 2, Brigham & Women's Genetics 1335 expressed	52838	0.48	0.46	0.44	1.10	-0.25	ns
OTTMUSG00000016644		667373	0.10	0.08	0.56	0.18	-0.52	ns
Depdc5	DEP domain containing 5	277854	0.28	0.34	0.38	0.73	-0.17	ns
Rsc1a1	regulatory solute carrier protein, family 1, member 1	69994	0.57	0.48	0.66	0.85	-0.45	ns
0610030E20Rik	RIKEN cDNA 0610030E20 gene	68364	0.55	0.59	0.73	0.76	-0.49	ns
Irgq	immunity-related GTPase family, Q	210146	0.34	0.40	0.42	0.78	-0.89	*
Cttnbp2nl	CTTNBP2 N-terminal like	80281	2.77	2.24	2.21	1.25	0.44	ns
Exosc6	exosome component 6	72544	0.88	1.04	0.79	1.11	0.37	ns
Trpm4	transient receptor potential cation channel, subfamily M, member 4	68667	0.88	0.81	0.95	0.93	-0.40	ns
Fhod3	formin homology 2 domain containing 3	225288	0.63	0.77	0.38	1.65	0.53	ns
Tmcc3	transmembrane and coiled coil domains 3	319880	0.97	1.04	1.55	0.63	-0.55	ns
Zfp597	zinc finger protein 597	71063	0.54	0.54	0.55	0.97	0.03	ns
Erf	Ets2 repressor factor	13875	0.54	0.55	0.51	1.07	0.63	ns
C230078M08Rik	RIKEN cDNA C230078M08 gene	319749	0.88	0.85	0.75	1.17	0.54	ns
Kntc1	kinetochore associated 1	208628	1.15	1.22	1.74	0.66	-0.33	ns
C230081A13Rik	RIKEN cDNA C230081A13 gene	244895	0.49	0.54	0.50	0.97	0.50	ns
Pcid2	PCI domain containing 2	234069	0.44	0.54	0.61	0.71	-0.48	ns
Ccdc85b	coiled-coil domain containing 85B	240514	0.44	0.33	0.24	1.79	0.90	*
Rps7	ribosomal protein S7	20115	24.32	24.84	22.79	1.06	-0.06	ns
Atad5	ATPase family, AAA domain containing 5	237877	1.14	1.19	1.04	1.09	0.35	ns
Sned1	sushi, nidogen and EGF-like domains 1	208777	0.50	0.55	0.17	2.94	0.08	ns
LOC631806		631806	0.55	0.47	0.58	0.95	-0.60	ns
Znrf3		407821	0.55	0.47	0.58	0.95	-0.60	ns
Cyp20a1	cytochrome P450, family 20, subfamily A, polypeptide 1	77951	1.40	1.33	0.89	1.56	0.07	ns
Acat2	acetyl-Coenzyme A acetyltransferase 2	110460	5.86	4.83	3.93	1.48	0.97	**
Pcmtd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	319263	0.66	0.60	0.36	1.83	0.39	ns
Gsk3a	glycogen synthase kinase 3 alpha	606496	0.81	0.89	0.91	0.88	0.12	ns
Ubb		22187	24.32	21.26	20.78	1.16	0.49	ns
Gnai2	guanine nucleotide binding protein, alpha inhibiting 2	14678	4.03	4.33	4.18	0.96	0.47	ns
Als2cr4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	381259	0.66	0.68	0.59	1.12	0.39	ns
Zfp397	zinc finger protein 397	69256	0.32	0.33	0.32	0.98	0.11	ns
Mast3	microtubule associated serine/threonine kinase 3	546071	0.52	0.59	0.53	0.98	-0.03	ns
Rhobtb2	Rho-related BTB domain containing 2	246710	0.26	0.30	0.36	0.72	-0.40	ns
Tbc1d12	TBC1D12: TBC1 domain family, member 12	209478	0.49	0.62	0.63	0.78	0.00	ns
Cep164	centrosomal protein 164	214552	0.53	0.57	0.57	0.93	-0.05	ns
Lars2	leucyl-tRNA synthetase, mitochondrial	102436	0.56	0.62	0.44	1.25	0.73	ns
2310008H09Rik	RIKEN cDNA 2310008H09 gene	66356	0.42	0.48	0.48	0.87	-0.53	ns
4921505C17Rik	RIKEN cDNA 4921505C17 gene	78757	1.64	1.44	2.19	0.74	-0.33	ns
EG545124		545124	3.76	3.55	3.35	1.12	0.05	ns
LOC624784		624784	3.76	3.55	3.35	1.12	0.05	ns
Tdg		21665	3.76	3.55	3.35	1.12	0.05	ns
Snrpn	small nuclear ribonucleoprotein N	20646	0.44	0.25	0.21	2.12	0.30	ns
EG241053		241053	27.00	24.48	18.04	1.49	0.71	ns
EG622589		622589	27.00	24.48	18.04	1.49	0.71	ns
EG633570		633570	27.00	24.48	18.04	1.49	0.71	ns
LOC546695		546695	27.00	24.48	18.04	1.49	0.71	ns
LOC630855		630855	27.00	24.48	18.04	1.49	0.71	ns
LOC639477		639477	27.00	24.48	18.04	1.49	0.71	ns
LOC668706		668706	27.00	24.48	18.04	1.49	0.71	ns
Rpl12		269261	27.00	24.48	18.04	1.49	0.71	ns
Lima1	LIM domain and actin binding 1	65970	1.67	1.60	1.30	1.28	-0.22	ns
Atp6v0c	ATPase, H+ transporting, lysosomal V0 subunit C	11984	9.38	8.80	10.50	0.89	-0.71	ns
Dus1l	dihydrouridine synthase 1-like (S. cerevisiae)	68730	0.90	0.94	0.88	1.01	0.57	ns
Nde1	nuclear distribution gene E homolog 1 (A nidulans)	67203	1.02	1.15	1.16	0.88	0.29	ns
Smek1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	68734	1.98	1.68	1.92	1.03	0.22	ns
6720401G13Rik	RIKEN cDNA 6720401G13 gene	103012	0.40	0.39	0.41	0.96	-0.10	ns
5031439G07Rik	RIKEN cDNA 5031439G07 gene	223739	0.77	0.93	1.00	0.76	-0.39	ns
Zyg11b	zyg-ll homolog B (C. elegans)	414872	0.53	0.62	0.65	0.81	-0.85	*
Samd10	sterile alpha motif domain containing 10	229011	0.28	0.31	0.34	0.81	-0.83	*
Pacs1	phosphofurin acidic cluster sorting protein 1	107975	0.53	0.59	0.48	1.10	0.11	ns
Tbc1d16	TBC1 domain family, member 16	207592	0.87	0.73	0.49	1.75	-0.21	ns
Gemin7	gem (nuclear organelle) associated protein 7	69731	0.49	0.49	0.44	1.11	0.75	ns
Arid4b	AT rich interactive domain 4B (Rbp1 like)	94246	1.70	1.59	1.71	0.99	-0.41	ns
Akap9	A kinase (PRKA) anchor protein (yotiao) 9	100986	1.38	1.27	1.38	1.00	-0.38	ns
4930547N16Rik	RIKEN cDNA 4930547N16 gene	75317	0.33	0.35	0.37	0.89	0.03	ns

Ankrd11	ankyrin repeat domain 11	77087	1.81	1.85	1.33	1.35	0.69	ns
Cep110	centrosomal protein 110	26920	0.36	0.43	0.32	1.12	-0.04	ns
Atg9a	autophagy-related 9A (yeast)	245860	0.47	0.43	0.43	1.07	0.26	ns
Klhl12	kelch-like 12 (Drosophila)	240756	0.70	0.64	0.58	1.20	0.88	*
Ppm1l	protein phosphatase 1 (formerly 2C)-like	242083	0.62	0.33	0.14	4.51	0.88	*
Rpl17	ribosomal protein L17	319195	17.48	19.02	14.78	1.18	0.70	ns
Sfrs14	splicing factor, arginine/serine-rich 14	234373	0.22	0.34	0.40	0.56	-0.66	ns
Csda	cold shock domain protein A	56449	10.31	9.35	11.02	0.93	-0.53	ns
Eif4e2	eukaryotic translation initiation factor 4E member 2	26987	1.82	1.89	1.72	1.05	-0.38	ns
5730455O13Rik	RIKEN cDNA 5730455O13 gene	70567	0.59	0.67	0.37	1.57	0.75	ns
Unc50	unc-50 homolog (C. elegans)	67387	0.92	1.38	1.01	0.91	-0.06	ns
LOC675985		675985	3.04	2.97	3.34	0.91	-0.59	ns
Suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit	20917	2.17	1.98	1.74	1.24	-0.06	ns
Cdc42bpa	Cdc42 binding protein kinase alpha	226751	0.63	0.60	0.48	1.31	0.38	ns
Psmc2	proteasome (prosome, macropain) 26S subunit, ATPase 2	19181	4.77	5.03	5.43	0.87	-0.54	ns
Commd6	COMM domain containing 6	66200	0.46	0.52	0.79	0.58	-0.77	ns
1810063B05Rik	RIKEN cDNA 1810063B05 gene	67892	1.26	1.07	0.61	2.07	0.87	*
Hist3h2a	histone cluster 3, H2a	319162	0.42	0.34	0.24	1.76	0.97	**
Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	11772	0.89	1.02	1.17	0.75	-0.50	ns
Sycp3	Synaptonemal complex protein 3	20962	1.70	1.48	1.13	1.50	0.29	ns
Zfp526		210172	17.51	18.10	15.47	1.13	0.15	ns
Prkab2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	108097	0.49	0.45	0.36	1.34	0.51	ns
Prkab2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	108097	0.46	0.56	0.46	0.98	0.01	ns
Stk38l	serine/threonine kinase 38 like	232533	0.43	0.42	0.58	0.73	-0.51	ns
Akt3	thymoma viral proto-oncogene 3	23797	0.72	0.68	0.66	1.09	0.71	ns
Ankrd50	ankrin repeat domain 50	99696	0.86	1.04	1.02	0.84	-0.38	ns
Itsn1	intersectin 1 (SH3 domain protein 1A)	16443	0.39	0.35	0.29	1.35	0.73	ns
Dnajb12	DnaJ (Hsp40) homolog, subfamily B, member 12	56709	0.36	0.31	0.31	1.16	0.35	ns
Rpl32	ribosomal protein L32	19951	16.63	16.79	15.50	1.07	0.49	ns
Gdi2	guanosine diphosphate (GDP) dissociation inhibitor 2	14569	9.78	8.90	9.22	1.06	0.52	ns
Zbtb43	zinc finger and BTB domain containing 43	71834	0.74	0.62	0.65	1.14	0.00	ns
Usp40	ubiquitin specific peptidase 40	227334	0.47	0.46	0.36	1.28	0.29	ns
Nudt18	nudix (nucleoside diphosphate linked moiety X)-type motif 18	213484	0.38	0.43	0.71	0.54	-0.63	ns
Ubxd7	UBX domain containing 7	224111	0.48	0.49	0.71	0.68	-0.42	ns
Fbxl19	F-box and leucine-rich repeat protein 19	233902	0.31	0.45	0.33	0.95	0.05	ns
Dennd3	DENN/MADD domain containing 3	105841	0.56	0.51	0.48	1.18	0.80	ns
E130308A19Rik	RIKEN cDNA E130308A19 gene	230259	0.33	0.38	0.39	0.83	-0.78	ns
Ckap2l	cytoskeleton associated protein 2-like	70466	1.24	1.40	1.71	0.72	-0.27	ns
Hr	hairless	15460	0.38	0.33	0.50	0.77	0.28	ns
Taok3	TAO kinase 3	330177	0.45	0.60	0.60	0.75	-0.69	ns
Cnot3	CCR4-NOT transcription complex, subunit 3	232791	0.79	0.83	1.00	0.78	-0.88	*
Hibadh	3-hydroxyisobutyrate dehydrogenase	58875	2.29	2.19	2.96	0.77	-0.69	ns
Btbd12	BTB (POZ) domain containing 12	52864	0.38	0.33	0.53	0.70	-0.59	ns
Nlk	nemo like kinase	18099	1.27	1.19	0.95	1.33	0.32	ns
Nav2	neuron navigator 2	78286	1.15	0.69	0.76	1.50	0.78	ns
Farp2	FERM, RhoGEF and pleckstrin domain protein 2	227377	0.78	0.79	0.55	1.41	-0.08	ns
Ik	IK cytokine	24010	1.87	2.80	2.34	0.79	0.06	ns
Mrpl22	mitochondrial ribosomal protein L22	216767	1.45	1.48	1.58	0.91	-0.31	ns
Thumpd1	THUMP domain containing 1	233802	0.64	0.69	0.81	0.78	-0.45	ns
Stk4	serine/threonine kinase 4	58231	3.16	2.74	3.15	1.00	-0.32	ns
Trappc1	trafficking protein particle complex 1	245828	1.32	1.33	1.91	0.69	-0.64	ns
Zfp703	zinc finger protein 703	353310	0.68	0.69	0.35	1.93	0.38	ns
Bicc1	bicaudal C homolog 1 (Drosophila)	83675	9.03	7.43	4.94	1.82	0.73	ns
Cep68	centrosomal protein 68	216543	0.78	0.69	0.79	0.99	-0.43	ns
Pigp	phosphatidylinositol glycan anchor biosynthesis, class P	56176	2.16	2.15	2.46	0.88	-0.56	ns
Exoc8	exocyst complex component 8	102058	0.45	0.48	0.30	1.49	0.51	ns
Hes6	hairy and enhancer of split 6 (Drosophila)	55927	0.59	0.62	0.52	1.13	-0.31	ns
Tbc1d22b	TBC1 domain family, member 22B	381085	0.38	0.37	0.25	1.49	0.72	ns
9130227C08Rik	RIKEN cDNA 9130227C08Rik gene	219094	0.56	0.48	0.51	1.10	0.24	ns
Kif13b	kinesin family member 13B	16554	0.96	1.02	1.29	0.74	-0.74	ns
Rfx1	regulatory factor X, 1 (influences HLA class II expression)	19724	0.41	0.42	0.39	1.05	-0.40	ns
Rps24	ribosomal protein S24	20088	23.27	22.35	18.31	1.26	0.85	*
Zbtb10		229055	0.19	0.20	0.52	0.36	-0.76	ns
Ing5	inhibitor of growth family, member 5	66262	0.68	0.69	0.51	1.33	0.61	ns
Ankrd26	ankyrin repeat domain 26	232339	0.24	0.27	0.33	0.72	-0.65	ns
A630007B06Rik		213993	1.34	1.32	0.94	1.42	0.82	*
Zfp414	zinc finger protein 414	328801	0.77	0.56	0.36	2.12	0.93	**
Zbtb34	zinc finger and BTB domain containing 34	241311	0.36	0.39	0.33	1.07	-0.24	ns
Rnf24	ring finger protein 24	51902	0.64	0.62	0.64	1.00	0.23	ns
St13	suppression of tumorigenicity 13	70356	5.38	4.73	4.47	1.20	0.41	ns
Nsmce1	non-SMC element 1 homolog (S. cerevisiae)	67711	0.95	1.17	1.30	0.73	-0.59	ns
Slc6a17	solute carrier family 6 (neurotransmitter transporter), member 17	229706	0.70	1.07	0.41	1.70	0.50	ns
Hbxip	hepatitis B virus x interacting protein	68576	3.13	4.08	3.69	0.84	-0.42	ns
Zmynd11	zinc finger, MYND domain containing 11	66505	1.52	1.68	2.14	0.70	-0.70	ns
Ccar1	cell division cycle and apoptosis regulator 1	67500	1.77	1.97	1.54	1.14	0.23	ns
Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	13688	1.16	1.00	1.01	1.14	0.19	ns
Usp32	ubiquitin specific peptidase 32	237898	2.84	2.48	2.58	1.10	0.44	ns
Kcnj16	potassium inwardly-rectifying channel, subfamily J, member 16	16517	0.09	0.18	0.20	0.45	-0.70	ns
Slc30a1	solute carrier family 30 (zinc transporter), member 1	22782	0.23	0.36	0.22	1.06	-0.30	ns
Atad2	ATPase family, AAA domain containing 2	70472	5.15	4.71	6.34	0.81	-0.12	ns
Leprel1	leprecan-like 1	210530	1.31	0.93	1.04	1.25	0.29	ns
Dnajc5	DnaJ (Hsp40) homolog, subfamily C, member 5	13002	1.64	1.75	1.63	1.00	-0.37	ns
Ddef2	development and differentiation enhancing factor 2	211914	1.10	1.12	1.15	0.96	-0.42	ns
Znf512b	zinc finger protein 512B	269401	0.37	0.35	0.37	1.01	-0.38	ns
E2f8	E2F transcription factor 8	108961	1.18	1.26	1.60	0.74	-0.44	ns
Arid4a	AT rich interactive domain 4A (Rbp1 like)	238247	0.41	0.52	0.50	0.81	-0.55	ns
BC046404	cDNA sequence BC046404	192976	0.60	0.52	0.77	0.78	-0.02	ns

Cdc42bpg	CDC42 binding protein kinase gamma (DMPK-like)	240505	1.35	1.19	1.14	1.18	0.54	ns
Trim14	tripartite motif-containing 14	74735	0.19	0.17	0.38	0.51	-0.45	ns
Ipmk	inositol polyphosphate multikinase	69718	0.74	0.82	0.79	0.94	-0.61	ns
2610204M08Rik	RIKEN cDNA 2610204M08 gene	70435	1.00	1.29	1.40	0.71	-0.47	ns
Gabpb1	GA repeat binding protein, beta 1	14391	0.64	0.52	0.57	1.12	0.22	ns
4732471D19Rik	RIKEN cDNA 4732471D19 gene	319719	0.30	0.30	0.31	0.98	-0.57	ns
Sost	sclerostin	74499	1.56	1.39	1.24	1.25	0.87	*
EG626571		626571	0.28	0.31	0.32	0.86	-0.70	ns
LOC630700		630700	0.28	0.31	0.32	0.86	-0.70	ns
Oaz1	ornithine decarboxylase antizyme	18245	11.60	10.65	10.34	1.12	0.17	ns
Gls	glutaminase	14660	2.52	2.63	1.99	1.26	0.24	ns
Ripk5	receptor interacting protein kinase 5	213452	0.34	0.40	0.39	0.86	-0.63	ns
Slc10a7	solute carrier family 10 (sodium/bile acid cotransporter family), member 7	76775	0.49	0.56	0.52	0.93	0.14	ns
Mllt4	myeloid/lymphoid or mixed lineage-leukemia translocation to 4 homolog (Drosophila)	17356	4.91	3.98	2.59	1.89	0.79	ns
Zfp292	zinc finger protein 292	30046	0.79	0.81	0.98	0.80	-0.52	ns
Gemin5	gem (nuclear organelle) associated protein 5	216766	0.39	0.43	0.48	0.82	-0.68	ns
Scyl2	SCY1-like 2 (S. cerevisiae)	213326	0.31	0.34	0.30	1.03	0.08	ns
Myst3	MYST histone acetyltransferase (monocytic leukemia) 3	244349	1.47	1.77	1.75	0.83	-0.26	ns
D230012E17Rik	RIKEN cDNA D230012E17 gene	241062	1.91	2.05	1.32	1.44	0.52	ns
B3gnt7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	227327	0.28	0.33	0.15	1.89	0.68	ns
Ptrh1	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)	329384	0.25	0.40	0.33	0.73	-0.45	ns
Hmbox1	homeobox containing 1	219150	0.75	0.72	0.48	1.57	0.67	ns
5830404H04Rik	RIKEN cDNA 5830404H04 gene	207781	0.29	0.29	0.31	0.94	0.26	ns
5730559C18Rik	RIKEN cDNA 5730559C18 gene	67313	0.66	0.71	0.74	0.89	-0.83	*
2700094K13Rik	RIKEN cDNA 2700094K13 gene	72657	5.15	3.97	4.00	1.28	0.60	ns
Dzip1l	DAZ interacting protein 1-like	72507	0.37	0.42	0.32	1.15	0.68	ns
Nfix	nuclear factor I/X	18032	0.70	0.58	0.72	0.97	0.38	ns
Srbd1	S1 RNA binding domain 1	78586	0.84	0.82	0.52	1.60	0.93	**
Gpr137	G protein-coupled receptor 137	107173	0.52	0.53	0.35	1.48	0.76	ns
3830406C13Rik	RIKEN cDNA 3830406C13 gene	218734	0.37	0.22	0.28	1.31	-0.27	ns
Clcc1	chloride channel CLIC-like 1	229725	0.59	0.79	0.89	0.65	-0.90	*
Ipo4	importin 4	75751	1.42	1.54	1.39	1.01	-0.39	ns
Kdelc1	KDEL (Lys-Asp-Glu-Leu) containing 1	72050	1.45	1.62	1.11	1.30	0.39	ns
Ptgs1	prostaglandin-endoperoxide synthase 1	19224	0.89	1.08	1.25	0.71	-0.54	ns
Fen1	flap structure specific endonuclease 1	14156	2.99	3.60	2.92	1.02	0.50	ns
Gpr161	G protein-coupled receptor 161	240888	0.38	0.54	0.30	1.26	-0.03	ns
Slfn9	schlafen 9	237886	0.47	0.53	0.73	0.64	-0.25	ns
Dpp7	dipeptidylpeptidase 7	83768	0.37	0.41	0.36	1.03	-0.01	ns
Trmt1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	212528	0.73	0.77	0.93	0.78	-0.47	ns
Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	23806	1.33	0.99	0.98	1.34	0.72	ns
Sgms1	sphingomyelin synthase 1	208449	1.93	2.49	0.99	1.93	0.64	ns
Irak2	interleukin-1 receptor-associated kinase 2	108960	0.26	0.34	0.34	0.77	-0.77	ns
2410014A08Rik	RIKEN cDNA 2410014A08 gene	109154	0.34	0.34	0.35	0.97	-0.28	ns
Lrrfip2	leucine rich repeat (in FLII) interacting protein 2	71268	0.95	1.18	1.25	0.76	-0.09	ns
BC031781	cDNA sequence BC031781	208768	0.95	0.90	0.66	1.44	0.65	ns
Map3k3	mitogen activated protein kinase kinase kinase 3	26406	0.61	0.67	0.71	0.85	0.04	ns
1810022K09Rik	RIKEN cDNA 1810022K09 gene	69126	3.20	3.09	3.03	1.05	-0.27	ns
Trove2	TROVE domain family, member 2	20822	1.49	1.32	1.01	1.47	0.39	ns
Zfp629	zinc finger protein 629	320683	0.40	0.38	0.39	1.03	0.33	ns
Ankrd37	ankyrin repeat domain 37	654824	0.42	0.36	0.80	0.52	-0.52	ns
Ptger1	Prostaglandin E receptor 1 (subtype EP1)	19216	0.40	0.49	0.36	1.11	0.32	ns
Dtx4	deltex 4 homolog (Drosophila)	207521	1.50	1.47	0.96	1.56	0.18	ns
Tmem139	transmembrane protein 139	109218	0.32	0.36	0.41	0.76	-0.61	ns
Psmd10	proteosome (prosome, macropain) 26S subunit, non-ATPase, 10	53380	0.46	0.48	0.93	0.49	-0.45	ns
Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	230073	0.29	0.27	0.84	0.34	-0.78	ns
Ccdc45	coiled-coil domain containing 45	320162	0.50	0.42	0.39	1.28	0.76	ns
Spry2	sprouty homolog 2 (Drosophila)	24064	0.81	0.75	0.68	1.18	0.91	*
BC023744	cDNA sequence BC023744	231668	1.24	1.25	0.90	1.38	0.36	ns
Lrpap1	low density lipoprotein receptor-related protein associated protein 1	16976	1.61	1.61	1.42	1.13	0.77	ns
Cetn4	centrin 4	207175	0.27	0.46	0.23	1.17	0.05	ns
Agpat4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	68262	2.02	1.79	1.01	1.98	0.69	ns
Cnot4	CCR4-NOT transcription complex, subunit 4	53621	0.73	0.95	1.04	0.70	-0.76	ns
Ltbp4	latent transforming growth factor beta binding protein 4	108075	0.23	0.27	0.17	1.34	0.60	ns
Riok2	RIO kinase 2 (yeast)	67045	0.36	0.65	0.31	1.14	0.21	ns
Aldh9a1	aldehyde dehydrogenase 9, subfamily A1	56752	1.81	1.84	1.60	1.12	-0.05	ns
Prdx1	peroxiredoxin 1	18477	14.04	14.10	13.60	1.03	0.42	ns
Slc35e4	solute carrier family 35, member E4	103710	0.27	0.41	0.34	0.78	-0.21	ns
Snapc2	small nuclear RNA activating complex, polypeptide 2	102209	1.77	1.96	2.34	0.76	-0.73	ns
Tmem32	transmembrane protein 32	236792	1.72	1.57	2.24	0.77	-0.41	ns
Ncaph	non-SMC condensin I complex, subunit H	215387	2.76	2.71	3.30	0.83	0.02	ns
Actr5	ARP5 actin-related protein 5 homolog (yeast)	109275	0.41	0.39	0.33	1.24	0.29	ns
Cdipt	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	52858	2.61	2.98	2.57	1.01	-0.26	ns
Cenpi	centromere protein I	102920	0.45	0.57	0.88	0.51	-0.09	ns
Lgtn	ligatin	16865	1.29	1.34	1.17	1.10	0.19	ns
Rtel1	regulator of telomere elongation helicase 1	269400	0.35	0.40	0.39	0.88	-0.29	ns
Afap1	actin filament associated protein 1	70292	1.39	1.35	1.16	1.20	-0.08	ns
D0H4S114	DNA segment, human D4S114	27528	0.42	0.55	0.58	0.72	-0.60	ns
Scyl1bp1	SCY1-like 1 binding protein 1	98376	0.35	0.43	0.36	0.98	-0.46	ns
Adck5	aarF domain containing kinase 5	268822	0.75	0.84	0.94	0.79	-0.28	ns
Cox6b1	cytochrome c oxidase, subunit VIb polypeptide 1	110323	9.46	9.01	10.06	0.94	-0.27	ns
Pgd	phosphogluconate dehydrogenase	110208	3.05	2.67	3.07	0.99	-0.21	ns
Sel1l	sel-1 suppressor of lin-12-like (C. elegans)	20338	2.06	2.07	2.15	0.96	-0.50	ns
Ankrd17	ankyrin repeat domain 17	81702	2.77	2.81	2.79	0.99	-0.52	ns

9630058J23Rik	RIKEN cDNA 9630058J23 gene	226744	0.66	0.63	0.35	1.85	0.74	ns
Surf4	surfeit gene 4	20932	1.08	1.11	0.94	1.14	0.48	ns
Cdc42ep4	CDC42 effector protein (Rho GTPase binding) 4	56699	0.70	0.74	0.60	1.15	0.79	ns
Scyl1	SCY1-like 1 (S. cerevisiae)	78891	0.78	0.94	0.78	1.00	0.06	ns
Mcm5	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	17218	7.44	7.71	8.43	0.88	0.14	ns
Spin1	spindlin 1	20729	6.78	5.05	5.13	1.32	0.83	*
Fkrp	fukutin related protein	243853	0.28	0.26	0.50	0.57	-0.69	ns
Khsrp	KH-type splicing regulatory protein	16549	1.74	1.96	1.27	1.37	0.48	ns
Exoc5	exocyst complex component 5	105504	1.13	1.03	0.84	1.33	0.87	*
Msi2	Musashi homolog 2 (Drosophila)	76626	2.19	1.33	1.40	1.56	0.19	ns
EG620155		620155	17.16	16.91	15.25	1.12	0.61	ns
Hk1		15275	17.16	16.91	15.25	1.12	0.61	ns
LOC676276		676276	17.16	16.91	15.25	1.12	0.61	ns
EG668155		668155	2.90	2.37	2.35	1.23	0.75	ns
Rnf26		213211	2.90	2.37	2.35	1.23	0.75	ns
Tmtc3	transmembrane and tetratricopeptide repeat containing 3	237500	0.90	0.78	0.63	1.42	0.65	ns
Gm944	gene model 944, (NCBI)	381126	0.99	0.85	0.50	1.95	0.44	ns
Ttll1	tubulin tyrosine ligase-like 1	319953	1.40	1.38	1.50	0.93	-0.58	ns
Mdh1	malate dehydrogenase 1, NAD (soluble)	17449	5.76	6.59	8.02	0.72	-0.79	ns
Cnn3	calponin 3, acidic	71994	10.57	11.13	7.23	1.45	0.42	ns
B230380D07Rik	RIKEN cDNA B230380D07 gene	235461	1.19	1.00	0.92	1.28	0.94	**
Cdca8	cell division cycle associated 8	52276	2.33	2.52	2.78	0.83	0.13	ns
Gaa	glucosidase, alpha, acid	14387	0.87	0.93	1.11	0.78	-0.13	ns
Pkn1		320795	0.44	0.37	0.27	1.61	0.98	***
2700007P21Rik	RIKEN cDNA 2700007P21 gene	212772	0.98	0.89	0.71	1.39	0.36	ns
Senp7	SUMO1/sentrin specific peptidase 7	66315	0.95	0.88	0.91	1.04	0.12	ns
Efna5	ephrin A5	13640	2.00	1.67	0.79	2.53	0.94	**
Afap1l2	actin filament associated protein 1-like 2	226250	1.33	1.28	1.17	1.13	0.66	ns
Slc25a5	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	11740	6.63	7.21	9.72	0.68	-0.68	ns
Mbtps2	membrane-bound transcription factor peptidase, site 2	270669	0.88	0.99	1.24	0.71	0.04	ns
Ewsr1	Ewing sarcoma breakpoint region 1	14030	4.28	4.42	4.93	0.86	-0.10	ns
Cherp	calcium homeostasis endoplasmic reticulum protein	27967	1.06	1.23	1.35	0.78	-0.60	ns
Uap1l1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	227620	2.00	1.68	1.30	1.52	0.28	ns
Leprot	leptin receptor overlapping transcript	230514	0.96	1.11	1.38	0.69	-0.65	ns
Rnf166	ring finger protein 166	68718	0.45	0.46	0.43	1.03	-0.02	ns
Nav1	neuron navigator 1	215690	0.25	0.32	0.09	2.78	0.63	ns
Rasal2	RAS protein activator like 2	226525	0.34	0.37	0.19	1.74	0.47	ns
Atp7a	ATPase, Cu++ transporting, alpha polypeptide	11977	1.04	0.86	1.54	0.67	-0.71	ns
EG665562		665562	23.62	21.85	17.77	1.32	0.76	ns
LOC638193		638193	23.62	21.85	17.77	1.32	0.76	ns
LOC638399		638399	23.62	21.85	17.77	1.32	0.76	ns
LOC665533		665533	23.62	21.85	17.77	1.32	0.76	ns
LOC673582		673582	23.62	21.85	17.77	1.32	0.76	ns
Esrrb	estrogen related receptor, beta	26380	3.69	3.36	5.43	0.68	-0.65	ns
EG623818		623818	0.49	0.48	0.70	0.70	-0.26	ns
Clns1a	chloride channel, nucleotide-sensitive, 1A	12729	4.60	4.54	5.05	0.91	-0.52	ns
Rbms3	RNA binding motif, single stranded interacting protein	207181	2.47	2.23	0.02	122.81	0.73	ns
Gm1752	gene model 1752, (NCBI)	385658	0.38	0.24	0.33	1.15	-0.08	ns
A930035D04Rik	RIKEN cDNA A930035D04 gene	320946	0.27	0.25	0.45	0.59	-0.77	ns
Gng5	guanine nucleotide binding protein (G protein), gamma 5 subunit	14707	9.18	9.17	10.19	0.90	-0.61	ns
Txnl1	thioredoxin-like 1	53382	4.95	5.70	6.00	0.82	-0.06	ns
Crkl	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	12929	1.70	1.40	1.47	1.16	0.51	ns
Txndc9	thioredoxin domain containing 9	98258	2.42	2.50	1.82	1.33	0.20	ns
Tssc1	tumor suppressing subtransferable candidate 1	380752	0.42	0.42	0.55	0.77	-0.80	ns
Nelf	nasal embryonic LHRH factor	56876	4.84	5.55	4.67	1.03	0.28	ns
Brd3	bromodomain containing 3	67382	0.92	0.91	0.71	1.29	0.32	ns
Yod1	YOD1 OTU deubiquitinating enzyme 1 homologue (S. cerevisiae)	226418	0.66	0.69	0.46	1.42	0.17	ns
Rbm14	RNA binding motif protein 14	56275	3.11	3.11	2.24	1.38	0.74	ns
Cnot2	CCR4-NOT transcription complex, subunit 2	72068	2.09	1.97	1.83	1.14	0.15	ns
Tnrc6b	trinucleotide repeat containing 6b	213988	1.62	1.68	1.69	0.95	-0.80	ns
Abi2	abl-interactor 2	329165	1.23	1.39	0.69	1.78	0.69	ns
Vdac1	voltage-dependent anion channel 1	22333	9.57	7.48	7.91	1.20	0.65	ns
Rpl26	ribosomal protein L26	19941	32.17	29.10	25.88	1.24	0.96	**
Sh3bgrl	SH3-binding domain glutamic acid-rich protein like	56726	2.32	2.52	2.50	0.92	-0.39	ns
Rpl18	ribosomal protein L18	19899	17.72	16.66	15.65	1.13	0.33	ns
Usp39	ubiquitin specific peptidase 39	28035	1.71	2.23	2.59	0.65	-0.68	ns
Tmem109	transmembrane protein 109	68539	3.64	4.51	3.97	0.91	-0.44	ns
EG637273		637273	1.11	1.08	1.64	0.67	-0.71	ns
Rap2c	RAP2C, member of RAS oncogene family	72065	0.70	0.74	1.33	0.52	-0.58	ns
Arl13b	ADP-ribosylation factor-like 13B	68146	0.40	0.39	0.55	0.72	-0.65	ns
D130059P03Rik	RIKEN cDNA D130059P03 gene	320538	0.86	1.04	0.89	0.96	-0.01	ns
BC057893	cDNA sequence BC057893	272027	0.46	0.52	0.73	0.62	-0.91	*
Rnps1	ribonucleic acid binding protein S1	19826	7.64	7.10	5.73	1.33	0.97	**
Arnt	aryl hydrocarbon receptor nuclear translocator	11863	1.26	1.33	1.23	1.02	-0.36	ns
Mapk8	mitogen activated protein kinase 8	26419	0.85	0.86	0.71	1.19	0.18	ns
Stxbp2	syntaxin binding protein 2	20911	0.73	1.01	0.90	0.81	0.14	ns
Sox21	SRY-box containing gene 21	223227	0.16	0.10	0.26	0.62	-0.71	ns
Osbpl8	oxysterol binding protein-like 8	237542	0.46	0.56	0.47	0.98	0.12	ns
Dcun1d2	DCN1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae)	102323	0.54	0.45	0.54	1.00	0.43	ns
Psmd11		69077	6.58	6.23	4.60	1.42	0.87	*
Sdad1	SDA1 domain containing 1	231452	0.50	0.56	0.61	0.81	-0.70	ns
Pim3	proviral integration site 3	223775	1.82	1.63	1.24	1.45	0.56	ns
Jarid1a	jumonji, AT rich interactive domain 1A (Rbp2 like)	214899	1.11	1.24	1.43	0.77	-0.94	**
Zc3h12c	zinc finger CCCH type containing 12C	244871	0.42	0.34	0.35	1.20	0.29	ns
Ern1	Endoplasmic reticulum (ER) to nucleus signalling 1	78943	0.41	0.41	0.64	0.64	-0.32	ns

A630033E08Rik	RIKEN cDNA A630033E08 gene	240041	0.32	0.38	0.32	0.97	-0.35	ns
Mrpl11	mitochondrial ribosomal protein L11	66419	2.09	2.81	1.52	1.37	0.67	ns
Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	18003	1.08	1.31	1.19	0.90	-0.21	ns
Akr1b3	aldo-keto reductase family 1, member B3 (aldose reductase)	11677	2.90	4.19	3.31	0.87	-0.54	ns
Txndc1	thioredoxin domain containing 1	72736	4.00	4.71	5.56	0.72	-0.46	ns
Psma6	proteasome (prosome, macropain) subunit, alpha type 6	26443	8.64	10.02	10.61	0.81	-0.54	ns
Arpc2	actin related protein 2/3 complex, subunit 2	76709	9.54	9.91	9.18	1.03	0.53	ns
Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	21366	1.83	1.45	1.76	1.03	0.30	ns
Usp22	ubiquitin specific peptidase 22	216825	2.53	2.23	2.56	0.98	-0.17	ns
Nipbl	Nipped-B homolog (Drosophila)	71175	2.09	2.18	2.21	0.94	-0.36	ns
Glb1	Galactosidase, beta 1	12091	0.37	0.43	0.31	1.17	0.43	ns
Rbpms	RNA binding protein gene with multiple splicing	19663	2.52	2.51	2.02	1.24	0.17	ns
EG432676		432676	1.85	1.59	2.99	0.62	-0.78	ns
Pcolce	procollagen C-endopeptidase enhancer protein	18542	5.30	6.43	7.71	0.68	-0.48	ns
Hadhb	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	231086	1.79	2.13	2.24	0.80	-0.75	ns
Pdik1l	PDLIM1 interacting kinase 1 like	230809	1.01	1.14	1.44	0.70	-0.61	ns
6530403A03Rik	RIKEN cDNA 6530403A03 gene	67797	0.88	0.82	0.95	0.93	-0.22	ns
Tmsb10	thymosin, beta 10	19240	24.98	22.79	21.51	1.16	0.93	**
E2f7	E2F transcription factor 7	52679	1.26	1.22	1.31	0.96	0.22	ns
Styk1	serine/threonine/tyrosine kinase 1	243659	0.55	0.64	0.60	0.92	-0.43	ns
Snrpb	small nuclear ribonucleoprotein B	20638	4.78	5.37	5.84	0.82	-0.46	ns
Rps16	ribosomal protein S16	20055	23.56	21.87	20.76	1.13	0.78	ns
Sorbs2	sorbin and SH3 domain containing 2	234214	2.30	2.13	1.84	1.24	0.27	ns
Lig3	ligase III, DNA, ATP-dependent	16882	0.41	0.34	0.50	0.83	-0.41	ns
Dusp5	dual specificity phosphatase 5	240672	0.23	0.42	0.35	0.67	0.10	ns
Fcho2	FCH domain only 2	218503	1.22	1.66	2.12	0.58	-0.99	***
Mysm1	myb-like, SWIRM and MPN domains 1	320713	0.35	0.39	0.33	1.05	0.47	ns
Sept10	septin 10	103080	0.95	0.96	0.65	1.46	0.74	ns
Brd2	bromodomain containing 2	14312	3.49	3.52	1.73	2.01	0.86	*
Xbp1	X-box binding protein 1	22433	3.60	3.81	3.33	1.08	-0.39	ns
Marcksl1	MARCKS-like 1	17357	4.41	4.36	5.18	0.85	-0.58	ns
Prmt2	protein arginine N-methyltransferase 2	15468	1.67	1.62	1.12	1.49	0.45	ns
Zfp110	zinc finger protein 110	65020	0.34	0.46	0.70	0.48	-0.61	ns
Nmd3	NMD3 homolog (S. cerevisiae)	97112	1.45	1.62	1.14	1.27	0.57	ns
Phc2	polyhomeotic-like 2 (Drosophila)	54383	1.73	1.86	2.28	0.75	-0.56	ns
Klf11	Kruppel-like factor 11	194655	1.22	1.14	1.58	0.77	-0.29	ns
Ttll12	tubulin tyrosine ligase-like family, member 12	223723	0.68	0.70	0.66	1.02	0.42	ns
Fosl2		14284	0.72	1.15	1.24	0.58	-0.92	*
LOC634417		634417	0.72	1.15	1.24	0.58	-0.92	*
Cdca2	cell division cycle associated 2	108912	0.64	0.72	0.96	0.67	-0.49	ns
Clcf1	cardiotrophin-like cytokine factor 1	56708	0.48	0.62	0.45	1.06	0.23	ns
Sdc1	syndecan 1	20969	5.60	7.34	9.25	0.60	-0.75	ns
Serbp1	Serpine1 mRNA binding protein 1	66870	14.76	14.99	16.11	0.91	-0.91	*
Xab2	XPA binding protein 2	67439	0.87	1.14	1.10	0.79	-0.21	ns
Tnpo2	transportin 2 (importin 3, karyopherin beta 2b)	212999	0.83	0.78	0.81	1.02	0.52	ns
Fzd1	frizzled homolog 1 (Drosophila)	14362	0.87	0.60	0.42	2.05	0.16	ns
1110020G09Rik	RIKEN cDNA 1110020G09 gene	68646	1.45	1.18	1.10	1.32	-0.05	ns
Impad1	inositol monophosphatase domain containing 1	242291	1.27	1.62	1.29	0.97	-0.24	ns
2700081O15Rik	RIKEN cDNA 2700081O15 gene	108899	0.72	0.70	0.36	2.03	0.85	*
Pkn2	protein kinase N2	109333	1.41	1.44	1.07	1.31	0.39	ns
Chd8	chromodomain helicase DNA binding protein 8	67772	1.60	1.43	1.38	1.16	0.56	ns
Wipf2	WAS/WASL interacting protein family, member 2	68524	0.88	0.91	0.92	0.95	-0.25	ns
Dvl1	dishevelled, dsh homolog 1 (Drosophila)	13542	3.05	2.75	3.16	0.96	-0.37	ns
Il6st	interleukin 6 signal transducer	16195	0.87	1.19	0.92	0.95	-0.04	ns
F2r	coagulation factor II (thrombin) receptor	14062	4.06	5.57	5.86	0.69	-0.64	ns
Rpa1	replication protein A1	68275	8.39	8.15	6.23	1.34	0.45	ns
Aldh18a1	aldehyde dehydrogenase 18 family, member A1	56454	3.41	4.27	2.24	1.51	0.57	ns
Enoph1	enolase-phosphatase 1	67870	0.78	0.88	0.84	0.92	0.00	ns
Arf3	ADP-ribosylation factor 3	11842	2.85	3.01	3.34	0.85	-0.67	ns
Parn	poly(A)-specific ribonuclease (deadenylation nuclease)	74108	1.23	1.05	1.31	0.94	-0.09	ns
Fuk	fucokinase	234730	0.37	0.39	0.39	0.94	-0.58	ns
Bscl2	Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	14705	0.65	0.65	0.31	2.06	0.66	ns
Fbxo28	F-box protein 28	67948	0.60	0.55	0.54	1.11	-0.13	ns
Ckap5	cytoskeleton associated protein 5	75786	1.33	1.13	1.31	1.01	0.23	ns
Wdfy1	WD repeat and FYVE domain containing 1	69368	0.97	0.97	0.59	1.63	0.71	ns
Pcdh19	protocadherin 19	279653	0.36	0.20	0.02	14.36	0.45	ns
Sgol2	shugoshin-like 2 (S. pombe)	68549	0.90	0.85	0.79	1.13	0.58	ns
9930021J17Rik	RIKEN cDNA 9930021J17 gene	229488	0.44	0.30	0.17	2.54	0.39	ns
Polrmt	polymerase (RNA) mitochondrial (DNA directed)	216151	1.02	0.98	0.95	1.07	-0.38	ns
Gpr172b	G protein-coupled receptor 172B	52710	0.48	0.38	0.52	0.92	-0.02	ns
Acvr2a	Activin receptor IIA	11480	1.63	1.47	1.33	1.22	-0.15	ns
Ccbe1	collagen and calcium binding EGF domains 1	320924	0.17	0.28	0.37	0.45	0.11	ns
Zcchc11	zinc finger, CCHC domain containing 11	230594	0.64	0.61	0.68	0.93	-0.62	ns
Gpr126	G protein-coupled receptor 126	215798	1.69	1.04	0.40	4.16	0.51	ns
Zfp217	zinc finger protein 217	228913	0.56	0.58	0.64	0.88	-0.59	ns
Sra1	steroid receptor RNA activator 1	24068	0.94	1.17	1.62	0.58	-0.61	ns
Syde2		214804	0.84	0.92	0.59	1.43	0.36	ns
EG620382	Predicted gene, EG620382	620382	0.48	0.44	0.25	1.91	0.42	ns
Ercc1	excision repair cross-complementing rodent repair deficiency, complementation group 1	13870	0.90	0.81	1.06	0.85	0.00	ns
Ctnnd1	catenin (cadherin associated protein), delta 1	12388	2.33	1.72	1.28	1.82	0.59	ns
Rsad1	radical S-adenosyl methionine domain containing 1	237926	0.81	0.62	0.68	1.18	0.34	ns
Pcsk9	proprotein convertase subtilisin/kexin type 9	100102	0.39	0.37	0.48	0.80	-0.79	ns
EG433144		433144	2.00	1.44	1.66	1.19	-0.02	ns
Txndc14		66958	2.00	1.44	1.66	1.19	-0.02	ns
Ythdf1	YTH domain family 1	228994	2.43	2.61	2.22	1.09	-0.08	ns

Rnpc3	RNA-binding region (RNP1, RRM) containing 3	67225	0.55	0.87	0.69	0.80	-0.58	ns
P4hb	prolyl 4-hydroxylase, beta polypeptide	18453	11.18	9.97	11.71	0.95	0.26	ns
Alcam	activated leukocyte cell adhesion molecule	11658	2.79	2.03	1.51	1.84	-0.12	ns
Fbxw11	F-box and WD-40 domain protein 11	103583	7.44	7.26	8.73	0.85	-0.56	ns
Pknox1	Pbx/knotted 1 homeobox	18771	0.49	0.43	0.39	1.24	0.75	ns
Lrrc45	leucine rich repeat containing 45	217366	0.74	0.83	0.90	0.81	-0.77	ns
Gatad2b	GATA zinc finger domain containing 2B	229542	1.27	1.22	0.91	1.39	0.60	ns
Zfp513	zinc finger protein 513	101023	0.32	0.35	0.38	0.84	-0.66	ns
Gprc5a	G protein-coupled receptor, family C, group 5, member A	232431	2.74	2.47	3.29	0.83	-0.70	ns
Noc3l	nucleolar complex associated 3 homolog (S. cerevisiae)	57753	0.38	0.45	0.30	1.27	0.61	ns
Ammecr1l	AMME chromosomal region gene 1-like	225339	3.87	4.79	4.60	0.84	0.12	ns
Coro7	coronin 7	78885	1.40	1.27	1.57	0.89	-0.70	ns
Polr3a	polymerase (RNA) III (DNA directed) polypeptide A	218832	0.56	0.59	0.73	0.77	-0.72	ns
Mcl1	myeloid cell leukemia sequence 1	17210	5.29	5.57	4.31	1.22	0.43	ns
Casp9	caspase 9	12371	0.46	0.42	0.45	1.02	0.04	ns
Prkaa1	protein kinase, AMP-activated, alpha 1 catalytic subunit	105787	0.34	0.40	0.63	0.54	-0.89	*
Fubp1	far upstream element (FUSE) binding protein 1	51886	2.17	2.34	1.14	1.90	0.47	ns
Dnajc14	DnaJ (Hsp40) homolog, subfamily C, member 14	74330	1.68	1.64	1.39	1.21	0.87	*
LOC633966	similar to guanine nucleotide binding protein-like 2 (nucleolar)	633966	0.42	0.56	0.71	0.59	-0.70	ns
Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2	18005	1.63	1.85	1.53	1.06	0.60	ns
Api5	apoptosis inhibitor 5	11800	7.97	6.83	7.47	1.06	-0.29	ns
Zbtb20	zinc finger and BTB domain containing 20	56490	1.98	1.56	0.91	2.18	0.77	ns
Rps8	ribosomal protein S8	20116	17.26	17.97	15.48	1.11	0.24	ns
Kif2c	kinesin family member 2C	73804	0.96	1.07	1.51	0.64	-0.33	ns
Vps37c	Vacuolar protein sorting 37C (yeast)	107305	1.61	1.47	0.70	2.29	0.88	*
Nudt16l1	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	66911	2.32	2.18	2.50	0.92	-0.19	ns
Zfp36l2	zinc finger protein 36, C3H type-like 2	12193	4.70	3.79	3.25	1.44	0.78	ns
Rhoa	ras homolog gene family, member A	11848	5.53	4.99	5.07	1.09	0.62	ns
Lsg1	large subunit GTPase 1 homolog (S. cerevisiae)	224092	0.55	0.59	0.69	0.80	-0.43	ns
Dcbld2	discoidin, CUB and LCCL domain containing 2	73379	1.21	1.18	1.71	0.71	-0.74	ns
Cenpj	centromere protein J	219103	0.39	0.35	0.53	0.73	-0.62	ns
D430020J02Rik	RIKEN cDNA D430020J02 gene	319545	0.39	0.40	0.46	0.85	-0.78	ns
Cd151	CD151 antigen	12476	2.00	2.35	3.03	0.65	-0.92	**
Prss23	protease, serine, 23	76453	0.97	0.96	0.71	1.36	0.12	ns
Fkbp9	FK506 binding protein 9	27055	3.20	3.62	3.30	0.97	-0.48	ns
Atp6ap2	ATPase, H+ transporting, lysosomal accessory protein 2	70495	4.38	5.43	8.96	0.49	-0.70	ns
Clu	clusterin	12759	1.84	3.85	9.01	0.20	-0.85	*
Csnk1d	casein kinase 1, delta	104318	3.51	3.50	3.19	1.10	0.71	ns
BC049807	cDNA sequence BC049807	381066	0.78	0.70	0.66	1.18	0.63	ns
Rps14		20044	23.30	21.92	18.99	1.22	0.79	ns
Vamp3	vesicle-associated membrane protein 3	22319	2.14	2.10	2.47	0.86	-0.18	ns
Apex1	apurinic/apyrimidinic endonuclease 1	11792	4.08	3.70	3.52	1.15	-0.23	ns
Kif22	kinesin family member 22	110033	1.79	2.42	4.01	0.44	-0.77	ns
Derl1	Der1-like domain family, member 1	67819	4.22	4.19	4.93	0.85	-0.73	ns
Pitpnm1	phosphatidylinositol membrane-associated 1	18739	2.64	2.82	1.97	1.34	0.82	*
Alkbh5	alkB, alkylation repair homolog 5 (E. coli)	268420	0.92	0.79	1.29	0.71	-0.53	ns
Ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	71978	2.38	2.18	2.19	1.08	0.64	ns
Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A	17931	3.69	3.39	2.76	1.33	0.48	ns
Atp2c1	ATPase, Ca++-sequestering	235574	1.33	1.29	1.00	1.32	0.60	ns
Rab21	RAB21, member RAS oncogene family	216344	1.82	1.77	1.89	0.96	-0.67	ns
Slc4a1ap	solute carrier family 4 (anion exchanger), member 1, adaptor protein	20534	0.41	0.39	0.51	0.79	-0.61	ns
Galnt12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12	230145	0.18	0.49	0.52	0.34	-0.83	*
Ddx17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	67040	9.18	9.47	8.67	1.05	-0.02	ns
Fancb	Fanconi anemia, complementation group B	237211	0.22	0.26	0.30	0.73	0.07	ns
Sp6	trans-acting transcription factor 6	83395	0.40	0.29	0.29	1.40	0.16	ns
Eml5	echinoderm microtubule associated protein like 5	319670	0.48	0.49	0.45	1.05	-0.07	ns
Ctnna1	catenin (cadherin associated protein), alpha 1	12385	10.77	11.30	10.96	0.98	-0.20	ns
Wdr46	WD repeat domain 46	57315	1.52	1.47	1.17	1.29	0.59	ns
Eef2k	eukaryotic elongation factor-2 kinase	13631	0.54	0.50	0.54	0.99	-0.51	ns
Pacsin3	protein kinase C and casein kinase substrate in neurons 3	80708	0.64	0.45	0.53	1.19	-0.06	ns
Poldip3	polymerase (DNA-directed), delta interacting protein 3	73826	4.74	4.72	4.78	0.99	0.09	ns
Grsf1	G-rich RNA sequence binding factor 1	231413	3.27	3.51	4.68	0.69	-0.87	*
Nupl1	Nucleoporin like 1	71844	3.18	3.52	3.04	1.04	0.44	ns
Cog1	component of oligomeric golgi complex 1	16834	0.67	0.56	0.65	1.03	0.43	ns
Pofut2	protein O-fucosyltransferase 2	80294	1.59	1.68	1.70	0.93	-0.37	ns
Cpsf3	cleavage and polyadenylation specificity factor 3	54451	2.39	2.54	2.98	0.80	-0.51	ns
Dusp18	dual specificity phosphatase 18	75219	0.28	0.33	0.31	0.91	-0.59	ns
3222402P14Rik	RIKEN cDNA 3222402P14 gene	235542	1.59	1.48	0.83	1.90	0.53	ns
Hexb	hexosaminidase B	15212	1.05	1.56	2.09	0.50	-0.84	*
Bicd2	bicaudal D homolog 2 (Drosophila)	76895	1.64	1.48	1.62	1.01	0.47	ns
Ttc14	tetratricopeptide repeat domain 14	67120	2.01	2.00	1.23	1.63	0.29	ns
Frs2	fibroblast growth factor receptor substrate 2	327826	1.29	1.12	0.89	1.44	0.47	ns
Ergic1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	67458	1.43	1.37	1.10	1.30	0.69	ns
Tmem39b	transmembrane protein 39b	230770	0.34	0.40	0.45	0.76	-0.97	**
6330416L07Rik	RIKEN cDNA 6330416L07 gene	319615	0.31	0.40	0.21	1.43	0.59	ns
Son	Son cell proliferation protein	20658	0.70	0.58	0.55	1.27	0.79	ns
Xpnpep3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	321003	0.66	0.67	0.60	1.09	0.34	ns
0610007P22Rik	RIKEN cDNA 0610007P22 gene	68327	0.50	0.53	0.34	1.47	0.87	*
Sf3b5	splicing factor 3b, subunit 5	66125	4.29	3.71	4.56	0.94	-0.51	ns
EG666448		666448	19.77	18.34	14.47	1.36	0.69	ns
EG666501		666501	19.77	18.34	14.47	1.36	0.69	ns
EG666548		666548	19.77	18.34	14.47	1.36	0.69	ns
EG666738		666738	19.77	18.34	14.47	1.36	0.69	ns
Rpl23a	ribosomal protein L23a	268449	24.49	22.10	17.41	1.40	0.84	*
Cox15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	226139	0.53	0.61	0.82	0.64	-0.80	ns

Rusc1	RUN and SH3 domain containing 1	72296	0.59	0.60	0.49	1.21	0.04	ns
Gja1	gap junction membrane channel protein alpha 1	14609	0.63	0.23	0.01	86.72	0.96	**
Qdpr	quinoid dihydropteridine reductase	110391	2.65	3.05	2.30	1.14	0.08	ns
Zfp622	zinc finger protein 622	52521	6.01	5.01	4.89	1.22	0.71	ns
Pols	polymerase (DNA directed) sigma	210106	0.48	0.81	1.00	0.48	-0.54	ns
Slc25a40	solute carrier family 25, member 40	319653	0.67	0.56	0.62	1.08	-0.24	ns
4933439F18Rik	RIKEN cDNA 4933439F18 gene	66771	0.62	0.61	0.83	0.75	-0.21	ns
Gga3	golgi associated, gamma adaptin ear containing, ARF binding protein 3	260302	0.45	0.43	0.42	1.07	0.73	ns
RP23-480B19.10	similar to histone 2a	665433	13.58	13.56	14.24	0.95	0.30	ns
Pcyt1a	phosphate cytidylyltransferase 1, choline, alpha isoform	13026	0.64	0.61	0.81	0.78	-0.39	ns
Dkc1	dyskeratosis congenita 1, dyskerin homolog (human)	245474	0.94	0.94	1.01	0.92	-0.52	ns
Hook1	hook homolog 1 (Drosophila)	77963	1.72	1.75	1.90	0.90	-0.12	ns
Rab11fip3	RAB11 family interacting protein 3 (class II)	215445	0.51	0.42	0.38	1.34	0.53	ns
Ccdc90a	coiled-coil domain containing 90A	76137	1.26	1.06	1.22	1.03	0.14	ns
Mtrf1l	mitochondrial translational release factor 1-like	108853	0.39	0.34	0.26	1.46	0.18	ns
Zfp560	zinc finger protein 560	434377	0.38	0.36	0.28	1.38	0.79	ns
Lrch1	leucine-rich repeats and calponin homology (CH) domain containing 1	380916	0.57	0.59	0.61	0.92	-0.29	ns
4930402H24Rik	RIKEN cDNA 4930402H24 gene	228602	0.91	1.07	0.81	1.12	0.00	ns
Pde7a	phosphodiesterase 7A	18583	1.58	1.44	1.24	1.27	0.11	ns
Eea1	early endosome antigen 1	216238	0.72	0.71	0.99	0.73	-0.71	ns
AU019823	expressed sequence AU019823	270156	0.52	0.47	0.35	1.48	0.95	**
Zfp384	zinc finger protein 384	269800	1.15	1.03	1.20	0.95	-0.49	ns
Ptov1	prostate tumor over expressed gene 1	84113	1.45	1.20	1.35	1.06	0.20	ns
Dtymk	deoxythymidylate kinase	21915	2.30	2.80	1.83	1.25	0.17	ns
Rab20	RAB20, member RAS oncogene family	19332	0.54	0.52	0.41	1.31	0.20	ns
Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	26941	5.36	4.49	4.19	1.27	0.36	ns
Irak1	interleukin-1 receptor-associated kinase 1	16179	1.11	1.18	2.35	0.47	-0.70	ns
Taf15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	70439	0.80	0.89	0.66	1.20	0.41	ns
Atxn2	ataxin 2	20239	1.31	1.23	1.12	1.16	-0.22	ns
Pigo	phosphatidylinositol glycan anchor biosynthesis, class O	56703	0.37	0.40	0.59	0.63	-0.72	ns
Slco4a1	solute carrier organic anion transporter family, member 4a1	108115	0.99	1.29	2.00	0.49	-0.92	*
Flot2	flotillin 2	14252	1.86	2.14	1.41	1.31	0.56	ns
Flcn	Folliculin	216805	0.43	0.48	0.59	0.73	-0.91	*
Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	68278	3.74	4.93	5.34	0.70	-0.55	ns
Frmd4b	FERM domain containing 4B	232288	0.71	0.83	0.75	0.94	-0.01	ns
Exod1	exonuclease domain containing 1	71151	0.40	0.54	0.63	0.63	-0.43	ns
1110031B06Rik	RIKEN cDNA 1110031B06 gene	67826	4.66	3.52	3.30	1.41	0.59	ns
Entpd4	ectonucleoside triphosphate diphosphohydrolase 4	67464	0.52	0.60	0.56	0.94	-0.55	ns
Atad3a	ATPase family, AAA domain containing 3A	108888	1.75	1.90	1.82	0.96	0.06	ns
Hax1		23897	11.60	11.55	8.42	1.37	0.80	ns
Silg111		20461	11.60	11.55	8.42	1.37	0.80	ns
Rnf40	ring finger protein 40	233900	0.52	0.43	0.49	1.07	0.26	ns
Baz2a	bromodomain adjacent to zinc finger domain, 2A	116848	1.26	1.08	1.09	1.15	0.40	ns
Gpd1l		333433	0.77	0.69	0.54	1.42	0.78	ns
AI316807	expressed sequence AI316807	102032	0.47	0.58	0.54	0.87	-0.15	ns
Dbp	D site albumin promoter binding protein	13170	0.34	0.41	0.45	0.76	-0.41	ns
Zbtb24	zinc finger and BTB domain containing 24	268294	0.37	0.30	0.35	1.08	-0.32	ns
Pggt1b	protein geranylgeranyltransferase type I, beta subunit	225467	0.62	0.87	0.68	0.91	0.13	ns
6030443O07Rik	RIKEN cDNA 6030443O07 gene	226151	2.68	3.21	1.95	1.37	0.67	ns
Rex2	reduced expression 2	19715	0.39	0.45	0.21	1.82	0.01	ns
Mid1	midline 1	17318	0.79	0.90	0.83	0.94	0.34	ns
Usp7	ubiquitin specific peptidase 7	252870	0.47	0.45	0.48	0.97	-0.12	ns
LOC545600		545600	1.84	2.76	4.01	0.46	-0.95	**
Adamtsl5	ADAMTS-like 5	66548	0.29	0.43	0.18	1.64	0.53	ns
Sumo1	SMT3 suppressor of mif two 3 homolog 1 (yeast)	22218	5.64	5.71	5.53	1.02	-0.15	ns
Adk	adenosine kinase	11534	2.61	2.74	1.76	1.48	0.68	ns
Atxn1	ataxin 1	20238	0.46	0.47	0.40	1.14	-0.11	ns
LOC626832		626832	1.21	1.14	0.57	2.11	0.51	ns
Ltbp3	latent transforming growth factor beta binding protein 3	16998	3.58	3.72	3.67	0.97	-0.41	ns
Akr7a5	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	110198	0.80	0.70	0.65	1.22	0.84	*
Ngdn	neuroguidin, EIF4E binding protein	68966	2.54	2.88	2.26	1.12	0.59	ns
Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)	17220	14.52	13.99	12.89	1.12	0.89	*
4930504E06Rik	RIKEN cDNA 4930504E06 gene	75007	1.49	1.80	1.62	0.91	-0.60	ns
Fdft1	farnesyl diphosphate farnesyl transferase 1	14137	3.02	2.75	3.15	0.95	-0.11	ns
Evi1	ecotropic viral integration site 1	14013	5.10	4.56	2.75	1.85	0.82	*
Laptm4b	lysosomal-associated protein transmembrane 4B	114128	3.59	3.40	3.29	1.08	0.07	ns
Clcn3	chloride channel 3	12725	4.17	3.86	3.68	1.13	0.77	ns
Matr3	matrin 3	17184	7.05	7.16	6.58	1.07	0.73	ns
Dos	downstream of Stk11	216164	0.36	0.39	0.42	0.85	-0.18	ns
Trim27	tripartite motif protein 27	19720	4.72	5.09	6.67	0.70	-0.90	*
Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	51792	11.81	10.09	8.20	1.43	0.84	*
Pttg1	pituitary tumor-transforming 1	30939	7.17	6.82	6.85	1.04	0.54	ns
4632411B12Rik	RIKEN cDNA 4632411B12 gene	226976	0.90	0.89	0.67	1.32	0.76	ns
Ubn1	ubinuclein 1	170644	0.93	1.02	1.00	0.93	-0.13	ns
Dsel	dermatan sulfate epimerase-like	319901	0.54	0.51	0.24	2.23	0.54	ns
Ankrd56	ankyrin repeat domain 56	78088	0.48	0.52	0.60	0.80	-0.84	*
Cep63	centrosomal protein 63	28135	0.30	0.43	0.44	0.67	-0.22	ns
4932432K03Rik	RIKEN cDNA 4932432K03 gene	74385	0.46	0.40	0.39	1.19	0.73	ns
Lrrc20	leucine rich repeat containing 20	216011	0.41	0.44	0.35	1.16	0.24	ns
Arhgap11a	Rho GTPase activating protein 11A	228482	2.59	3.08	2.80	0.92	0.36	ns
Phca	phytoceramidase, alkaline	66190	0.50	0.52	0.56	0.89	-0.02	ns
Lrrc8e	leucine rich repeat containing 8 family, member E	72267	0.51	0.58	0.66	0.78	0.13	ns
Ddx11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	320209	0.44	0.47	0.35	1.23	0.42	ns

Grit	Rho GTPase-activating protein	330914	0.57	0.42	0.35	1.63	0.73	ns
B430203M17Rik	RIKEN cDNA B430203M17 gene	320193	0.86	0.87	0.67	1.28	0.21	ns
Thyn1	thymocyte nuclear protein 1	77862	0.43	0.38	0.34	1.26	0.61	ns
Edf1		59022	3.76	4.13	3.77	0.99	-0.30	ns
LOC665181		665181	3.76	4.13	3.77	0.99	-0.30	ns
LOC674653		674653	3.76	4.13	3.77	0.99	-0.30	ns
Rnasen	ribonuclease III, nuclear	14000	4.08	3.87	4.35	0.93	-0.50	ns
Hars	histidyl-tRNA synthetase	15115	2.19	2.79	2.52	0.87	0.17	ns
LOC433745		433745	0.91	1.12	1.02	0.89	-0.60	ns
EG433326		433326	1.24	1.44	2.45	0.50	-0.74	ns
EG623402		623402	1.24	1.44	2.45	0.50	-0.74	ns
LOC630624		630624	1.24	1.44	2.45	0.50	-0.74	ns
Tor2a	torsin family 2, member A	30933	0.80	1.15	0.81	0.98	-0.32	ns
Eif4h	eukaryotic translation initiation factor 4H	22384	9.53	9.89	10.63	0.89	-0.43	ns
Muc4	mucin 4	140474	0.13	0.37	0.95	0.14	-0.70	ns
Slc44a2	solute carrier family 44, member 2	68682	8.91	5.77	6.40	1.39	0.49	ns
Tmem180	transmembrane protein 180	75146	1.41	1.47	1.25	1.13	0.34	ns
Ptpn2	protein tyrosine phosphatase, non-receptor type 2	19255	2.28	2.93	2.96	0.77	0.12	ns
Mrps24	mitochondrial ribosomal protein S24	64660	1.07	1.14	1.37	0.78	-0.64	ns
Vwa2	von Willebrand factor A domain containing 2	240675	0.75	0.61	0.28	2.71	0.48	ns
Btbd10	BTB (POZ) domain containing 10	68815	0.53	0.60	0.67	0.78	-0.92	**
Zcchc7	zinc finger, CCHC domain containing 7	319885	0.38	0.35	0.32	1.19	-0.18	ns
Clic4	chloride intracellular channel 4 (mitochondrial)	29876	2.11	2.43	3.65	0.57	-0.66	ns
Cryz	Crystallin, zeta	12972	1.81	2.05	0.88	2.05	0.21	ns
Pctk1	PCTAIRE-motif protein kinase 1	18555	3.24	3.40	5.32	0.61	-0.66	ns
Rpl14	ribosomal protein L14	67115	16.13	17.76	13.76	1.17	0.59	ns
Grn	granulin	14824	7.40	6.61	6.92	1.06	0.65	ns
Ttc13	tetratricopeptide repeat domain 13	234875	0.94	1.18	0.89	1.05	-0.15	ns
Sf3b2	splicing factor 3b, subunit 2	319322	3.92	4.46	4.11	0.95	-0.38	ns
Commd9	COMM domain containing 9	76501	1.49	1.23	1.07	1.39	0.24	ns
2510039O18Rik	RIKEN cDNA 2510039O18 gene	77034	0.59	0.67	0.71	0.83	-0.67	ns
Cetn2	centrin 2	26370	1.49	1.56	2.80	0.53	-0.69	ns
Pebp1	phosphatidylethanolamine binding protein 1	23980	15.88	12.70	13.60	1.16	0.38	ns
Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	14755	4.96	4.44	2.94	1.68	0.96	**
Atxn10	ataxin 10	54138	11.99	11.40	11.31	1.05	-0.25	ns
Timm17b	translocase of inner mitochondrial membrane 17b	21855	0.77	0.93	1.28	0.60	-0.18	ns
EG667723		667723	10.52	11.36	10.34	1.01	-0.18	ns
Ptp4a1		19243	10.52	11.36	10.34	1.01	-0.18	ns
Chchd6	coiled-coil-helix-coiled-coil-helix domain containing 6	66098	0.74	0.94	1.01	0.73	-0.49	ns
Atxn2l	ataxin 2-like	233871	0.67	0.54	0.63	1.07	-0.12	ns
Wdr40a	WD repeat domain 40A	68970	0.51	0.57	0.67	0.75	-0.37	ns
Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	218756	0.82	0.77	0.67	1.21	-0.42	ns
Nuak1	NUAK family, SNF1-like kinase, 1	77976	0.39	0.43	0.29	1.33	0.46	ns
Zmym6	zinc finger, MYM-type 6	100177	0.49	0.50	0.46	1.06	-0.19	ns
Srrm2	serine/arginine repetitive matrix 2	75956	6.06	6.20	3.65	1.65	0.80	ns
Zzef1	zinc finger, ZZ-type with EF hand domain 1	195018	0.35	0.34	0.41	0.84	-0.21	ns
Tmem110	transmembrane protein 110	69179	0.37	0.41	0.32	1.15	0.38	ns
Bicd1	bicaudal D homolog 1 (Drosophila)	12121	0.44	0.32	0.31	1.43	0.73	ns
Zfp207	zinc finger protein 207	22680	3.71	3.40	2.68	1.38	0.76	ns
Rps10		67097	27.80	24.87	19.73	1.40	0.87	*
Wdr32	WD repeat domain 32	242418	0.27	0.27	0.37	0.74	-0.81	ns
Adi1	acireductone dioxygenase 1	104923	1.23	1.40	1.31	0.93	-0.49	ns
Adam15	a disintegrin and metallopeptidase domain 15 (metargidin)	11490	0.48	0.53	0.37	1.31	0.71	ns
Odc1		18263	3.95	4.29	4.73	0.83	-0.14	ns
EG383032		383032	8.35	9.02	8.98	0.93	-0.46	ns
EG625298		625298	9.61	10.29	10.37	0.92	-0.70	ns
EG628061		628061	9.61	10.29	10.37	0.92	-0.70	ns
LOC637251		637251	9.61	10.29	10.37	0.92	-0.70	ns
LOC668239		668239	9.61	10.29	10.37	0.92	-0.70	ns
Rps13		68052	9.61	10.29	10.37	0.92	-0.70	ns
Snx16	sorting nexin 16	74718	0.90	0.88	0.82	1.08	0.00	ns
Eftud2	elongation factor Tu GTP binding domain containing 2	20624	4.16	4.19	4.41	0.94	0.30	ns
Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	22627	13.99	13.54	11.49	1.21	0.75	ns
Ddx54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	71990	1.52	1.80	2.00	0.76	-0.84	*
Tnfaip2	tumor necrosis factor, alpha-induced protein 2	21928	2.47	3.37	2.38	1.03	-0.09	ns
LOC629957		629957	31.01	29.66	27.04	1.14	0.66	ns
LOC637599		637599	31.01	29.66	27.04	1.14	0.66	ns
Rps29		20090	31.01	29.66	27.04	1.14	0.66	ns
Hsp90aa1	heat shock protein 90kDa alpha (cytosolic), class A member 1	15519	16.43	15.44	16.81	0.97	-0.63	ns
Map3k12	mitogen activated protein kinase kinase kinase 12	26404	0.63	0.70	0.65	0.96	-0.53	ns
Stom	stomatin	13830	0.20	0.31	0.41	0.48	-0.21	ns
Ninj1	ninjurin 1	18081	1.70	1.81	1.90	0.89	0.06	ns
Sema4a	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	20351	0.07	0.24	0.65	0.11	-0.64	ns
Phb2	prohibitin 2	12034	5.40	5.29	3.29	1.63	0.82	*
Ampd2	adenosine monophosphate deaminase 2 (isoform L)	109674	1.88	2.35	1.91	0.98	-0.37	ns
Nup54	nucleoporin 54	269113	1.48	2.04	2.25	0.66	-0.89	*
Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	110911	2.23	2.57	2.79	0.80	-0.42	ns
Blmh	bleomycin hydrolase	104184	2.78	2.93	2.01	1.37	0.77	ns
Tfpt	TCF3 (E2A) fusion partner	69714	0.40	0.47	0.51	0.78	-0.68	ns
Spint2	serine protease inhibitor, Kunitz type 2	20733	8.58	8.36	10.43	0.82	-0.73	ns
Ube2h	ubiquitin-conjugating enzyme E2H	22214	1.42	1.64	2.00	0.71	-0.45	ns
AI413782	expressed sequence AI413782	104799	1.44	1.54	1.86	0.77	-0.82	*
Hn1	hematological and neurological expressed sequence 1	15374	2.96	4.97	6.15	0.48	-0.55	ns
Nfat5	nuclear factor of activated T-cells 5	54446	2.95	2.69	1.63	1.81	0.53	ns
Zfp319	zinc finger protein 319	79233	0.21	0.26	0.17	1.21	0.25	ns

Gnl3l	guanine nucleotide binding protein-like 3 (nucleolar)-like	237107	0.36	0.41	0.73	0.49	-0.32	ns
Dck	deoxycytidine kinase	13178	2.36	2.86	3.94	0.60	-0.84	*
Adipor1	adiponectin receptor 1	72674	2.57	2.09	1.82	1.41	0.76	ns
Fras1	Fraser syndrome 1 homolog (human)	231470	0.89	1.03	0.35	2.53	-0.22	ns
AW146020	expressed sequence AW146020	330361	0.43	0.34	0.35	1.20	0.75	ns
Bag4	BCL2-associated athanogene 4	67384	0.51	0.49	0.44	1.14	0.60	ns
C330023M02Rik	RIKEN cDNA C330023M02 gene	231713	0.66	0.62	0.67	0.99	-0.50	ns
Cep27	centrosomal protein 27	66296	0.43	0.38	0.27	1.59	0.83	*
Zfp322a	zinc finger protein 322a	218100	0.66	0.53	0.60	1.11	0.13	ns
Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	11931	12.46	11.12	9.86	1.26	-0.06	ns
Ccdc55	coiled-coil domain containing 55	237859	0.42	0.50	0.28	1.45	0.51	ns
Zdhhc6	zinc finger, DHHC domain containing 6	66980	2.62	2.57	2.22	1.17	0.90	*
BC031748	CDNA sequence BC031748	245622	0.61	0.82	0.99	0.61	-0.11	ns
Wipi1	WD repeat domain, phosphoinositide interacting 1	52639	0.33	0.33	0.40	0.81	0.04	ns
Polr3f	polymerase (RNA) III (DNA directed) polypeptide F	70408	0.69	0.52	0.50	1.36	0.10	ns
2310035C23Rik	RIKEN cDNA 2310035C23 gene	227446	1.05	1.08	0.75	1.39	0.07	ns
Pfkl	phosphofructokinase, liver, B-type	18641	9.41	8.70	8.85	1.06	0.62	ns
Mthfsd	methenyltetrahydrofolate synthetase domain containing	234814	0.38	0.45	0.22	1.69	0.43	ns
Gm962	gene model 962, (NCBI)	381201	0.61	0.59	0.58	1.05	-0.26	ns
D630023B12Rik	RIKEN cDNA D630023B12 gene	329679	1.20	1.40	1.20	1.00	-0.28	ns
Nfatc2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	18019	0.72	0.66	0.63	1.14	-0.06	ns
Tnrc6a	trinucleotide repeat containing 6a	233833	1.57	1.20	1.33	1.18	0.68	ns
Prelid1	PRELI domain containing 1	66494	8.66	8.77	10.76	0.80	-0.33	ns
Gpr137b		83924	1.10	1.26	1.76	0.62	-0.84	*
Rpn1	ribophorin I	103963	7.35	7.57	7.54	0.97	0.38	ns
Abhd4	abhydrolase domain containing 4	105501	3.67	3.19	3.31	1.10	-0.10	ns
Adar	Adenosine deaminase, RNA-specific	56417	0.38	0.65	0.66	0.57	-0.76	ns
Rad51l1	RAD51-like 1 (S. cerevisiae)	19363	0.45	0.76	0.69	0.65	0.02	ns
Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	65962	0.34	0.45	0.25	1.32	0.55	ns
Timm44	translocase of inner mitochondrial membrane 44	21856	1.60	1.79	1.94	0.82	0.13	ns
Cdc20	cell division cycle 20 homolog (S. cerevisiae)	107995	4.78	5.17	5.82	0.82	-0.08	ns
2310061F22Rik	RIKEN cDNA 2310061F22 gene	66965	0.96	1.34	0.75	1.27	0.43	ns
Bcar1	breast cancer anti-estrogen resistance 1	12927	1.65	1.63	0.84	1.95	0.85	*
Myadm	myeloid-associated differentiation marker	50918	3.04	3.51	4.07	0.74	-0.61	ns
Ppp2r4	protein phosphatase 2A, regulatory subunit B (PR 53)	110854	1.42	1.77	1.07	1.32	0.57	ns
Cntd1	Cyclin N-terminal domain containing 1	68107	7.00	6.75	7.88	0.88	0.12	ns
Slc25a39	solute carrier family 25, member 39	68066	14.21	11.98	12.79	1.11	0.54	ns
Xpo7	exportin 7	65246	2.15	2.10	2.76	0.78	-0.60	ns
Cldn9	claudin 9	56863	2.12	1.17	0.37	5.64	0.74	ns
Dtx2	deltex 2 homolog (Drosophila)	74198	0.62	0.74	0.65	0.95	-0.08	ns
Slc35a2	solute carrier family 35 (UDP-galactose transporter), member A2	22232	0.26	0.34	0.56	0.46	-0.67	ns
Incenp	inner centromere protein	16319	5.05	6.30	5.51	0.91	0.30	ns
EG625193		625193	2.74	3.05	2.74	1.00	-0.14	ns
Twf2	twinfilin, actin-binding protein, homolog 2 (Drosophila)	23999	0.35	0.53	0.50	0.71	-0.19	ns
Lats2	large tumor suppressor 2	50523	0.29	0.54	0.66	0.44	-0.80	ns
Tkt	transketolase	21881	13.32	12.79	12.79	1.04	0.55	ns
Tmed9	transmembrane emp24 protein transport domain containing 9	67511	2.23	2.38	3.61	0.62	-0.61	ns
A230046K03Rik	RIKEN cDNA A230046K03 gene	319277	0.73	0.71	0.42	1.74	0.42	ns
Rnaseh2c	ribonuclease H2, subunit C	68209	2.93	2.92	2.71	1.08	0.13	ns
Capza1	capping protein (actin filament) muscle Z-line, alpha 1	12340	4.29	5.75	5.40	0.79	-0.75	ns
LOC634748		634748	1.54	1.96	2.67	0.57	-0.76	ns
LOC637733		637733	6.32	6.65	7.04	0.89	-0.64	ns
Tex10	testis expressed gene 10	269536	1.76	2.16	2.54	0.69	-0.87	*
Bud31	BUD31 homolog (yeast)	231889	3.76	3.79	3.70	1.01	0.00	ns
Dsg2	desmoglein 2	13511	3.95	4.93	4.52	0.87	0.14	ns
Acot2	acyl-CoA thioesterase 2	171210	1.19	1.09	1.79	0.66	-0.31	ns
Zfp608		269023	0.68	0.79	0.64	1.06	0.29	ns
Dot1l	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	208266	0.92	0.76	0.81	1.13	0.32	ns
Nr2c1	nuclear receptor subfamily 2, group C, member 1	22025	0.64	0.60	0.32	1.99	0.56	ns
4933407H18Rik	RIKEN cDNA 4933407H18 gene	71101	0.42	0.48	0.60	0.71	-0.96	**
Punc	putative neuronal cell adhesion molecule	19289	0.56	0.49	0.17	3.28	0.92	**
4930573I19Rik	RIKEN cDNA 4930573I19 gene	104859	0.45	0.52	0.53	0.84	-0.49	ns
Dtl	denticleless homolog (Drosophila)	76843	0.84	0.91	0.66	1.27	0.71	ns
EG668830		668830	3.75	3.97	4.06	0.92	0.20	ns
LOC621832		621832	3.75	3.97	4.06	0.92	0.20	ns
EG432995	predicted gene, EG432995	432995	1.86	1.41	2.47	0.75	-0.19	ns
Tmem186	transmembrane protein 186	66690	0.44	0.48	0.45	0.97	0.13	ns
Uck2	uridine-cytidine kinase 2	80914	1.95	1.96	1.17	1.66	0.68	ns
Igf2bp2	insulin-like growth factor 2 mRNA binding protein 2	319765	3.07	3.06	4.50	0.68	-0.63	ns
Krt42	keratin 42	68239	0.65	0.61	0.60	1.08	0.69	ns
Brwd3	bromodomain and WD repeat domain containing 3	382236	0.23	0.25	0.45	0.51	-0.57	ns
Stk35	serine/threonine kinase 35	67333	0.43	0.44	0.47	0.91	-0.14	ns
Heatr5b		320473	0.55	0.46	0.46	1.19	0.66	ns
LOC670614		670614	0.55	0.46	0.46	1.19	0.66	ns
Chm	choroidermia	12662	0.53	0.53	0.84	0.63	-0.61	ns
LOC675366	similar to mitogen activated protein kinase kinase kinase 5	675366	0.99	0.84	0.85	1.16	-0.23	ns
Tmem170	transmembrane protein 170	66817	0.59	0.64	0.48	1.22	0.51	ns
Pbx1	pre B-cell leukemia transcription factor 1	18514	1.50	1.64	0.99	1.50	0.10	ns
Kctd7	potassium channel tetramerisation domain containing 7	212919	0.42	0.35	0.35	1.18	0.75	ns
Ibrdc1	IBR domain containing 1	268291	1.60	1.24	1.19	1.34	0.52	ns
Ankrd12	ankyrin repeat domain 12	106585	0.62	0.60	0.30	2.08	0.74	ns
Zfp760	zinc finger protein 760	240034	0.48	0.38	0.26	1.83	0.63	ns
Mtap9	microtubule-associated protein 9	213582	0.34	0.50	0.23	1.42	0.01	ns
Psmd11	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	69077	4.55	4.22	3.23	1.40	0.66	ns
LOC100045398	hypothetical protein LOC100045398	#######	0.53	0.56	0.36	1.47	0.87	*
Ap4e1	adaptor-related protein complex AP-4, epsilon 1	108011	1.19	1.10	1.17	1.02	0.39	ns

Nrp	neural regeneration protein	654309	0.59	0.63	0.58	1.01	0.57	ns
Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A	243725	0.99	1.00	0.62	1.58	0.44	ns
E330016A19Rik	RIKEN cDNA E330016A19 gene	214763	0.85	0.84	0.90	0.93	0.42	ns
Kctd12b	potassium channel tetramerisation domain containing 12b	207474	0.10	0.10	0.02	5.97	0.38	ns
Arl15	ADP-ribosylation factor-like 15	218639	1.67	2.74	2.54	0.65	-0.75	ns
Dclre1b	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae)	140917	0.38	0.36	0.30	1.26	0.25	ns
Ctdspl2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	329506	1.76	1.52	1.26	1.39	0.58	ns
Rabep2	rabaptin, RAB GTPase binding effector protein 2	70314	1.43	1.28	1.81	0.78	-0.67	ns
Zfp771	zinc finger protein 771	244216	0.81	0.76	0.57	1.42	0.68	ns
BC059842	cDNA sequence BC059842	230676	0.40	0.36	0.50	0.80	-0.66	ns
Reps1	RalBP1 associated Eps domain containing protein	19707	1.42	1.23	1.22	1.16	-0.13	ns
Bach1	BTB and CNC homology 1	12013	1.57	1.53	1.64	0.95	-0.64	ns
Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	19106	0.32	0.34	0.41	0.77	-0.41	ns
Mppe1	metallophosphoesterase 1	225651	0.31	0.36	0.20	1.51	0.27	ns
Zfp809	zinc finger protein 809	235047	0.85	0.97	0.62	1.38	0.78	ns
2510049J12Rik	RIKEN cDNA 2510049J12 gene	70291	0.42	0.40	0.61	0.68	-0.45	ns
D630037F22Rik	RIKEN cDNA D630037F22 gene	544696	0.69	0.51	0.43	1.62	0.62	ns
Zfp697	zinc finger protein 697	242109	0.43	0.40	0.30	1.43	0.72	ns
Zdhhc23	zinc finger, DHHC domain containing 23	332175	0.31	0.31	0.34	0.89	-0.74	ns
1110038B12Rik	RIKEN cDNA 1110038B12 gene	68763	3.29	2.77	1.60	2.04	0.44	ns
Elovl7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	74559	0.22	0.35	0.30	0.74	-0.50	ns
Dmrta2	doublesex and mab-3 related transcription factor like family A2	242620	0.55	0.44	0.36	1.52	0.43	ns
Tmem161b	Transmembrane protein 161B	72745	0.46	0.63	0.52	0.88	-0.02	ns
BC021891	cDNA sequence BC021891	234878	1.11	0.74	0.06	17.74	0.96	**
Exph5	exophilin 5	320051	0.92	0.50	0.52	1.78	0.75	ns
2700097O09Rik	RIKEN cDNA 2700097O09 gene	72658	1.58	1.72	1.74	0.90	0.13	ns
Rfx3	Regulatory factor X, 3 (influences HLA class II expression)	19726	0.31	0.37	0.25	1.23	0.58	ns
Ift122	intraflagellar transport 122 homolog (Chlamydomonas)	81896	0.95	0.93	1.03	0.92	-0.65	ns
Pi4kb	Phosphatidylinositol 4-kinase, catalytic, beta polypeptide	107650	0.30	0.41	0.28	1.05	-0.12	ns
LOC667106	Hypothetical protein LOC667106	667106	0.83	0.78	0.51	1.61	0.37	ns
Olfml2a	Olfactomedin-like 2A	241327	0.37	0.34	0.30	1.23	0.32	ns
Ipo9	importin 9	226432	2.39	2.11	1.66	1.44	0.41	ns
Psma3	Proteasome (prosome, macropain) subunit, alpha type 3	19167	0.51	0.54	0.55	0.93	-0.01	ns
Aatf	Apoptosis antagonizing transcription factor	56321	3.08	2.87	2.25	1.36	0.31	ns
Rassf1	Ras association (RalGDS/AF-6) domain family 1	56289	0.96	0.82	1.08	0.88	-0.04	ns
Rnf39	ring finger protein 39	386454	1.04	0.88	1.02	1.01	0.18	ns
Zmiz1	zinc finger, MIZ-type containing 1	328365	0.37	0.44	0.31	1.16	0.04	ns
Akap10	A kinase (PRKA) anchor protein 10	56697	0.34	0.38	0.38	0.89	-0.43	ns
4930534B04Rik	RIKEN cDNA 4930534B04 gene	75216	0.68	0.67	0.67	1.01	0.54	ns
Pkd2	polycystic kidney disease 2	18764	3.74	3.71	2.97	1.25	-0.07	ns
Elovl7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	74559	0.96	1.05	0.80	1.20	0.03	ns
Grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	56149	0.93	0.93	1.25	0.74	-0.57	ns
Ccne1	cyclin E1	12447	0.53	0.48	0.54	0.98	-0.22	ns
Tmem40	transmembrane protein 40	94346	0.57	0.67	0.72	0.80	-0.42	ns
Vat1	Vesicle amine transport protein 1 homolog (T californica)	26949	1.06	1.69	1.62	0.65	-0.75	ns
Abhd14a	abhydrolase domain containing 14A	68644	0.38	0.42	0.34	1.13	0.64	ns
Zfand3	zinc finger, AN1-type domain 3	21769	3.31	2.64	1.82	1.81	0.79	ns
Lynx1	Ly6/neurotoxin 1	23936	0.13	0.15	0.43	0.29	-0.58	ns
1200003C05Rik	RIKEN cDNA 1200003C05 gene	104771	1.31	1.53	1.61	0.81	-0.77	ns
Prosapip1	ProSAPiP1 protein	241638	0.66	0.82	0.41	1.58	-0.08	ns
Mbd5	methyl-CpG binding domain protein 5	109241	0.43	0.58	0.32	1.33	0.46	ns
Ppp1r3e	Protein phosphatase 1, regulatory (inhibitor) subunit 3E	105651	0.26	0.38	0.32	0.80	-0.64	ns
Nbeal1	neurobeachin like 1	269198	1.19	1.26	0.73	1.62	-0.05	ns
Psmc3ip	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	19183	0.64	0.68	0.88	0.73	-0.37	ns
Prr11	proline rich 11	270906	0.32	0.29	0.39	0.81	-0.20	ns
Cpne5	copine V	240058	0.57	0.55	0.47	1.21	0.56	ns
Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	16975	0.14	0.20	0.43	0.34	-0.92	**
Sulf2	sulfatase 2	72043	1.26	1.29	1.71	0.73	-0.93	**
Fut8	Fucosyltransferase 8	53618	2.76	2.52	2.70	1.02	-0.17	ns
Ell3	elongation factor RNA polymerase II-like 3	269344	0.39	0.30	0.25	1.56	0.22	ns
Zfp609	Zinc finger protein 609	214812	0.57	0.40	0.40	1.43	0.66	ns
Eya4	eyes absent 4 homolog (Drosophila)	14051	0.50	0.16	0.01	64.99	0.81	*
Tnfrsf23	tumor necrosis factor receptor superfamily, member 23	79201	0.33	0.43	2.18	0.15	-0.63	ns
Ypel1	Yippee-like 1 (Drosophila)	106369	0.38	0.32	0.31	1.22	0.78	ns
Pdlim5	PDZ and LIM domain 5	56376	1.95	1.79	1.28	1.51	-0.06	ns
Tbrg4	transforming growth factor beta regulated gene 4	21379	0.70	0.81	0.75	0.93	-0.37	ns
Rgmb	RGM domain family, member B	68799	0.45	0.41	0.19	2.34	0.85	*
Rhbdl2	rhomboid, veinlet-like 2 (Drosophila)	230726	0.44	0.39	0.39	1.12	0.52	ns
Adm2	adrenomedullin 2	223780	0.47	0.44	0.52	0.89	-0.16	ns
Ccdc66	coiled-coil domain containing 66	320234	0.56	0.63	0.54	1.04	0.36	ns
Magi1	Membrane associated guanylate kinase, WW and PDZ domain containing 1	14924	0.66	0.72	0.68	0.96	-0.34	ns
Polr3b	polymerase (RNA) III (DNA directed) polypeptide B	70428	0.37	0.42	0.33	1.10	0.38	ns
Cog7	Component of oligomeric golgi complex 7	233824	0.25	0.29	0.38	0.64	-0.81	ns
Syvn1	synovial apoptosis inhibitor 1, synoviolin	74126	0.99	0.91	0.85	1.16	0.82	*
Fbxo39	F-box protein 39	628100	0.13	0.17	0.91	0.14	-0.69	ns
D3Ertd300e	DNA segment, Chr 3, ERATO Doi 300, expressed	56790	0.50	0.50	0.30	1.67	0.72	ns
Sbf2	SET binding factor 2	319934	0.83	1.01	1.26	0.65	-0.48	ns
Lcor	ligand dependent nuclear receptor corepressor	212391	2.18	2.93	2.63	0.82	-0.65	ns
Cisd1	CDGSH iron sulfur domain 1	52637	0.28	0.41	0.29	0.96	-0.33	ns
Wdr48	WD repeat domain 48	67561	1.10	0.99	0.99	1.10	0.69	ns
LOC433546	similar to ribosomal protein L9	433546	31.08	28.19	25.53	1.21	0.76	ns
Urod	uroporphyrinogen decarboxylase	22275	1.14	1.03	1.16	0.97	-0.19	ns

Rabep1	rabaptin, RAB GTPase binding effector protein 1	54189	0.41	0.46	0.42	0.95	0.12	ns
EG667823	Predicted gene, EG667823	667823	0.18	0.28	0.61	0.29	-0.80	ns
Mbtd1	Mbt domain containing 1	103537	0.64	0.46	0.52	1.23	0.28	ns
Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	239273	1.66	1.55	0.68	2.43	0.10	ns
Zbtb39	zinc finger and BTB domain containing 39	320080	0.34	0.32	0.38	0.89	-0.58	ns
Pofut1	protein O-fucosyltransferase 1	140484	0.51	0.55	0.45	1.13	0.04	ns
Tbc1d5	TBC1 domain family, member 5	72238	0.61	0.55	0.32	1.92	0.65	ns
BC032203	cDNA sequence BC032203	210982	0.53	0.61	0.36	1.43	0.55	ns
Rad18	RAD18 homolog (S. cerevisiae)	58186	0.82	0.90	1.00	0.82	0.10	ns
1700094D03Rik	RIKEN cDNA 1700094D03 gene	73545	0.57	0.51	0.33	1.74	0.47	ns
Thoc2	THO complex 2	331401	0.81	0.77	0.80	1.00	0.06	ns
Dock9		105445	2.02	1.88	2.18	0.92	-0.44	ns
Jarid1c	jumonji, AT rich interactive domain 1C (Rbp2 like)	20591	0.35	0.27	0.48	0.74	-0.04	ns
Ube2v1		66589	5.00	5.07	4.89	1.02	-0.32	ns
Myo9a	Myosin IXa	270163	0.64	0.53	0.42	1.52	0.63	ns
EG240038	predicted gene, EG240038	240038	0.38	0.36	0.27	1.43	0.85	*
Herc4	Hect domain and RLD 4	67345	0.39	0.47	0.34	1.14	0.26	ns
Mettl2	Methyltransferase like 2	52686	0.49	0.53	0.43	1.14	0.59	ns
Ptbp2	Polypyrimidine tract binding protein 2	56195	2.16	2.56	1.16	1.85	0.58	ns
Scfd1	Sec1 family domain containing 1	76983	0.32	0.38	0.25	1.30	0.12	ns
Usp6nl	USP6 N-terminal like	98910	0.92	0.97	0.51	1.80	0.65	ns
Col4a4	procollagen, type IV, alpha 4	12829	1.01	1.18	0.13	7.97	0.60	ns
Dtnb	dystrobrevin, beta	13528	0.77	0.91	0.84	0.91	-0.05	ns
Vti1a	Vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	53611	0.51	0.46	0.34	1.51	0.82	*
Pawr	PRKC, apoptosis, WT1, regulator	114774	0.30	0.32	0.17	1.73	0.47	ns
Hdac2	histone deacetylase 2	15182	2.80	3.06	2.78	1.00	0.30	ns
LOC630474		630474	0.36	0.40	0.39	0.93	-0.52	ns
LOC638081		638081	0.36	0.40	0.39	0.93	-0.52	ns
Ifi35	interferon-induced protein 35	70110	0.93	1.19	2.98	0.31	-0.73	ns
Slc12a5	solute carrier family 12, member 5	57138	0.39	0.34	0.31	1.27	0.62	ns
Lcorl	Ligand dependent nuclear receptor corepressor-like	209707	0.32	0.33	0.35	0.93	0.32	ns
Prkca	Protein kinase C, alpha	18750	0.33	0.32	0.34	0.98	0.30	ns
Dnajc17		69408	2.25	2.25	1.97	1.14	-0.10	ns
Lias	lipoic acid synthetase	79464	1.50	1.58	1.52	0.98	0.08	ns
Ssr3	signal sequence receptor, gamma	67437	6.61	6.75	6.58	1.00	0.13	ns
Arl1	ADP-ribosylation factor-like 1	104303	4.66	4.21	3.77	1.23	0.81	ns
5730508B09Rik	RIKEN cDNA 5730508B09 gene	70617	2.17	2.37	1.77	1.22	0.12	ns
Cryl1	crystallin, lambda 1	68631	0.43	0.43	0.40	1.06	-0.03	ns
Psmd1	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	70247	0.57	0.55	0.37	1.53	0.54	ns
Pcyox1	prenylcysteine oxidase 1	66881	3.06	3.22	2.61	1.17	0.28	ns
Ep400	E1A binding protein p400	75560	1.49	1.39	1.40	1.06	0.53	ns
Bub1b	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	12236	1.41	1.27	1.42	0.98	0.48	ns
Zfp263	zinc finger protein 263	74120	0.79	0.96	1.07	0.74	-0.75	ns
Mrps6	mitochondrial ribosomal protein S6	121022	3.79	3.25	3.45	1.09	0.04	ns
Stox2	storkhead box 2	71069	0.76	0.66	0.25	2.99	0.80	ns
Pbx3	pre B-cell leukemia transcription factor 3	18516	1.79	1.73	0.89	2.00	0.69	ns
Bms1	BMS1 homolog, ribosome assembly protein (yeast)	213895	4.39	4.63	3.90	1.12	0.69	ns
Neo1	neogenin	18007	1.23	1.15	0.82	1.49	0.89	*
Pde2a	phosphodiesterase 2A, cGMP-stimulated	207728	0.35	0.42	0.42	0.84	-0.59	ns
Prkaca	protein kinase, cAMP dependent, catalytic, alpha	18747	1.84	1.77	2.47	0.74	-0.45	ns
Tufm		233870	0.40	0.44	0.48	0.84	-0.15	ns
Plekhh1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	211945	0.97	1.24	1.62	0.60	-0.82	*
Oxnad1	oxidoreductase NAD-binding domain containing 1	218885	0.46	0.54	0.56	0.83	-0.70	ns
Polh	Polymerase (DNA directed), eta (RAD 30 related)	80905	0.78	0.73	0.57	1.36	0.90	*
Tcn2	Transcobalamin 2	21452	0.90	0.89	1.00	0.90	-0.27	ns
Hist2h2be	histone cluster 2, H2be	319190	1.79	1.79	0.99	1.80	0.26	ns
Fgfrl1	fibroblast growth factor receptor-like 1	116701	0.60	0.54	0.41	1.45	0.76	ns
Map1lc3a	microtubule-associated protein 1 light chain 3 alpha	66734	2.74	3.00	3.67	0.74	-0.69	ns
LOC631721		631721	0.49	0.40	0.33	1.48	0.84	*
Vps52		224705	0.49	0.40	0.33	1.48	0.84	*
Pan3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	72587	0.81	0.97	1.42	0.56	-0.85	*
Fnta	farnesyltransferase, CAAX box, alpha	14272	4.42	4.52	3.97	1.11	0.82	*
Nup62	nucleoporin 62	18226	4.59	4.66	3.92	1.17	0.86	*
Selk	selenoprotein K	80795	2.54	2.32	3.01	0.84	-0.30	ns
Ntan1	N-terminal Asn amidase	18203	2.75	2.64	2.55	1.07	0.52	ns
Car5b	carbonic anhydrase 5b, mitochondrial	56078	0.14	0.15	0.38	0.37	-0.67	ns
Ssh3	slingshot homolog 3 (Drosophila)	245857	0.48	0.50	0.40	1.19	0.11	ns
Whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	234135	1.70	1.62	1.97	0.86	-0.02	ns
Fancm	Fanconi anemia, complementation group M	104806	0.21	0.25	0.18	1.18	-0.41	ns
2410006H16Rik	RIKEN cDNA 2410006H16 gene	69221	4.28	4.36	3.97	1.07	-0.23	ns
Yeats2	YEATS domain containing 2	208146	0.87	0.84	0.90	0.96	-0.36	ns
Mrpl38	mitochondrial ribosomal protein L38	60441	0.93	0.86	1.04	0.89	-0.28	ns
Sash1	SAM and SH3 domain containing 1	70097	1.00	1.12	1.05	0.95	-0.14	ns
Usp24	ubiquitin specific peptidase 24	329908	0.40	0.51	0.58	0.69	-0.72	ns
Sass6	spindle assembly 6 homolog (C. elegans)	72776	0.56	0.62	0.49	1.14	0.64	ns
Tbc1d24	TBC1 domain family, member 24	224617	0.83	0.77	0.76	1.09	0.40	ns
4833439L19Rik	RIKEN cDNA 4833439L19 gene	97820	2.66	2.51	4.01	0.66	-0.49	ns
Wdr61	WD repeat domain 61	66317	2.39	2.37	2.24	1.06	0.64	ns
Nono	non-POU-domain-containing, octamer binding protein	53610	9.10	7.87	10.49	0.86	-0.29	ns
Aldh6a1	aldehyde dehydrogenase family 6, subfamily A1	104776	0.96	0.99	0.87	1.10	-0.40	ns
Necap1	NECAP endocytosis associated 1	67602	0.47	0.42	0.56	0.84	-0.52	ns
Serinc1	serine incorporator 1	56442	3.23	2.76	2.29	1.41	0.79	ns
Ctps2	cytidine 5'-triphosphate synthase 2	55936	0.85	0.64	0.84	1.00	0.40	ns
Cox7c	cytochrome c oxidase, subunit VIIc	12867	3.46	5.15	6.89	0.50	-0.88	*
Ctsd	cathepsin D	13033	4.02	4.44	5.36	0.75	-0.90	*
Wbp2	WW domain binding protein 2	22378	1.72	1.46	1.69	1.01	0.33	ns

Tcp1	t-complex protein 1	21454	10.25	8.89	6.51	1.57	0.90	*
Gusb	glucuronidase, beta	110006	0.56	0.76	0.70	0.80	-0.13	ns
Ctsa	cathepsin A	19025	3.19	3.01	3.62	0.88	-0.70	ns
Arpc5	actin related protein 2/3 complex, subunit 5	67771	2.96	3.42	3.08	0.96	-0.41	ns
Mfn2	mitofusin 2	170731	0.38	0.43	0.46	0.83	-0.63	ns
X99384	cDNA sequence X99384	27355	0.64	0.83	0.63	1.02	0.35	ns
Atf4	activating transcription factor 4	11911	6.92	7.06	6.19	1.11	0.48	ns
Aldh2	aldehyde dehydrogenase 2, mitochondrial	11669	0.25	0.52	0.08	3.24	0.41	ns
Wwp2	WW domain containing E3 ubiquitin protein ligase 2	66894	0.52	0.48	0.46	1.12	0.64	ns
Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	15568	2.41	2.44	2.50	0.96	-0.09	ns
Ndrg2	N-myc downstream regulated gene 2	29811	0.16	0.32	0.37	0.42	-0.45	ns
Rpl10	ribosomal protein 10	110954	20.06	18.07	17.67	1.13	0.82	*
Casp2	caspase 2	12366	2.25	2.09	2.37	0.94	0.07	ns
Psmb1	proteasome (prosome, macropain) subunit, beta type 1	19170	5.22	4.56	4.04	1.28	0.91	*
Ifngr1	interferon gamma receptor 1	15979	0.53	0.54	0.51	1.04	0.69	ns
Krt18	keratin 18	16668	25.71	22.32	19.13	1.34	0.82	*
Siah2	seven in absentia 2	20439	0.36	0.34	0.35	1.04	0.19	ns
Cul1	cullin 1	26965	1.33	1.45	1.68	0.79	-0.88	*
Usmg5	upregulated during skeletal muscle growth 5	66477	4.16	5.21	3.43	1.21	0.54	ns
Cd24a	CD24a antigen	12484	18.84	16.73	15.11	1.24	0.45	ns
Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	64209	1.24	1.03	1.28	0.96	0.32	ns
Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)	22228	0.74	0.73	0.62	1.18	0.75	ns
Mrpl33	mitochondrial ribosomal protein L33	66845	0.60	0.65	1.24	0.48	-0.80	ns
Plk1	polo-like kinase 1 (Drosophila)	18817	1.03	0.90	1.18	0.86	0.12	ns
Prps1		19139	0.92	1.04	1.06	0.87	0.11	ns
Taf5l	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor	102162	0.54	0.44	0.36	1.49	0.54	ns
Mat2b	methionine adenosyltransferase II, beta	108645	1.95	1.54	2.13	0.91	-0.49	ns
Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	67264	4.78	5.19	2.89	1.65	0.78	ns
Atp5l	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	27425	4.64	3.79	3.40	1.36	0.81	ns
Sav1	salvador homolog 1 (Drosophila)	64010	2.21	1.97	2.20	1.00	0.07	ns
Ccnb1		268697	2.05	2.91	3.19	0.64	-0.36	ns
Psma2	proteasome (prosome, macropain) subunit, alpha type 2	19166	4.50	4.85	5.44	0.82	-0.27	ns
Anxa1	annexin A1	16952	16.83	14.34	8.82	1.90	0.81	ns
Dpp3	dipeptidylpeptidase 3	75221	1.24	1.12	0.97	1.27	0.99	***
Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	22631	13.42	11.49	12.21	1.09	0.55	ns
Bat1a	HLA-B-associated transcript 1A	53817	6.92	5.88	4.79	1.44	0.82	*
Tfam	transcription factor A, mitochondrial	21780	2.20	2.03	1.76	1.24	-0.02	ns
Gpaa1	GPI anchor attachment protein 1	14731	0.58	0.66	0.77	0.74	-0.22	ns
Grb7	growth factor receptor bound protein 7	14786	1.60	1.35	1.44	1.11	-0.22	ns
Usp10	ubiquitin specific peptidase 10	22224	1.47	1.63	1.09	1.34	0.50	ns
Tuba1c		22146	1.00	1.05	1.08	0.92	-0.38	ns
Prnp	prion protein	19122	1.28	1.13	1.77	0.72	-0.12	ns
Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	23950	2.87	2.87	3.58	0.80	-0.47	ns
EG432959		432959	1.18	1.40	1.87	0.63	-0.95	**
Rdx	radixin	19684	3.30	3.72	2.68	1.23	0.57	ns
2700060E02Rik	RIKEN cDNA 2700060E02 gene	68045	4.99	4.86	4.59	1.08	0.02	ns
Mbtps1	membrane-bound transcription factor peptidase, site 1	56453	1.85	1.90	1.43	1.29	0.49	ns
Gm2a	GM2 ganglioside activator protein	14667	1.20	1.21	1.97	0.60	-0.56	ns
Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha	108124	1.18	1.00	1.41	0.84	-0.31	ns
Lypla1	lysophospholipase 1	18777	0.73	0.78	0.80	0.91	-0.59	ns
Rpsa	ribosomal protein SA	16785	22.26	21.86	15.28	1.45	0.92	**
Hdac1	histone deacetylase 1	433759	2.22	2.41	2.86	0.77	-0.89	*
Bcl7b	B-cell CLL/lymphoma 7B	12054	0.47	0.47	0.56	0.83	-0.07	ns
Crk	v-crk sarcoma virus CT10 oncogene homolog (avian)	12928	3.22	2.90	2.35	1.36	0.85	*
Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	14555	0.49	0.54	0.96	0.50	-0.76	ns
Eef1b2	eukaryotic translation elongation factor 1 beta 2	55949	11.53	11.92	9.42	1.22	0.33	ns
Spcs1	signal peptidase complex subunit 1 homolog (S. cerevisiae)	69019	6.48	6.67	6.17	1.05	0.25	ns
Cdh1	cadherin 1	12550	10.11	11.01	8.19	1.23	0.03	ns
Psmb2	proteasome (prosome, macropain) subunit, beta type 2	26445	1.82	1.86	2.16	0.84	-0.36	ns
Cndp2	CNDP dipeptidase 2 (metallopeptidase M20 family)	66054	1.68	3.00	3.03	0.55	-0.17	ns
Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	56200	0.74	0.82	0.84	0.88	-0.59	ns
Gss	glutathione synthetase	14854	0.41	0.53	0.79	0.52	-0.69	ns
Tspan4	tetraspanin 4	64540	0.67	0.68	0.67	0.99	-0.35	ns
Pold2	polymerase (DNA directed), delta 2, regulatory subunit	18972	2.09	2.01	2.75	0.75	-0.50	ns
Arpc3	actin related protein 2/3 complex, subunit 3	56378	3.48	3.49	4.97	0.70	-0.77	ns
Plrg1	pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	53317	2.55	2.50	2.08	1.22	0.86	*
Ndufc1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	66377	5.54	5.63	5.03	1.10	0.06	ns
Hsd17b10	hydroxysteroid (17-beta) dehydrogenase 10	15108	1.70	1.93	2.53	0.67	0.00	ns
Uqcr	ubiquinol-cytochrome c reductase (6.4kD) subunit	66594	3.28	2.81	2.43	1.34	0.17	ns
Med10	mediator of RNA polymerase II transcription, subunit 10 homolog (NUT2, S. cerevisiae)	28077	1.28	1.85	2.22	0.57	-0.67	ns
Tnk2		51789	1.14	1.07	1.47	0.77	-0.69	ns
Mgst3	microsomal glutathione S-transferase 3	66447	1.86	1.87	1.40	1.32	0.83	*
Kctd20	potassium channel tetramerisation domain containing 20	66989	0.72	0.56	0.44	1.62	0.89	*
Rab6	RAB6, member RAS oncogene family	19346	2.52	2.57	3.11	0.81	-0.52	ns
Ap3m1	adaptor-related protein complex 3, mu 1 subunit	55946	0.77	0.69	0.74	1.03	-0.42	ns
Usp5	ubiquitin specific peptidase 5 (isopeptidase T)	22225	0.81	0.99	0.96	0.84	-0.11	ns
Tpp1	tripeptidyl peptidase I	12751	2.36	2.57	3.25	0.72	-0.94	**
Cdc2a	cell division cycle 2 homolog A (S. pombe)	12534	5.22	4.77	4.91	1.06	0.64	ns
Pycr2	pyrroline-5-carboxylate reductase family, member 2	69051	1.08	1.17	0.86	1.24	0.11	ns
Tmem128	transmembrane protein 128	66309	1.63	1.62	1.66	0.98	-0.61	ns
Adfp	adipose differentiation related protein	11520	1.97	2.02	4.91	0.40	-0.45	ns
Smoc1	SPARC related modular calcium binding 1	64075	0.92	0.18	0.08	11.12	0.69	ns
Cox4i1	cytochrome c oxidase subunit IV isoform 1	12857	10.92	11.02	7.68	1.42	0.80	ns

Myd116	myeloid differentiation primary response gene 116	17872	1.08	1.09	0.89	1.21	-0.12	ns
Adprh	ADP-ribosylarginine hydrolase	11544	0.53	0.51	1.08	0.49	-0.50	ns
Drg1	developmentally regulated GTP binding protein 1	13494	2.55	2.43	2.92	0.87	-0.11	ns
Tmem30a	transmembrane protein 30A	69981	1.70	1.45	1.27	1.33	0.87	*
Nbr1	neighbor of Brca1 gene 1	17966	3.80	3.56	3.32	1.14	0.81	ns
Tomm34	translocase of outer mitochondrial membrane 34	67145	1.41	1.18	1.30	1.08	-0.05	ns
Caprin1	cell cycle associated protein 1	53872	9.00	8.14	7.66	1.17	-0.18	ns
Asl	argininosuccinate lyase	109900	0.52	0.68	0.50	1.03	0.32	ns
Coro1b	coronin, actin binding protein 1B	23789	2.89	2.79	2.56	1.12	0.83	*
G6pdx	glucose-6-phosphate dehydrogenase X-linked	14381	0.99	0.93	1.97	0.50	-0.78	ns
Prss16	protease, serine, 16 (thymus)	54373	0.41	0.51	0.60	0.69	-0.43	ns
EG666609		666609	8.68	9.27	8.89	0.97	0.13	ns
Snrpg		68011	8.68	9.27	8.89	0.97	0.13	ns
Angel2	angel homolog 2 (Drosophila)	52477	1.21	1.29	1.00	1.21	0.29	ns
Ttc3	tetratricopeptide repeat domain 3	22129	7.49	6.71	6.54	1.14	0.49	ns
Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	56354	2.12	1.93	2.16	0.98	0.37	ns
Yap1	yes-associated protein 1	22601	2.46	1.85	0.91	2.69	0.94	**
Exosc7	exosome component 7	66446	0.92	1.11	1.01	0.92	0.30	ns
Pola2	polymerase (DNA directed), alpha 2	18969	1.80	1.95	1.30	1.37	0.85	*
Ulk1	Unc-51 like kinase 1 (C. elegans)	22241	0.83	0.63	0.83	0.99	-0.39	ns
Mrpl18	mitochondrial ribosomal protein L18	67681	1.94	1.83	1.75	1.10	0.58	ns
Wrnip1	Werner helicase interacting protein 1	78903	1.00	0.97	1.31	0.76	-0.33	ns
Pot1a	protection of telomeres 1A	101185	0.63	0.69	0.76	0.82	-0.45	ns
Mmp14	matrix metallopeptidase 14 (membrane-inserted)	17387	1.49	1.99	1.25	1.18	-0.14	ns
Slc15a4	solute carrier family 15, member 4	100561	0.47	0.47	0.57	0.83	-0.48	ns
Rbx1	ring-box 1	56438	6.04	6.42	6.77	0.89	-0.38	ns
1110002B05Rik	RIKEN cDNA 1110002B05 gene	104725	4.34	4.32	4.26	1.01	-0.42	ns
Rab9	RAB9, member RAS oncogene family	56382	1.30	1.33	1.90	0.68	-0.12	ns
Cldn7	claudin 7	53624	7.55	7.48	7.55	1.00	0.21	ns
Tmem131	transmembrane protein 131	56030	1.75	2.02	1.82	0.95	-0.43	ns
Tax1bp1	Tax1 (human T-cell leukemia virus type I) binding protein 1	52440	1.93	2.37	2.96	0.65	-0.86	*
Smarcd2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	83796	3.15	3.71	3.36	0.93	0.34	ns
Tln1	talin 1	21894	1.24	1.25	1.46	0.84	-0.28	ns
Lars	leucyl-tRNA synthetase	107045	1.48	1.96	1.64	0.90	0.15	ns
Eid1	EP300 interacting inhibitor of differentiation 1	58521	1.86	1.84	2.18	0.85	-0.29	ns
Ube4b	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)	63958	0.65	0.58	0.80	0.81	-0.55	ns
Wfs1	Wolfram syndrome 1 homolog (human)	22393	0.73	0.78	0.36	2.05	0.47	ns
Tsc22d4	TSC22 domain family 4	78829	1.16	1.11	1.10	1.05	-0.20	ns
2410016O06Rik	RIKEN cDNA 2410016O06 gene	71952	0.70	0.81	0.90	0.77	-0.49	ns
Rad1	RAD1 homolog (S. pombe)	19355	0.65	0.55	0.75	0.86	-0.19	ns
Wdr23	WD repeat domain 23	28199	3.14	2.98	2.37	1.32	0.25	ns
Pop4	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	66161	0.31	0.28	0.41	0.76	-0.74	ns
Tmed4	transmembrane emp24 protein transport domain containing 4	103694	2.11	1.85	2.75	0.76	-0.55	ns
Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	67130	4.51	4.21	4.01	1.12	0.29	ns
Rnf103	ring finger protein 103	22644	0.95	0.88	0.93	1.02	-0.38	ns
Irf1	interferon regulatory factor 1	16362	0.49	0.60	0.86	0.57	-0.81	*
Derl2	Der1-like domain family, member 2	116891	1.32	1.33	1.63	0.80	-0.20	ns
Psma3	proteasome (prosome, macropain) subunit, alpha type 3	19167	8.33	8.32	8.86	0.94	0.02	ns
Acp6	acid phosphatase 6, lysophosphatidic	66659	0.41	0.41	0.28	1.46	0.90	*
Vps28	vacuolar protein sorting 28 (yeast)	66914	3.29	3.43	4.51	0.73	-0.42	ns
Chkb	choline kinase beta	12651	1.30	1.21	0.95	1.36	0.92	*
Ak2	adenylate kinase 2	11637	1.09	1.29	1.36	0.80	-0.35	ns
Acvr1	activin A receptor, type 1	11477	0.44	0.40	0.40	1.10	0.21	ns
Thoc7	THO complex 7 homolog (Drosophila)	66231	2.72	2.85	3.11	0.87	-0.42	ns
4933434E20Rik	RIKEN cDNA 4933434E20 gene	99650	4.32	3.91	2.91	1.48	0.79	ns
Ykt6	YKT6 homolog (S. Cerevisiae)	56418	2.95	2.37	3.05	0.96	0.22	ns
Nipsnap1	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	18082	0.65	0.65	0.64	1.01	-0.23	ns
Ehbp1l1	EH domain binding protein 1-like 1	114601	0.38	0.36	0.28	1.36	0.88	*
Vars	valyl-tRNA synthetase	22321	1.84	1.68	1.17	1.57	0.84	*
Nap1l4	nucleosome assembly protein 1-like 4	17955	1.69	1.69	1.67	1.01	-0.22	ns
Psmd3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	22123	1.96	1.86	2.05	0.95	-0.18	ns
Nip7	nuclear import 7 homolog (S. cerevisiae)	66164	1.31	1.42	0.97	1.34	0.69	ns
Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	68198	2.36	2.54	2.84	0.83	-0.71	ns
Amd1	S-adenosylmethionine decarboxylase 1	11702	3.04	2.36	2.55	1.19	0.46	ns
Ggt1	gamma-glutamyltransferase 1	14598	0.26	0.29	0.48	0.54	-0.46	ns
Mrps5	mitochondrial ribosomal protein S5	77721	0.50	0.51	0.58	0.85	-0.40	ns
Pafah2	platelet-activating factor acetylhydrolase 2	100163	0.47	0.38	0.46	1.00	-0.49	ns
Ech1	enoyl coenzyme A hydratase 1, peroxisomal	51798	1.60	1.80	1.79	0.89	-0.60	ns
Psmd12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	66997	2.44	2.31	2.85	0.85	0.03	ns
Paip2	polyadenylate-binding protein-interacting protein 2	67869	3.52	3.58	3.48	1.01	0.57	ns
Tsta3	tissue specific transplantation antigen P35B	22122	1.42	1.35	1.95	0.72	-0.58	ns
Ing1	inhibitor of growth family, member 1	26356	1.58	2.08	1.88	0.83	0.19	ns
Ercc3	excision repair cross-complementing rodent repair deficiency, complementation group 3	13872	0.45	0.44	0.50	0.90	0.24	ns
Rps6ka4	ribosomal protein S6 kinase, polypeptide 4	56613	1.29	1.21	1.01	1.27	0.86	*
LOC633016		633016	7.58	7.60	7.75	0.97	-0.95	**
C1d	nuclear DNA binding protein	57316	2.37	2.42	2.76	0.86	-0.32	ns
Efhd1	EF hand domain containing 1	98363	1.64	1.61	2.12	0.77	-0.61	ns
Traf3ip2	Traf3 interacting protein 2	103213	0.32	0.29	0.31	1.03	-0.47	ns
Npc2	Niemann Pick type C2	67963	8.47	9.23	12.11	0.70	-0.50	ns
Tsn	translin	22099	2.26	2.52	1.70	1.33	0.44	ns
Timm22	translocase of inner mitochondrial membrane 22 homolog (yeast)	56322	0.93	0.86	0.81	1.15	0.60	ns
Tead2	TEA domain family member 2	21677	0.78	0.83	0.93	0.84	-0.69	ns
Brd7		26992	0.98	1.02	1.05	0.92	0.21	ns
LOC634327		634327	0.98	1.02	1.05	0.92	0.21	ns

Ssr4	signal sequence receptor, delta	20832	1.80	1.80	2.68	0.67	-0.59	ns
Kpnb1	karyopherin (importin) beta 1	16211	3.66	3.56	4.10	0.89	-0.73	ns
Pdcd10	programmed cell death 10	56426	3.78	3.64	3.64	1.03	-0.25	ns
Thbd	thrombomodulin	21824	0.14	0.21	0.33	0.42	-0.48	ns
Lmnb2	lamin B2	16907	0.31	0.41	0.26	1.22	0.19	ns
Tbcb	tubulin folding cofactor B	66411	2.05	2.37	2.32	0.88	-0.40	ns
Lsm3	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	67678	2.92	3.03	3.31	0.88	-0.06	ns
Ttc1	tetratricopeptide repeat domain 1	66827	1.17	1.14	1.17	0.99	0.03	ns
LOC638521		638521	1.06	1.18	1.39	0.76	-0.59	ns
Bccip	BRCA2 and CDKN1A interacting protein	66165	1.01	1.09	1.02	0.98	-0.01	ns
Slmo2	slowmo homolog 2 (Drosophila)	66390	0.99	1.11	1.36	0.73	-0.62	ns
Rassf3	Ras association (RalGDS/AF-6) domain family 3	192678	0.93	0.90	0.86	1.07	-0.39	ns
Tulp4	tubby like protein 4	68842	1.71	1.16	0.81	2.09	0.66	ns
Dpagt1	dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	13478	0.51	0.59	0.47	1.07	0.59	ns
Lbp	lipopolysaccharide binding protein	16803	0.57	0.73	1.08	0.52	-0.81	ns
Pla2g4a	phospholipase A2, group IVA (cytosolic, calcium-dependent)	18783	1.15	0.87	0.74	1.54	-0.14	ns
Flot1	flotillin 1	14251	0.73	0.61	0.39	1.84	0.82	*
Cib1	calcium and integrin binding 1 (calmyrin)	23991	0.65	0.69	1.15	0.57	-0.78	ns
Ppp1r11	protein phosphatase 1, regulatory (inhibitor) subunit 11	76497	1.53	1.23	1.18	1.29	0.89	*
Tmem115	transmembrane protein 115	56395	0.46	0.38	0.38	1.20	0.66	ns
Slc20a1	solute carrier family 20, member 1	20515	0.76	1.03	1.71	0.44	-0.64	ns
Cd8b1	CD8 antigen, beta chain 1	12526	2.21	2.16	2.12	1.04	0.38	ns
Gmfb	glia maturation factor, beta	63985	2.56	2.66	2.42	1.05	0.06	ns
Pafah1b1	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	18472	1.82	1.61	1.91	0.95	-0.14	ns
Glg1	golgi apparatus protein 1	20340	2.65	2.86	1.84	1.44	0.54	ns
Ctnnbl1	catenin, beta like 1	66642	1.44	1.45	1.28	1.12	0.58	ns
AA960436	expressed sequence AA960436	101985	0.42	0.39	0.40	1.03	0.16	ns
Rsrc1	arginine/serine-rich coiled-coil 1	66880	0.90	0.84	0.88	1.01	0.48	ns
Gtf2h4	general transcription factor II H, polypeptide 4	14885	1.11	1.08	0.84	1.31	0.85	*
Hspa14	heat shock protein 14	50497	1.56	1.55	1.49	1.05	0.30	ns
Tbc1d10a	TBC1 domain family, member 10a	103724	0.76	0.88	1.08	0.70	-0.72	ns
Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	66046	4.26	3.55	3.25	1.31	0.58	ns
Crtap	cartilage associated protein	56693	0.71	0.92	0.69	1.02	0.22	ns
Bex1	brain expressed gene 1	19716	14.23	17.14	17.93	0.79	0.07	ns
Cstf1	cleavage stimulation factor, 3' pre-RNA, subunit 1	67337	0.86	0.77	0.77	1.11	-0.12	ns
Sod2	superoxide dismutase 2, mitochondrial	20656	1.87	1.59	1.22	1.52	0.67	ns
Wwc2	WW, C2 and coiled-coil domain containing 2	52357	3.11	2.89	1.41	2.20	0.94	**
Sfn	stratifin	55948	0.45	0.51	0.46	0.97	0.41	ns
Ecm1	extracellular matrix protein 1	13601	0.23	0.30	0.67	0.34	-0.55	ns
Ccs	copper chaperone for superoxide dismutase	12460	0.95	0.83	0.50	1.87	0.98	***
Dhcr7	7-dehydrocholesterol reductase	13360	0.42	0.41	0.55	0.76	-0.85	*
Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal	20597	0.78	0.68	0.65	1.19	0.48	ns
Lsm4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	50783	2.33	2.44	2.20	1.06	0.65	ns
Tmem123	transmembrane protein 123	71929	1.45	1.39	0.54	2.65	0.73	ns
Golga2	golgi autoantigen, golgin subfamily a, 2	99412	0.94	1.11	1.05	0.89	-0.36	ns
Cdk5rap1	CDK5 regulatory subunit associated protein 1	66971	1.14	1.04	1.34	0.84	-0.29	ns
Pbk	PDZ binding kinase	52033	2.85	3.10	4.00	0.71	0.01	ns
Hps4	Hermansky-Pudlak syndrome 4 homolog (human)	192232	0.51	0.52	0.58	0.87	-0.38	ns
Sdhc	succinate dehydrogenase complex, subunit C, integral membrane protein	66052	2.34	2.08	1.94	1.20	0.04	ns
Psmb10	proteasome (prosome, macropain) subunit, beta type 10	19171	0.18	0.30	0.42	0.42	-0.77	ns
Prpf31	PRP31 pre-mRNA processing factor 31 homolog (yeast)	68988	0.38	0.49	0.57	0.66	-0.75	ns
Ralbp1	ralA binding protein 1	19765	1.80	1.52	1.11	1.61	0.93	**
Smc2	structural maintenance of chromosomes 2	14211	2.74	2.91	3.69	0.74	-0.52	ns
Med25	mediator of RNA polymerase II transcription, subunit 25 homolog (yeast)	75613	0.51	0.36	0.44	1.16	0.58	ns
Mtbp	Mdm2, transformed 3T3 cell double minute p53 binding protein	105837	0.66	0.57	0.72	0.91	-0.33	ns
Spata5	spermatogenesis associated 5	57815	0.65	0.69	0.49	1.33	0.24	ns
Mbtd1	mbt domain containing 1	103537	2.49	2.25	2.20	1.13	0.35	ns
Pcbp1	poly(rC) binding protein 1	23983	9.56	9.27	10.73	0.89	-0.39	ns
Ssna1	Sjogren's syndrome nuclear autoantigen 1	68475	1.63	1.72	1.48	1.10	-0.08	ns
Pef1	penta-EF hand domain containing 1	67898	0.56	0.47	0.71	0.78	-0.22	ns
Msl31	male-specific lethal-3 homolog 1 (Drosophila)	17692	1.16	1.32	1.62	0.71	0.07	ns
Wdr12	WD repeat domain 12	57750	0.59	0.52	0.37	1.58	0.35	ns
Man2a1	mannosidase 2, alpha 1	17158	0.17	0.51	0.15	1.19	0.43	ns
Pole	polymerase (DNA directed), epsilon	18973	1.59	1.69	1.72	0.92	0.28	ns
Nudt5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	53893	1.19	1.12	0.93	1.27	0.08	ns
Ift88	intraflagellar transport 88 homolog (Chlamydomonas)	21821	0.37	0.40	0.29	1.26	0.24	ns
Eed	embryonic ectoderm development	13626	1.32	1.38	1.66	0.80	-0.82	*
Lrp1	low density lipoprotein receptor-related protein 1	16971	0.36	0.45	0.24	1.47	0.12	ns
Cacnb3	calcium channel, voltage-dependent, beta 3 subunit	12297	1.04	1.00	1.30	0.79	-0.80	ns
Sart1	squamous cell carcinoma antigen recognized by T-cells 1	20227	1.02	1.00	0.72	1.41	0.92	**
Casp7	caspase 7	12369	0.41	0.76	0.95	0.43	-0.56	ns
Arhgdig	Rho GDP dissociation inhibitor (GDI) gamma	14570	1.01	0.93	0.56	1.79	0.84	*
Plcb3	phospholipase C, beta 3	18797	1.42	1.50	0.88	1.61	0.81	*
Mvd	mevalonate (diphospho) decarboxylase	192156	0.39	0.45	0.31	1.27	0.58	ns
Dmd	dystrophin, muscular dystrophy	13405	0.36	0.33	0.09	4.16	0.37	ns
Tob2	transducer of ERBB2, 2	57259	0.99	1.15	1.01	0.97	0.40	ns
Ube2e3	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast)	22193	5.06	4.31	2.79	1.80	0.57	ns
Pvrl3	poliovirus receptor-related 3	58998	1.01	0.33	0.01	129.91	0.69	ns
Rnf25	ring finger protein 25	57751	0.47	0.48	0.39	1.20	0.20	ns
Cox4nb	COX4 neighbor	18117	1.03	1.10	0.67	1.53	0.82	*
Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2	66849	2.90	2.80	2.63	1.10	0.35	ns
2900010M23Rik	RIKEN cDNA 2900010M23 gene	67267	3.36	3.25	2.27	1.47	0.96	**
Podxl	podocalyxin-like	27205	0.72	0.91	0.82	0.88	-0.51	ns
Kcnk1	potassium channel, subfamily K, member 1	16525	5.56	3.32	2.33	2.37	0.90	*
Ubqln4	ubiquilin 4	94232	2.10	2.62	1.75	1.20	0.14	ns
Rpl36al	ribosomal protein L36a-like	66483	12.98	12.47	13.15	0.98	-0.16	ns

Mrpl54	mitochondrial ribosomal protein L54	66047	0.92	0.83	0.80	1.13	-0.08 ns
Krit1	KRIT1, ankyrin repeat containing	79264	0.39	0.46	0.50	0.78	-0.92 *
Ier3ip1	immediate early response 3 interacting protein 1	66191	0.88	1.14	1.12	0.78	-0.27 ns
Lsm8	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	76522	3.08	3.48	4.20	0.73	-0.44 ns
H47	histocompatibility 47	109815	0.87	0.87	0.93	0.93	-0.32 ns
Zbtb22	zinc finger and BTB domain containing 22	81630	1.44	1.12	0.87	1.64	0.85 *
Ttrap	Traf and Tnf receptor associated protein	56196	2.44	2.12	2.87	0.85	-0.36 ns
Taf13	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor	99730	1.24	1.34	1.10	1.12	0.67 ns
Arid1a		93760	2.21	1.96	2.34	0.94	-0.60 ns
LOC675933		675933	2.21	1.96	2.34	0.94	-0.60 ns
Mcm3ap	minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	54387	0.94	0.85	0.90	1.04	-0.23 ns
Ccrn4l		12457	21.00	19.21	17.52	1.19	0.81 *
Cog6		67542	21.00	19.21	17.52	1.19	0.81 *
Sgip1		73094	21.00	19.21	17.52	1.19	0.81 *
Gcdh	glutaryl-Coenzyme A dehydrogenase	270076	0.31	0.42	0.24	1.31	0.55 ns
Lrrc40	leucine rich repeat containing 40	67144	1.67	1.98	1.56	1.06	0.07 ns
Cish	cytokine inducible SH2-containing protein	12700	0.25	0.31	0.39	0.63	-0.29 ns
Parg	poly (ADP-ribose) glycohydrolase	26430	1.08	1.10	1.19	0.91	-0.52 ns
Sept4	septin 4	18952	1.06	0.73	1.20	0.88	-0.06 ns
Hprt1	hypoxanthine guanine phosphoribosyl transferase 1	15452	2.19	2.33	5.32	0.41	-0.69 ns
Ssx2ip	synovial sarcoma, X breakpoint 2 interacting protein	99167	0.62	0.74	0.65	0.95	-0.23 ns
Galns	galactosamine (N-acetyl)-6-sulfate sulfatase	50917	0.36	0.36	0.26	1.39	0.21 ns
Nbn	nibrin	27354	0.43	0.34	0.45	0.94	-0.38 ns
Car2	carbonic anhydrase 2	12349	2.72	2.44	2.05	1.32	-0.30 ns
Pml	promyelocytic leukemia	18854	0.48	0.38	0.42	1.14	0.63 ns
Nrbf2		641340	0.70	0.68	0.73	0.95	-0.60 ns
Zfp68	zinc finger protein 68	24135	0.87	1.04	1.08	0.81	-0.86 *
Copg2	coatomer protein complex, subunit gamma 2	54160	1.01	0.84	1.26	0.80	-0.64 ns
Rad17	RAD17 homolog (S. pombe)	19356	0.78	1.01	1.46	0.53	-0.74 ns
Atad1	ATPase family, AAA domain containing 1	67979	1.21	1.25	1.21	1.00	-0.07 ns
Slc35b1	solute carrier family 35, member B1	110172	1.37	1.34	1.44	0.95	-0.18 ns
Atpif1	ATPase inhibitory factor 1	11983	3.43	3.67	4.83	0.71	-0.73 ns
Fth1	ferritin heavy chain 1	14319	12.05	12.49	11.42	1.05	0.42 ns
Ube2a	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	22209	1.30	1.32	2.72	0.47	-0.59 ns
Stoml2	stomatin (Epb7.2)-like 2	66592	1.07	1.19	1.25	0.85	-0.14 ns
Mcm2	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	17216	3.83	3.65	4.13	0.92	-0.52 ns
Sfrs4	splicing factor, arginine/serine-rich 4 (SRp75)	57317	1.93	1.85	2.21	0.87	-0.17 ns
Ciz1	CDKN1A interacting zinc finger protein 1	68379	0.96	0.91	0.72	1.32	0.16 ns
Taf10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	24075	2.87	2.64	3.64	0.78	-0.42 ns
Moap1	modulator of apoptosis 1	64113	1.12	1.09	1.36	0.82	-0.38 ns
Snx5	sorting nexin 5	69178	3.28	3.23	3.76	0.87	-0.37 ns
Elk3	ELK3, member of ETS oncogene family	13713	1.27	1.26	0.82	1.55	0.28 ns
Mrps12	mitochondrial ribosomal protein S12	24030	0.91	0.96	1.04	0.87	-0.33 ns
Nufip1	nuclear fragile X mental retardation protein interacting protein 1	27275	0.74	0.67	0.83	0.90	-0.24 ns
Nme2	expressed in non-metastatic cells 2, protein	18103	12.51	10.01	8.98	1.39	0.38 ns
Cse1l	chromosome segregation 1-like (S. cerevisiae)	110750	3.56	3.81	4.31	0.82	-0.77 ns
Mrpl2	mitochondrial ribosomal protein L2	27398	1.90	1.56	1.12	1.68	0.94 **
Hpcal1	hippocalcin-like 1	53602	3.29	3.11	4.61	0.71	-0.63 ns
Psmb6	proteasome (prosome, macropain) subunit, beta type 6	19175	3.72	3.66	4.21	0.88	-0.19 ns
Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2	18604	0.38	0.22	0.16	2.34	0.37 ns
Smc6	structural maintenance of chromosomes 6	67241	2.30	2.49	2.81	0.81	-0.43 ns
Dusp1	dual specificity phosphatase 1	19252	1.36	1.14	0.66	2.04	0.37 ns
Angpt2	angiopoietin 2	11601	2.44	1.24	0.21	11.33	0.40 ns
E2f6	E2F transcription factor 6	50496	0.41	0.51	0.60	0.68	-0.66 ns
Topors	topoisomerase I binding, arginine/serine-rich	106021	1.38	1.93	2.05	0.67	-0.46 ns
LOC670211		670211	14.46	13.16	10.51	1.37	0.97 **
Tor1b	torsin family 1, member B	30934	1.48	1.49	1.03	1.44	0.62 ns
Mrpl40	mitochondrial ribosomal protein L40	18100	1.66	1.39	1.88	0.88	-0.45 ns
Synj2bp	synaptojanin 2 binding protein	24071	2.66	2.61	2.56	1.03	-0.21 ns
Msra	methionine sulfoxide reductase A	110265	0.22	0.27	0.26	0.84	0.35 ns
Zdhhc12	zinc finger, DHHC domain containing 12	66220	0.28	0.31	0.42	0.66	-0.79 ns
Traf5	Tnf receptor-associated factor 5	22033	0.47	0.41	0.30	1.55	0.92 **
Tnfaip1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	21927	2.62	2.57	1.88	1.38	0.74 ns
Snrk	SNF related kinase	20623	0.68	0.69	0.93	0.73	-0.22 ns
Senp3	SUMO/sentrin specific peptidase 3	80886	2.01	2.22	2.24	0.89	-0.17 ns
Tmem9b	TMEM9 domain family, member B	56786	1.09	1.05	1.41	0.77	-0.67 ns
Scand1	SCAN domain-containing 1	19018	2.00	1.99	2.32	0.86	-0.41 ns
Mrps16	mitochondrial ribosomal protein S16	66242	1.53	1.50	1.48	1.03	-0.19 ns
Mapk13	mitogen activated protein kinase 13	26415	1.69	1.78	1.23	1.37	0.70 ns
Ocln	occludin	18260	1.66	1.84	2.33	0.71	-0.90 *
Sh2b1	SH2B adaptor protein 1	20399	0.47	0.36	0.45	1.05	0.15 ns
Zhx1	zinc fingers and homeoboxes protein 1	22770	1.74	1.44	1.45	1.20	0.26 ns
Mxd3	Max dimerization protein 3	17121	0.58	0.56	0.53	1.09	0.57 ns
Ube2l3	ubiquitin-conjugating enzyme E2L 3	22195	4.32	3.64	4.83	0.89	-0.46 ns
Tmem93	transmembrane protein 93	66048	1.20	1.26	1.38	0.86	-0.80 ns
Lgmn	legumain	19141	1.48	1.58	2.26	0.65	-0.87 *
Gtf2e2	general transcription factor II E, polypeptide 2 (beta subunit)	68153	1.65	1.78	2.66	0.62	-0.65 ns
Gata3	GATA binding protein 3	14462	2.84	2.81	1.60	1.76	0.53 ns
Klf2	Kruppel-like factor 2 (lung)	16598	0.32	0.27	0.11	2.89	0.60 ns
Dock7	dedicator of cytokinesis 7	67299	2.85	2.58	2.16	1.31	0.29 ns
Ncor2	nuclear receptor co-repressor 2	20602	1.15	0.99	0.97	1.17	0.44 ns
Akr1b8	aldo-keto reductase family 1, member B8	14187	0.17	0.23	0.78	0.22	-0.32 ns
Pigf	phosphatidylinositol glycan anchor biosynthesis, class F	18701	1.49	1.25	1.09	1.36	0.95 **
Nme3	expressed in non-metastatic cells 3	79059	0.76	0.75	0.55	1.37	0.05 ns

Cdh16	cadherin 16	12556	12.06	11.37	10.20	1.18	0.46	ns
Thop1	thimet oligopeptidase 1	50492	0.95	0.90	0.65	1.45	0.58	ns
Mrpl39	mitochondrial ribosomal protein L39	27393	3.97	3.54	4.38	0.90	-0.67	ns
Smarcd1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	83797	0.51	0.46	0.35	1.47	0.85	*
Mafg	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	17134	0.69	0.65	0.77	0.90	0.15	ns
Mrps9	mitochondrial ribosomal protein S9	69527	0.55	0.52	0.54	1.02	0.59	ns
Prkra	protein kinase, interferon inducible double stranded RNA dependent activator	23992	0.58	0.56	0.36	1.61	0.37	ns
Hoxa5	homeo box A5	15402	0.72	0.74	0.64	1.12	-0.20	ns
Hdac6		15185	1.32	1.41	2.61	0.50	-0.10	ns
F2rl1	coagulation factor II (thrombin) receptor-like 1	14063	0.54	1.04	1.98	0.27	-0.70	ns
Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	67273	2.86	2.90	2.29	1.24	0.42	ns
Stx12	syntaxin 12	100226	1.35	1.43	1.72	0.79	-0.64	ns
Slc35b3	solute carrier family 35, member B3	108652	0.52	0.51	0.62	0.84	-0.35	ns
Rpa3	replication protein A3	68240	1.94	2.01	2.60	0.75	-0.56	ns
Usp25	ubiquitin specific peptidase 25	30940	0.90	0.91	1.76	0.51	-0.84	*
Nrp1	neuropilin 1	18186	2.25	1.14	0.53	4.19	0.90	*
Kif3c	kinesin family member 3C	16570	0.47	0.51	0.57	0.82	-0.98	***
2810004N23Rik	RIKEN cDNA 2810004N23 gene	66523	0.85	0.88	0.42	2.03	0.72	ns
Rag1ap1	recombination activating gene 1 activating protein 1	19729	0.80	0.91	0.77	1.03	-0.19	ns
Il1r1	interleukin 1 receptor, type I	16177	0.76	1.00	0.95	0.80	-0.62	ns
Blm	Bloom syndrome homolog (human)	12144	0.46	0.59	0.74	0.61	-0.42	ns
Nrip3	nuclear receptor interacting protein 3	78593	0.45	0.41	0.17	2.68	0.37	ns
Stard10	START domain containing 10	56018	1.72	1.76	2.31	0.74	-0.85	*
Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	17993	1.02	1.42	2.00	0.51	-0.73	ns
Cxxc5	CXXC finger 5	67393	1.93	1.87	1.59	1.21	0.36	ns
Plscr2	phospholipid scramblase 2	18828	0.30	0.42	0.46	0.64	-0.88	*
Nfyc	nuclear transcription factor-Y gamma	18046	1.32	1.35	1.24	1.05	0.52	ns
Nipsnap3a	nipsnap homolog 3A (C. elegans)	66536	0.33	0.49	0.56	0.60	-0.89	*
Sult1d1	sulfotransferase family 1D, member 1	53315	0.93	0.20	0.14	6.43	0.13	ns
Tfip11	tuftelin interacting protein 11	54723	0.51	0.58	0.55	0.93	-0.49	ns
Ngef	neuronal guanine nucleotide exchange factor	53972	0.31	0.39	0.25	1.22	0.33	ns
Muted	muted	17828	0.61	0.74	0.63	0.97	0.10	ns
Dusp22	dual specificity phosphatase 22	105352	0.54	0.63	0.74	0.74	-0.85	*
Acadl	acyl-Coenzyme A dehydrogenase, long-chain	11363	3.28	2.85	3.11	1.05	-0.31	ns
Atg3	autophagy-related 3 (yeast)	67841	2.09	1.99	1.88	1.11	0.00	ns
D10Jhu81e	DNA segment, Chr 10, Johns Hopkins University 81 expressed	28295	1.32	1.19	1.09	1.21	-0.23	ns
Ivd	isovaleryl coenzyme A dehydrogenase	56357	0.57	0.48	0.54	1.05	-0.05	ns
Phlda3	pleckstrin homology-like domain, family A, member 3	27280	0.74	0.68	0.91	0.82	-0.80	ns
Vti1b	vesicle transport through interaction with t-SNAREs 1B homolog	53612	3.74	4.01	4.89	0.76	-0.34	ns
Mrpl46	mitochondrial ribosomal protein L46	67308	0.58	0.57	0.55	1.06	0.46	ns
Btg3		12228	1.36	1.13	1.40	0.96	0.24	ns
Tulp3	tubby-like protein 3	22158	0.61	0.57	0.39	1.54	0.22	ns
Lactb	lactamase, beta	80907	0.55	0.50	0.55	1.00	0.34	ns
Pfn1	profilin 1	18643	10.37	9.51	9.45	1.09	0.69	ns
Akap1	A kinase (PRKA) anchor protein 1	11640	0.90	0.83	0.95	0.94	-0.55	ns
Plscr3	phospholipid scramblase 3	70310	1.72	1.78	1.88	0.91	-0.49	ns
Rpp21	ribonuclease P 21 subunit (human)	67676	0.80	0.72	0.59	1.35	0.94	**
Nes	nestin	18008	0.63	0.75	0.44	1.41	0.57	ns
Ezh1	enhancer of zeste homolog 1 (Drosophila)	14055	1.04	0.97	1.05	0.98	0.39	ns
Hexa	hexosaminidase A	15211	0.78	0.60	1.03	0.76	-0.61	ns
Ifit3	interferon-induced protein with tetratricopeptide repeats 3	15959	0.42	0.24	1.11	0.38	-0.53	ns
Ifnar1	interferon (alpha and beta) receptor 1	15975	0.66	0.68	0.75	0.87	-0.77	ns
Rhou	ras homolog gene family, member U	69581	1.15	1.18	0.61	1.89	0.49	ns
Sephs2	selenophosphate synthetase 2	20768	0.77	0.96	1.06	0.72	-0.66	ns
Trip6	thyroid hormone receptor interactor 6	22051	2.60	2.50	2.06	1.26	0.77	ns
Naga	N-acetyl galactosaminidase, alpha	17939	1.08	1.01	1.05	1.02	-0.14	ns
Eef1e1	eukaryotic translation elongation factor 1 epsilon 1	66143	1.36	1.38	1.70	0.79	-0.66	ns
Afg3l1	AFG3(ATPase family gene 3)-like 1 (yeast)	114896	0.69	0.73	0.56	1.23	0.58	ns
Rab4a	RAB4A, member RAS oncogene family	19341	0.46	0.35	0.21	2.21	0.64	ns
Dnmt3b	DNA methyltransferase 3B	13436	0.35	0.54	0.38	0.91	0.19	ns
Oxct1	3-oxoacid CoA transferase 1	67041	3.65	4.44	2.59	1.40	0.28	ns
LOC631653		631653	0.51	0.48	0.67	0.75	0.01	ns
Prim1	DNA primase, p49 subunit	19075	6.04	5.48	4.07	1.47	0.77	ns
Sec22b	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	20333	1.40	1.24	1.13	1.23	0.86	*
Arhgef7	Rho guanine nucleotide exchange factor (GEF7)	54126	0.79	0.82	0.80	0.98	0.40	ns
Zfp148	zinc finger protein 148	22661	1.67	1.49	1.61	1.03	-0.02	ns
N6amt2	N-6 adenine-specific DNA methyltransferase 2 (putative)	68043	0.70	0.78	0.73	0.94	0.17	ns
Exdl2	exonuclease 3''-5'' domain-like 2	97827	0.36	0.30	0.38	0.93	0.16	ns
St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	54613	1.44	1.05	0.62	2.31	0.24	ns
Sh3d19	SH3 domain protein D19	27059	2.52	2.98	2.36	1.06	-0.38	ns
Phf10	PHD finger protein 10	72057	2.52	2.80	2.14	1.17	0.65	ns
Yes1	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	22612	0.55	0.62	0.75	0.72	-0.45	ns
Cldn8	claudin 8	54420	6.34	4.68	2.65	2.38	-0.09	ns
Ctf1	cardiotrophin 1	13019	0.50	0.40	0.47	1.05	-0.18	ns
Vps54	vacuolar protein sorting 54 (yeast)	245944	1.53	1.28	1.64	0.93	-0.07	ns
Txnrd2	thioredoxin reductase 2	26462	0.47	0.35	0.34	1.36	0.62	ns
Lrba	LPS-responsive beige-like anchor	80877	4.37	4.08	2.30	1.89	0.60	ns
Pard6a	par-6 (partitioning defective 6,) homolog alpha (C. elegans)	56513	0.32	0.37	0.40	0.82	-0.13	ns
Fdx1	ferredoxin 1	14148	1.46	1.11	1.09	1.34	0.68	ns
Socs2	suppressor of cytokine signaling 2	216233	0.63	0.58	0.80	0.79	-0.56	ns
Rhob	ras homolog gene family, member B	11852	5.64	5.14	4.78	1.17	0.45	ns
Grb2	growth factor receptor bound protein 2	14784	0.82	0.78	0.93	0.88	0.16	ns
Gpbp1l1	GC-rich promoter binding protein 1-like 1	77110	0.59	0.55	0.68	0.86	-0.18	ns
Dbt	dihydrolipoamide branched chain transacylase E2	13171	0.51	0.47	0.27	1.84	0.13	ns

Tnfaip8l1	tumor necrosis factor, alpha-induced protein 8-like 1	66443	0.56	0.44	0.35	1.58	0.87 *
Sprr1a	small proline-rich protein 1A	20753	0.41	0.52	1.40	0.29	-0.85 *
Sf3b1	splicing factor 3b, subunit 1	81898	5.30	4.87	4.70	1.12	0.27 ns
2310008M10Rik	RIKEN cDNA 2310008M10 gene	66357	2.68	2.76	2.73	0.98	0.13 ns
Fblim1	filamin binding LIM protein 1	74202	0.56	0.49	0.54	1.02	-0.03 ns
Gna11	guanine nucleotide binding protein, alpha 11	14672	2.15	1.84	1.92	1.11	0.09 ns
Cav1	caveolin, caveolae protein 1	12389	2.54	2.43	3.44	0.73	-0.02 ns
Phtf1	putative homeodomain transcription factor 1	18685	0.98	1.07	0.85	1.15	-0.18 ns
Pctk3	PCTAIRE-motif protein kinase 3	18557	0.62	0.66	0.53	1.17	-0.17 ns
Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	12579	1.02	0.87	0.96	1.05	-0.20 ns
Pop7	processing of precursor 7, ribonuclease P family, (S. cerevisiae)	74097	0.60	0.70	0.68	0.88	-0.70 ns
Sigirr	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	24058	0.45	0.53	0.62	0.71	-0.67 ns
Cd68	CD68 antigen	12514	0.15	0.25	0.47	0.33	-0.77 ns
S100a14	S100 calcium binding protein A14	66166	1.44	2.13	2.63	0.54	-0.64 ns
Epb4.1l4a	erythrocyte protein band 4.1-like 4a	13824	1.67	1.66	0.94	1.77	0.56 ns
Ttk	Ttk protein kinase	22137	0.60	0.65	0.72	0.83	0.29 ns
Pdgfa	platelet derived growth factor, alpha	18590	0.78	0.95	0.97	0.80	-0.83 *
Midn	midnolin	59090	0.97	0.75	0.70	1.39	0.18 ns
BC003266	cDNA sequence BC003266	80284	0.37	0.44	0.40	0.94	0.29 ns
Mrps25	mitochondrial ribosomal protein S25	64658	0.83	0.90	1.12	0.74	-0.43 ns
EG619900		619900	25.70	24.34	21.73	1.18	0.65 ns
EG667035		667035	25.70	24.34	21.73	1.18	0.65 ns
LOC639567		639567	25.70	24.34	21.73	1.18	0.65 ns
Rps27a		78294	25.70	24.34	21.73	1.18	0.65 ns
Muc1	mucin 1, transmembrane	17829	1.15	2.47	1.76	0.65	-0.60 ns
Nup155	nucleoporin 155	170762	1.86	1.69	1.92	0.96	-0.08 ns
Sema4g	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	26456	0.72	0.66	0.17	4.24	-0.28 ns
Kif20a	kinesin family member 20A	19348	0.68	0.77	0.96	0.71	0.14 ns
Bpnt1	bisphosphate 3'-nucleotidase 1	23827	0.88	0.86	0.79	1.11	-0.25 ns
Lage3	L antigen family, member 3	66192	0.90	0.93	1.31	0.68	-0.41 ns
Casp8ap2	caspase 8 associated protein 2	26885	1.64	1.74	2.09	0.78	-0.38 ns
Cdkl2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	53886	0.34	0.40	0.37	0.91	0.22 ns
Rps19	ribosomal protein S19	20085	12.06	12.45	10.83	1.11	0.20 ns
Prcc	papillary renal cell carcinoma (translocation-associated)	94315	0.40	0.43	0.33	1.19	0.69 ns
Spp1	secreted phosphoprotein 1	20750	1.83	2.33	6.25	0.29	-0.79 ns
Rpl15	ribosomal protein L15	66480	18.96	18.30	16.44	1.15	0.55 ns
Rab11a	RAB11a, member RAS oncogene family	53869	3.39	2.76	3.40	0.99	-0.22 ns
D11Wsu99e	DNA segment, Chr 11, Wayne State University 99, expressed	28081	1.11	1.01	1.15	0.96	0.36 ns
Hebp2	heme binding protein 2	56016	0.64	0.75	0.50	1.27	-0.23 ns
Eif2ak3	eukaryotic translation initiation factor 2 alpha kinase 3	13666	0.83	0.83	0.92	0.90	-0.78 ns
Nrtn	neurturin	18188	0.43	0.35	0.16	2.72	0.96 **
Mapk12	mitogen-activated protein kinase 12	29857	1.54	1.49	1.18	1.29	0.87 *
B2m	beta-2 microglobulin	12010	2.35	2.39	5.17	0.45	-0.20 ns
Dpysl5	dihydropyrimidinase-like 5	65254	0.51	0.46	0.32	1.62	0.72 ns
Dcbld1	discoidin, CUB and LCCL domain containing 1	66686	0.51	0.48	0.21	2.41	0.57 ns
Sap30bp	SAP30 binding protein	57230	0.32	0.39	0.49	0.65	-0.29 ns
Abca2	ATP-binding cassette, sub-family A (ABC1), member 2	11305	0.47	0.48	0.31	1.52	0.67 ns
Sesn3	sestrin 3	75747	0.63	0.49	0.32	1.94	0.66 ns
Zfpm2	zinc finger protein, multitype 2	22762	1.09	0.77	1.13	0.96	-0.06 ns
LOC674810		674810	26.40	25.49	20.42	1.29	0.84 *
Rpl3		27367	26.40	25.49	20.42	1.29	0.84 *
Ly75	lymphocyte antigen 75	17076	0.32	0.37	0.33	0.96	-0.41 ns
Sf3a1	splicing factor 3a, subunit 1	67465	0.99	0.99	1.26	0.78	-0.70 ns
Timp3	tissue inhibitor of metalloproteinase 3	21859	1.14	0.91	1.74	0.65	-0.71 ns
D10Ertd641e	DNA segment, Chr 10, ERATO Doi 641, expressed	52717	1.53	1.31	1.27	1.20	0.21 ns
Ptplb	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	70757	1.79	1.46	1.77	1.01	0.02 ns
Sin3a	transcriptional regulator, SIN3A (yeast)	20466	1.27	1.02	1.07	1.17	0.75 ns
Ccdc34	coiled-coil domain containing 34	68201	1.06	0.75	1.09	0.96	0.08 ns
Riok1	RIO kinase 1 (yeast)	71340	0.57	0.58	0.58	0.96	0.01 ns
Mpp6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	56524	1.16	1.42	1.53	0.76	-0.23 ns
Nudt1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	17766	1.28	1.38	1.37	0.93	-0.22 ns
Zmat3	zinc finger matrin type 3	22401	0.64	0.66	0.94	0.68	-0.76 ns
Eps15l1	epidermal growth factor receptor pathway substrate 15-like 1	13859	0.56	0.40	0.55	1.01	0.20 ns
2310030G06Rik	RIKEN cDNA 2310030G06 gene	66952	0.72	0.54	0.62	1.16	0.47 ns
Mink1	misshapen-like kinase 1 (zebrafish)	50932	0.53	0.46	0.67	0.79	-0.67 ns
Atf3	activating transcription factor 3	11910	0.46	0.68	0.40	1.13	0.19 ns
Nicn1	nicolin 1	66257	0.38	0.52	0.40	0.94	0.41 ns
Adssl1	adenylosuccinate synthetase like 1	11565	0.44	0.73	0.57	0.78	-0.07 ns
Hoxb2	homeo box B2	103889	0.98	0.66	0.59	1.66	0.45 ns
1810046J19Rik	RIKEN cDNA 1810046J19 gene	103742	1.72	1.59	2.13	0.80	-0.64 ns
Zfp53	zinc finger protein 53	24132	0.73	0.67	0.39	1.88	0.83 *
Chd1l	chromodomain helicase DNA binding protein 1-like	68058	0.89	1.00	1.08	0.82	-0.69 ns
Dock8	dedicator of cytokinesis 8	76088	0.50	0.56	0.12	4.26	0.59 ns
Plek2	pleckstrin 2	27260	0.42	0.52	0.61	0.68	-0.36 ns
Fkbp1b	FK506 binding protein 1b	14226	0.51	0.49	0.42	1.20	0.66 ns
B4galt3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	57370	0.77	0.73	0.69	1.10	-0.19 ns
EG667759		667759	23.06	20.36	17.95	1.28	0.97 **
D6Wsu163e	DNA segment, Chr 6, Wayne State University 163, expressed	28040	0.61	0.61	0.64	0.95	-0.44 ns
Dpm1	dolichol-phosphate (beta-D) mannosyltransferase 1	13480	0.90	0.82	1.04	0.86	-0.71 ns
Klf7	Kruppel-like factor 7 (ubiquitous)	93691	1.13	1.17	0.78	1.45	0.12 ns
Wbp1	WW domain binding protein 1	22377	1.14	1.16	1.43	0.79	-0.58 ns
Mfap1a	microfibrillar-associated protein 1A	67532	2.67	2.20	1.58	1.68	0.84 *
Ccdc59	coiled-coil domain containing 59	52713	0.37	0.35	0.30	1.22	0.57 ns
Med9	mediator of RNA polymerase II transcription, subunit 9 homolog (yeast)	192191	0.52	0.55	0.76	0.68	-0.57 ns
Bst1	bone marrow stromal cell antigen 1	12182	0.25	0.61	1.86	0.14	-0.73 ns

Rage	renal tumor antigen	26448	0.61	0.61	0.54	1.13	-0.24	ns
Slc25a13	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13	50799	1.20	0.79	0.86	1.38	-0.08	ns
Polk	polymerase (DNA directed), kappa	27015	0.36	0.49	0.74	0.48	-0.91	*
Ripk1	receptor (TNFRSF)-interacting serine-threonine kinase 1	19766	0.71	0.67	0.93	0.76	-0.59	ns
Mbd4	methyl-CpG binding domain protein 4	17193	0.44	0.42	0.35	1.22	-0.11	ns
Card10	caspase recruitment domain family, member 10	105844	1.70	1.68	1.44	1.18	-0.13	ns
Hoxa7	homeo box A7	15404	0.22	0.24	0.28	0.80	-0.70	ns
Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	66656	7.26	7.70	6.70	1.08	0.55	ns
Ssbp4	single stranded DNA binding protein 4	76900	0.81	0.88	0.90	0.90	-0.72	ns
Gadd45a	growth arrest and DNA-damage-inducible 45 alpha	13197	0.93	1.21	0.97	0.96	-0.07	ns
Bcl7c	B-cell CLL/lymphoma 7C	12055	0.67	0.68	0.86	0.78	-0.83	*
Gdpd3	glycerophosphodiester phosphodiesterase domain containing 3	68616	0.94	0.91	0.87	1.07	-0.22	ns
LOC635918		635918	0.23	0.39	0.28	0.82	-0.39	ns
Zfp617	zinc finger protein 617	170938	0.79	0.87	0.93	0.85	-0.81	*
C920025E04Rik		667803	0.44	0.43	0.98	0.45	-0.53	ns
H2-T23		15040	0.44	0.43	0.98	0.45	-0.53	ns
Gstp1	glutathione S-transferase, pi 1	14870	10.80	10.67	9.51	1.13	0.73	ns
Sh3yl1	Sh3 domain YSC-like 1	24057	2.29	2.32	2.56	0.89	-0.55	ns
AI314976		106821	0.66	0.67	0.47	1.39	0.50	ns
Golga3	golgi autoantigen, golgin subfamily a, 3	269682	0.77	0.78	0.78	0.98	-0.20	ns
2900092E17Rik	RIKEN cDNA 2900092E17 gene	67278	0.60	0.70	0.72	0.84	-0.18	ns
Atp6ap1	ATPase, H+ transporting, lysosomal accessory protein 1	54411	1.37	1.67	3.07	0.45	-0.70	ns
Txnrd3	thioredoxin reductase 3	232223	0.38	0.49	0.38	0.98	-0.42	ns
Stard7	START domain containing 7	99138	3.38	2.85	2.36	1.42	0.59	ns
Nt5c3l	5'-nucleotidase, cytosolic III-like	68106	0.53	0.57	0.56	0.93	0.28	ns
Btf3	basic transcription factor 3	218490	6.19	7.45	9.01	0.68	-0.90	*
Coro1c	coronin, actin binding protein 1C	23790	0.69	0.95	1.09	0.63	-0.52	ns
Rnf20	ring finger protein 20	109331	0.45	0.67	0.73	0.62	-0.64	ns
Fnip1	folliculin interacting protein 1	216742	0.64	0.68	1.40	0.46	-0.85	*
Pdcd6ip	programmed cell death 6 interacting protein	18571	1.28	1.37	1.52	0.84	0.01	ns
Stx5a	syntaxin 5A	56389	3.65	3.39	2.55	1.42	0.74	ns
Scp2	sterol carrier protein 2, liver	20280	1.70	1.96	2.63	0.65	-0.84	*
Mfn1	mitofusin 1	67414	1.11	1.09	0.98	1.12	-0.01	ns
C330027C09Rik	RIKEN cDNA C330027C09 gene	224171	1.36	1.41	2.17	0.62	-0.65	ns
Chek1	checkpoint kinase 1 homolog (S. pombe)	12649	1.39	1.47	1.37	1.01	0.58	ns
Atp6v1e1	VATPase, H+ transporting, lysosomal V1 subunit E1	11973	2.33	2.61	3.17	0.73	-0.68	ns
5730472N09Rik	RIKEN cDNA 5730472N09 gene	108958	0.80	0.71	0.53	1.51	0.15	ns
D8Ertd738e	DNA segment, Chr 8, ERATO Doi 738, expressed	101966	2.44	2.43	2.77	0.88	-0.08	ns
Bbs4	Bardet-Biedl syndrome 4 homolog (human)	102774	0.24	0.24	0.17	1.41	0.64	ns
Tfb1m	transcription factor B1, mitochondrial	224481	0.47	0.42	0.36	1.28	0.52	ns
Pkp2	plakophilin 2	67451	2.44	2.39	2.68	0.91	-0.10	ns
Phf7	PHD finger protein 7	71838	0.25	0.30	0.43	0.58	-0.57	ns
Ssbp2	single-stranded DNA binding protein 2	66970	0.25	0.20	0.47	0.53	-0.59	ns
Memo1		76890	1.00	0.97	0.58	1.71	0.64	ns
Casp3	caspase 3	12367	1.79	1.89	1.80	0.99	0.44	ns
Kif3a	kinesin family member 3A	16568	0.58	0.80	0.91	0.63	-0.90	*
Ephb4	Eph receptor B4	13846	0.49	0.52	0.45	1.09	0.50	ns
Fbxl6	F-box and leucine-rich repeat protein 6	30840	0.34	0.37	0.47	0.73	-0.83	*
Ehd4	EH-domain containing 4	98878	1.28	1.18	1.29	0.99	-0.09	ns
Uchl3		50933	1.47	1.75	2.08	0.71	-0.71	ns
Uchl4		93841	1.47	1.75	2.08	0.71	-0.71	ns
Nek4	NIMA (never in mitosis gene a)-related expressed kinase 4	23955	0.37	0.38	0.38	0.95	-0.62	ns
H2-T22		15039	0.72	0.86	0.91	0.79	0.09	ns
H2-T9		15051	0.72	0.86	0.91	0.79	0.09	ns
Kifc1		16580	0.58	0.42	0.32	1.83	0.78	ns
Ociad1	OCIA domain containing 1	68095	2.86	2.78	2.81	1.01	-0.02	ns
Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	16206	0.31	0.34	0.44	0.71	-0.82	*
Mtcp1	mature T-cell proliferation 1	17763	0.31	0.26	0.58	0.53	-0.35	ns
Dynlt3	dynein light chain Tctex-type 3	67117	2.09	2.15	2.97	0.70	0.04	ns
Ssr2	signal sequence receptor, beta	66256	1.66	2.00	2.07	0.80	-0.79	ns
Dnaja3	DnaJ (Hsp40) homolog, subfamily A, member 3	83945	1.28	1.58	1.98	0.64	-0.94	**
Eif2b4	eukaryotic translation initiation factor 2B, subunit 4 delta	13667	1.15	1.05	1.06	1.08	0.38	ns
Ilk	integrin linked kinase	16202	2.03	1.68	1.64	1.23	0.89	*
Sec61a2	Sec61, alpha subunit 2 (S. cerevisiae)	57743	0.66	0.72	0.55	1.19	0.78	ns
Nfkbil1	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	18038	0.46	0.47	0.34	1.36	0.74	ns
Sim1	single-minded homolog 1 (Drosophila)	20464	0.72	0.53	0.56	1.28	-0.06	ns
Acot10		64833	1.22	1.50	2.20	0.55	-0.21	ns
Acot9		56360	1.22	1.50	2.20	0.55	-0.21	ns
BC018101	cDNA sequence BC018101	449000	0.62	0.71	0.65	0.95	0.42	ns
Hsd17b12	hydroxysteroid (17-beta) dehydrogenase 12	56348	3.22	2.56	2.81	1.14	0.38	ns
Ywhag	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	22628	4.77	4.77	4.84	0.98	-0.31	ns
Ubqln2	ubiquilin 2	54609	3.49	4.02	3.96	0.88	0.24	ns
Gtpbp1	GTP binding protein 1	14904	0.62	0.67	0.76	0.80	-0.31	ns
Sufu	suppressor of fused homolog (Drosophila)	24069	0.62	0.66	0.60	1.02	0.38	ns
B3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	53625	1.65	1.42	1.55	1.06	-0.19	ns
Lancl2	LanC (bacterial lantibiotic synthetase component C)-like 2	71835	1.48	1.65	1.42	1.04	0.48	ns
Aff4	AF4/FMR2 family, member 4	93736	2.94	2.79	3.88	0.75	-0.80	ns
Stat1	signal transducer and activator of transcription 1	20846	0.26	0.29	0.71	0.37	-0.82	*
Fzd7	frizzled homolog 7 (Drosophila)	14369	0.23	0.30	0.33	0.69	-0.63	ns
Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	269951	2.34	2.15	2.10	1.11	0.53	ns
Kif2a	Kinesin family member 2A	16563	0.87	1.14	1.08	0.80	-0.59	ns
Add1	adducin 1 (alpha)	11518	3.33	3.44	3.29	1.01	-0.17	ns
Maged1	melanoma antigen, family D, 1	94275	1.23	1.36	1.50	0.82	-0.44	ns

Ubr1	ubiquitin protein ligase E3 component n-recognin 1	22222	0.97	0.73	0.55	1.75	0.80	ns
1810034K20Rik	RIKEN cDNA 1810034K20 gene	67881	0.49	0.57	0.64	0.77	-0.79	ns
Pak1	p21 (CDKN1A)-activated kinase 1	18479	0.26	0.27	0.06	4.16	0.26	ns
Ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)	192195	1.27	1.48	1.33	0.95	-0.48	ns
Zfp101	zinc finger protein 101	22643	0.60	0.63	0.51	1.16	0.61	ns
Gba	glucosidase, beta, acid	14466	1.27	1.38	1.25	1.01	0.06	ns
Amfr	autocrine motility factor receptor	23802	1.46	1.84	2.58	0.56	-0.69	ns
Adam10	a disintegrin and metallopeptidase domain 10	11487	0.55	0.44	0.48	1.13	0.02	ns
Adh7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	11529	0.16	0.86	0.69	0.23	-0.53	ns
Nudt8	nudix (nucleoside diphosphate linked moiety X)-type motif 8	66387	0.58	0.63	0.51	1.12	0.29	ns
Tcf3	transcription factor 3	21415	1.85	1.39	1.28	1.43	0.34	ns
Socs6	suppressor of cytokine signaling 6	54607	0.61	0.55	0.65	0.93	0.25	ns
Bspry	B-box and SPRY domain containing	192120	0.57	0.68	0.61	0.93	0.23	ns
Serpinb6a	serine (or cysteine) peptidase inhibitor, clade B, member 6a	20719	4.32	3.64	4.60	0.93	0.17	ns
Cdkn2a	cyclin-dependent kinase inhibitor 2A	12578	0.48	0.40	0.35	1.37	0.17	ns
Ppp1cc		19047	12.23	11.51	11.34	1.07	0.69	ns
Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	14683	11.55	10.51	11.26	1.02	0.27	ns
Galt	galactose-1-phosphate uridyl transferase	14430	0.58	0.59	0.45	1.29	-0.13	ns
Hoxd4	homeo box D4	15436	0.38	0.27	0.11	3.40	0.65	ns
Map4k2	mitogen activated protein kinase kinase kinase kinase 2	26412	0.35	0.44	0.34	1.03	-0.01	ns
Chka	choline kinase alpha	12660	2.91	3.02	1.47	1.96	0.61	ns
Ube2f	ubiquitin-conjugating enzyme E2F (putative)	67921	1.01	0.96	0.76	1.32	0.08	ns
Scin	scinderin	20259	7.39	6.96	5.62	1.31	0.21	ns
Avpr2	arginine vasopressin receptor 2	12000	1.33	1.28	1.32	1.00	0.25	ns
Gata2	GATA binding protein 2	14461	0.31	0.37	0.07	4.19	0.66	ns
Capg	capping protein (actin filament), gelsolin-like	12332	3.52	4.74	5.59	0.63	-0.78	ns
Mxi1	Max interacting protein 1	17859	2.16	2.09	2.06	1.05	-0.18	ns
Kpna3	karyopherin (importin) alpha 3	16648	1.42	1.14	1.54	0.92	-0.46	ns
Twsg1	twisted gastrulation homolog 1 (Drosophila)	65960	3.77	2.62	1.89	1.99	0.65	ns
Scamp4	secretory carrier membrane protein 4	56214	0.50	0.49	0.49	1.02	0.16	ns
Golph3	golgi phosphoprotein 3	66629	1.82	1.89	3.15	0.57	-0.83	*
Slc22a5	solute carrier family 22 (organic cation transporter), member 5	20520	0.56	0.58	0.67	0.83	-0.86	*
4930570C03Rik	RIKEN cDNA 4930570C03 gene	67739	1.38	1.16	1.01	1.36	0.73	ns
Pdgfb	platelet derived growth factor, B polypeptide	18591	1.39	1.59	1.31	1.05	0.30	ns
Bxdc1	brix domain containing 1	67239	0.70	0.87	0.52	1.35	0.45	ns
2700062C07Rik	RIKEN cDNA 2700062C07 gene	68046	0.20	0.33	0.45	0.44	-0.99	***
Nedd4	neural precursor cell expressed, developmentally down-regulted gene 4	17999	7.73	5.69	4.92	1.56	0.90	*
L1cam	L1 cell adhesion molecule	16728	3.51	3.40	3.75	0.93	-0.01	ns
Narfl	nuclear prelamin A recognition factor-like	67563	0.60	0.40	0.48	1.26	0.53	ns
Akr1c12	aldo-keto reductase family 1, member C12	622402	0.48	0.36	0.39	1.22	0.07	ns
2810433K01Rik	RIKEN cDNA 2810433K01 gene	66468	0.30	0.48	0.53	0.57	0.07	ns
Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	28169	1.07	0.89	0.88	1.20	0.73	ns
Ppp2r5d	protein phosphatase 2, regulatory subunit B (B56), delta isoform	21770	1.36	1.26	0.92	1.47	0.84	*
Surf1	surfeit gene 1	20930	1.23	1.18	0.88	1.39	0.46	ns
Gnb2	guanine nucleotide binding protein, beta 2	14693	7.44	6.09	6.98	1.06	0.31	ns
Manba	mannosidase, beta A, lysosomal	110173	0.94	0.98	0.77	1.22	0.20	ns
Slc2a8	solute carrier family 2, (facilitated glucose transporter), member 8	56017	0.40	0.34	0.24	1.69	0.85	*
LOC433749		433749	5.53	4.82	5.46	1.01	0.45	ns
LOC631743		631743	5.53	4.82	5.46	1.01	0.45	ns
Pdcd5	programmed cell death 5	56330	2.87	3.32	3.73	0.76	-0.13	ns
3110001I20Rik	RIKEN cDNA 3110001I20 gene	70354	0.83	0.88	1.22	0.68	-0.74	ns
Zfp36l1	zinc finger protein 36, C3H type-like 1	12192	6.41	7.26	6.26	1.02	0.11	ns
Cyp51	cytochrome P450, family 51	13121	2.06	1.90	2.46	0.84	-0.43	ns
Gng10	guanine nucleotide binding protein (G protein), gamma 10	14700	1.29	1.43	1.15	1.12	0.32	ns
Dhdds	dehydrodolichyl diphosphate synthase	67422	0.55	0.65	0.81	0.68	-0.50	ns
Ppie	peptidylprolyl isomerase E (cyclophilin E)	56031	0.49	0.64	0.53	0.91	0.07	ns
Pts	6-pyruvoyl-tetrahydropterin synthase	19286	1.04	1.01	0.70	1.48	0.86	*
Gabpa	GA repeat binding protein, alpha	14390	1.59	1.53	1.99	0.79	-0.69	ns
Cs	citrate synthase	12974	5.59	5.87	4.93	1.13	0.02	ns
Hspe1	heat shock protein 1 (chaperonin 10)	15528	3.46	3.20	2.28	1.51	0.34	ns
Map3k11	mitogen activated protein kinase kinase kinase 11	26403	0.50	0.55	0.29	1.72	0.84	*
Cdk5	cyclin-dependent kinase 5	12568	0.73	0.66	0.77	0.94	0.11	ns
Arpp19	cAMP-regulated phosphoprotein 19	59046	2.00	1.71	1.05	1.89	0.93	**
Rgl2	ral guanine nucleotide dissociation stimulator-like 2	19732	0.95	0.73	0.62	1.52	0.69	ns
Ranbp2	RAN binding protein 2	19386	2.55	2.15	1.84	1.38	0.36	ns
Caskin2	cask-interacting protein 2	140721	0.47	0.50	0.48	0.97	0.39	ns
Kif4	kinesin family member 4	16571	0.44	0.54	1.02	0.43	-0.39	ns
Fkbp2	FK506 binding protein 2	14227	4.01	3.57	2.70	1.47	0.92	**
Slc30a7	solute carrier family 30 (zinc transporter), member 7	66500	0.51	0.55	0.55	0.94	-0.26	ns
Selenbp1	selenium binding protein 1	20341	2.09	2.40	4.00	0.52	-0.58	ns
Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3	260409	0.71	0.57	0.26	2.66	0.61	ns
Gtf2h2	general transcription factor II H, polypeptide 2	23894	0.35	0.40	0.50	0.69	-0.87	*
Rdbp	RD RNA-binding protein	27632	2.34	2.44	1.79	1.30	0.84	*
Arl3	ADP-ribosylation factor-like 3	56350	3.55	3.19	2.30	1.54	0.91	*
Brd4	bromodomain containing 4	57261	2.91	2.61	1.83	1.58	0.93	**
Azin1	antizyme inhibitor 1	54375	1.54	1.33	1.70	0.90	-0.03	ns
Adamts1	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1	11504	3.58	2.50	3.22	1.11	-0.13	ns
Acp1	acid phosphatase 1, soluble	11431	5.24	5.18	5.58	0.93	-0.11	ns
Asah2	N-acylsphingosine amidohydrolase 2	54447	0.52	0.60	0.45	1.14	-0.35	ns
Poldip2	polymerase (DNA-directed), delta interacting protein 2	67811	0.72	0.74	0.58	1.25	0.18	ns
Hs2st1	heparan sulfate 2-O-sulfotransferase 1	23908	1.72	1.52	1.23	1.39	0.41	ns
Tnfrsf21	tumor necrosis factor receptor superfamily, member 21	94185	0.15	0.20	0.47	0.31	-0.87	*
Pno1	partner of NOB1 homolog (S. cerevisiae)	66249	1.22	1.28	1.35	0.90	-0.73	ns
Mapre1	microtubule-associated protein, RP/EB family, member 1	13589	4.98	4.92	4.89	1.01	0.34	ns
Ell2	elongation factor RNA polymerase II 2	192657	0.60	0.81	1.15	0.52	-0.97	**

Keap1	kelch-like ECH-associated protein 1	50868	0.82	0.52	0.77	1.06	0.26	ns
Agpat6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	102247	0.80	0.79	0.83	0.96	0.32	ns
Xrn2	5'-3' exoribonuclease 2	24128	0.91	0.97	1.13	0.80	-0.42	ns
Wnt4	wingless-related MMTV integration site 4	22417	0.55	0.61	0.36	1.50	0.20	ns
Ifit1	interferon-induced protein with tetratricopeptide repeats 1	15957	0.17	0.19	1.78	0.09	-0.72	ns
Syt8	synaptotagmin VIII	55925	0.43	0.36	0.41	1.03	0.19	ns
2410018M08Rik		71970	5.72	5.05	7.32	0.78	-0.36	ns
Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	66416	5.78	4.95	4.15	1.39	0.72	ns
Rpl39	ribosomal protein L39	67248	23.73	24.27	17.73	1.33	0.84	*
Cenpa	centromere protein A	12615	2.47	2.54	3.28	0.75	-0.12	ns
Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	12406	0.70	0.46	0.81	0.87	-0.21	ns
Dap3	death associated protein 3	65111	3.63	3.59	2.82	1.28	0.64	ns
Wdr1	WD repeat domain 1	22388	4.08	4.53	5.33	0.76	-0.54	ns
Tle4	transducin-like enhancer of split 4, homolog of Drosophila E(spl)	21888	1.42	0.97	0.58	2.43	0.91	*
Arvcf	armadillo repeat gene deleted in velo-cardio-facial syndrome	11877	0.54	0.53	0.43	1.27	0.55	ns
Lap3	leucine aminopeptidase 3	66988	0.97	0.99	0.98	0.99	0.16	ns
Rad54l	RAD54 like (S. cerevisiae)	19366	0.63	0.72	0.86	0.73	-0.09	ns
Mrpl17	mitochondrial ribosomal protein L17	27397	1.07	1.13	1.56	0.68	-0.86	*
Hgsnat	heparan-alpha-glucosaminide N-acetyltransferase	52120	0.80	0.65	0.79	1.00	-0.04	ns
Bcat1	branched chain aminotransferase 1, cytosolic	12035	0.89	0.74	0.11	8.23	0.27	ns
Gtpbp4	GTP binding protein 4	69237	1.31	1.39	1.68	0.78	-0.72	ns
BC005537	cDNA sequence BC005537	79555	3.40	2.99	3.71	0.91	-0.01	ns
Sri	sorcin	109552	2.57	2.28	2.26	1.13	0.65	ns
Atp9b	ATPase, class II, type 9B	50771	0.48	0.44	0.45	1.05	0.56	ns
Mrpl16	mitochondrial ribosomal protein L16	94063	1.89	2.04	1.46	1.28	0.78	ns
Dffa	DNA fragmentation factor, alpha subunit	13347	0.53	0.44	0.49	1.08	-0.07	ns
Gsg2	germ cell-specific gene 2	14841	0.29	0.29	0.39	0.72	-0.41	ns
Rqcd1	rcd1 (required for cell differentiation) homolog 1 (S. pombe)	58184	1.85	1.64	1.39	1.33	0.86	*
Hltf	helicase-like transcription factor	20585	1.28	1.12	1.00	1.27	0.33	ns
Srp19	signal recognition particle 19	66384	1.46	1.51	1.42	1.02	0.45	ns
Usp4	ubiquitin specific peptidase 4 (proto-oncogene)	22258	0.62	0.70	0.70	0.88	0.25	ns
Ubap1	ubiquitin-associated protein 1	67123	0.50	0.50	0.55	0.91	-0.43	ns
Ap2m1	adaptor protein complex AP-2, mu1	11773	7.75	6.95	8.26	0.93	-0.14	ns
Arhgap5	Rho GTPase activating protein 5	11855	2.68	2.90	3.46	0.77	-0.84	*
Nedd1	neural precursor cell expressed, developmentally down-regulated gene 1	17997	1.26	0.91	0.95	1.32	0.49	ns
Smek2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	104570	1.15	0.92	1.06	1.08	0.18	ns
Eif4e		13684	3.52	3.49	3.23	1.08	-0.16	ns
LOC630527		630527	3.52	3.49	3.23	1.08	-0.16	ns
Ppib	peptidylprolyl isomerase B	19035	7.55	6.41	5.85	1.28	0.85	*
B4galt6		56386	0.23	0.40	0.16	1.40	0.28	ns
Ppp1r14b	protein phosphatase 1, regulatory (inhibitor) subunit 14B	18938	5.55	5.50	3.90	1.41	0.91	*
Stau2	staufen (RNA binding protein) homolog 2 (Drosophila)	29819	0.32	0.31	0.30	1.07	-0.17	ns
Src	Rous sarcoma oncogene	20779	0.46	0.46	0.48	0.97	-0.44	ns
Mpp1	membrane protein, palmitoylated	17524	0.52	0.49	0.73	0.72	-0.15	ns
Ccnb2	cyclin B2	12442	2.86	2.34	2.56	1.11	0.63	ns
Eif4a2	eukaryotic translation initiation factor 4A2	13682	13.06	12.42	9.00	1.44	0.59	ns
Lin7c	lin-7 homolog C (C. elegans)	22343	2.01	1.66	1.38	1.45	0.73	ns
Sdcbp	syndecan binding protein	53378	0.87	0.73	0.77	1.12	-0.31	ns
2610528J11Rik	RIKEN cDNA 2610528J11 gene	66451	0.57	0.53	0.74	0.76	-0.70	ns
Katna1	katanin p60 (ATPase-containing) subunit A1	23924	1.27	1.29	1.08	1.17	-0.06	ns
Smc3	structural maintenace of chromosomes 3	13006	3.15	3.34	2.30	1.36	0.66	ns
Ciao1	cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	26371	1.27	1.14	1.17	1.08	0.61	ns
Yme1l1	YME1-like 1 (S. cerevisiae)	27377	1.20	0.97	0.62	1.91	0.68	ns
Sqstm1	sequestosome 1	18412	5.56	4.55	5.26	1.05	0.13	ns
Tm4sf1	transmembrane 4 superfamily member 1	17112	0.37	0.78	1.64	0.23	-0.80	ns
D930014E17Rik	RIKEN cDNA D930014E17 gene	57373	0.81	0.79	0.94	0.86	-0.58	ns
Tex261	testis expressed gene 261	21766	1.25	0.99	1.45	0.85	-0.22	ns
Crot	carnitine O-octanoyltransferase	74114	0.86	0.76	0.75	1.14	0.32	ns
Ptplad2	protein tyrosine phosphatase-like A domain containing 2	66775	0.47	0.62	0.14	3.31	0.54	ns
Uqcrfs1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	66694	3.44	3.15	3.98	0.86	-0.17	ns
Pccb	propionyl Coenzyme A carboxylase, beta polypeptide	66904	0.44	0.38	0.31	1.38	0.68	ns
Got1	glutamate oxaloacetate transaminase 1, soluble	14718	1.33	1.39	1.02	1.30	0.60	ns
Gadd45b	growth arrest and DNA-damage-inducible 45 beta	17873	1.14	1.08	1.08	1.05	-0.23	ns
Gtpbp3	GTP binding protein 3	70359	0.24	0.31	0.43	0.56	-0.81	ns
Cnn2	calponin 2	12798	5.39	4.78	3.01	1.78	0.63	ns
Akap8	A kinase (PRKA) anchor protein 8	56399	1.86	1.68	1.22	1.51	0.74	ns
Tjp2	tight junction protein 2	21873	3.36	3.57	2.48	1.35	0.79	ns
Nol5	nucleolar protein 5	55989	1.08	1.25	0.81	1.34	0.39	ns
2310004I24Rik	RIKEN cDNA 2310004I24 gene	66358	0.40	0.43	0.40	0.98	-0.45	ns
Pask	PAS domain containing serine/threonine kinase	269224	0.59	0.56	0.47	1.24	0.20	ns
Tmem126a	transmembrane protein 126A	66271	1.37	1.21	1.29	1.06	0.48	ns
Aco2	aconitase 2, mitochondrial	11429	4.48	3.97	4.47	1.00	0.28	ns
Zfp358	zinc finger protein 358	140482	0.41	0.25	0.30	1.35	0.63	ns
Ifrd2	interferon-related developmental regulator 2	15983	0.36	0.43	0.43	0.83	0.25	ns
Klf5	Kruppel-like factor 5	12224	3.15	3.03	2.88	1.09	0.40	ns
Ftsj3	FtsJ homolog 3 (E. coli)	56095	0.44	0.62	0.57	0.78	-0.12	ns
Spg21	spastic paraplegia 21 homolog (human)	27965	1.11	1.10	1.06	1.04	0.61	ns
Ptpn9	protein tyrosine phosphatase, non-receptor type 9	56294	0.81	0.74	0.78	1.04	0.50	ns
2610027L16Rik	RIKEN cDNA 2610027L16 gene	67842	0.69	0.81	0.87	0.79	-0.48	ns
Dtd1	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	66044	0.70	0.64	0.49	1.43	0.53	ns
Mina	myc induced nuclear antigen	67014	0.85	0.91	0.87	0.97	-0.48	ns
Sip1	survivor of motor neuron protein interacting protein 1	66603	0.64	0.75	0.92	0.69	-0.67	ns
Zfpm1	zinc finger protein, multitype 1	22761	0.34	0.44	0.18	1.91	0.32	ns
Bcap31	B-cell receptor-associated protein 31	27061	3.99	3.78	5.91	0.67	-0.42	ns
Nt5c3	5'-nucleotidase, cytosolic III	107569	0.79	1.01	1.16	0.68	-0.93	**
Cog8	component of oligomeric golgi complex 8	97484	1.05	1.15	0.61	1.73	0.64	ns

Psmd7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	17463	1.00	1.13	0.72	1.39	0.74	ns
Dnm2	dynamin 2	13430	0.65	0.49	0.59	1.10	0.57	ns
Mcts2	malignant T cell amplified sequence 2	66405	0.48	0.47	0.44	1.10	0.06	ns
Stxbp4	syntaxin binding protein 4	20913	0.65	0.60	0.41	1.56	0.12	ns
Psat1	phosphoserine aminotransferase 1	107272	5.98	6.97	5.29	1.12	0.37	ns
Sgta	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	52551	1.88	1.69	1.45	1.29	0.98	***
Rps25	ribosomal protein S25	75617	14.32	12.51	11.42	1.25	0.87	*
Gdi1	guanosine diphosphate (GDP) dissociation inhibitor 1	14567	1.32	1.39	2.50	0.53	-0.77	ns
Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	11928	8.83	9.40	8.73	1.01	-0.46	ns
Sppl3	signal peptide peptidase 3	74585	0.96	1.23	0.99	0.96	-0.14	ns
Rnf13	ring finger protein 13	24017	1.64	1.63	1.41	1.15	-0.03	ns
Ctdsp2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	52468	7.24	5.94	4.71	1.53	0.53	ns
EG665407		665407	1.01	1.18	1.14	0.89	-0.16	ns
Usp1	ubiquitin specific peptdiase 1	230484	4.20	4.35	4.14	1.01	0.31	ns
1300018I05Rik	RIKEN cDNA 1300018I05 gene	74157	0.93	0.75	0.82	1.12	0.68	ns
Aars	alanyl-tRNA synthetase	234734	3.56	3.99	2.22	1.60	0.62	ns
Etfdh	electron transferring flavoprotein, dehydrogenase	66841	1.34	1.42	1.41	0.95	0.26	ns
Rac1	RAS-related C3 botulinum substrate 1	19353	9.45	7.78	8.90	1.06	0.19	ns
Oxa1l	oxidase assembly 1-like	69089	0.67	0.53	0.56	1.19	0.25	ns
Arcn1	archain 1	213827	3.03	2.47	2.39	1.27	0.86	*
Asns	asparagine synthetase	27053	3.13	3.78	3.37	0.92	0.00	ns
Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	226646	4.37	4.33	3.54	1.23	0.33	ns
Vasp	vasodilator-stimulated phosphoprotein	22323	1.31	1.62	2.12	0.62	-0.84	*
Chmp1a	chromatin modifying protein 1A	234852	1.25	1.37	1.04	1.19	0.65	ns
Mbc2	membrane bound C2 domain containing protein	23943	0.99	1.08	0.62	1.58	0.45	ns
Rps28	ribosomal protein S28	54127	27.63	26.24	19.19	1.43	0.85	*
Cnot8	CCR4-NOT transcription complex, subunit 8	69125	0.85	0.84	0.84	1.01	0.25	ns
D14Ertd500e	DNA segment, Chr 14, ERATO Doi 500, expressed	219072	1.59	1.81	1.82	0.87	-0.33	ns
Snrp70	U1 small nuclear ribonucleoprotein polypeptide A	20637	0.89	0.96	1.14	0.78	-0.36	ns
Dap	death-associated protein	223453	3.35	3.87	4.72	0.71	-0.81	ns
Cmtm6	CKLF-like MARVEL transmembrane domain containing 6	67213	0.70	0.75	0.78	0.89	0.33	ns
Pias3	protein inhibitor of activated STAT 3	229615	0.72	0.61	0.62	1.15	-0.06	ns
Tom1l1	target of myb1-like 1 (chicken)	71943	0.44	0.45	0.38	1.17	0.22	ns
Idi1	isopentenyl-diphosphate delta isomerase	319554	3.11	2.53	2.49	1.25	0.69	ns
C330016O10Rik	RIKEN cDNA C330016O10 gene	212706	0.28	0.28	0.44	0.65	-0.85	*
Sod1	superoxide dismutase 1, soluble	20655	7.13	6.57	6.20	1.14	0.46	ns
Paip2b	poly(A) binding protein interacting protein 2B	232164	1.81	1.70	1.52	1.18	0.57	ns
Pbxip1	pre-B-cell leukemia transcription factor interacting protein 1	229534	1.22	1.09	0.51	2.39	0.53	ns
Tm2d2	TM2 domain containing 2	69742	1.17	1.11	1.02	1.14	0.95	**
Gtf2b	general transcription factor IIB	229906	1.60	1.28	1.15	1.38	0.36	ns
Mier2	mesoderm induction early response 1, family member 2	70427	0.40	0.30	0.43	0.94	-0.42	ns
Prkag2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	108099	0.35	0.30	0.31	1.14	0.12	ns
Mettl8	methyltransferase like 8	228019	0.36	0.32	0.19	1.84	0.16	ns
Exoc1	exocyst complex component 1	69940	0.65	0.68	0.81	0.80	-0.86	*
1110006G06Rik	RIKEN cDNA 1110006G06 gene	73833	0.38	0.26	0.37	1.01	-0.15	ns
Bxdc2	brix domain containing 2	67832	2.41	2.12	2.48	0.97	-0.02	ns
Tmem111	transmembrane protein 111	66087	2.82	2.91	3.04	0.92	-0.08	ns
Zfp386		56220	1.15	1.10	1.23	0.93	-0.53	ns
Pgm2	phosphoglucomutase 2	72157	1.31	1.29	2.22	0.59	-0.55	ns
Zfp410	zinc finger protein 410	52708	1.47	1.81	2.48	0.59	-0.78	ns
Pvr	poliovirus receptor	52118	0.24	0.27	0.63	0.38	-0.62	ns
Hsbp1	heat shock factor binding protein 1	68196	3.32	3.24	3.04	1.09	0.72	ns
Tinf2	Terf1 (TRF1)-interacting nuclear factor 2	28113	0.83	0.82	1.20	0.69	-0.57	ns
Mrps18b	mitochondrial ribosomal protein S18B	66973	1.32	1.21	0.78	1.69	0.85	*
Ccdc101	coiled-coil domain containing 101	75565	0.33	0.45	0.42	0.77	-0.01	ns
Arhgdia	Rho GDP dissociation inhibitor (GDI) alpha	192662	6.10	5.50	5.38	1.13	0.72	ns
Nomo1	nodal modulator 1	211548	0.85	0.84	1.11	0.76	-0.40	ns
2310008H04Rik	RIKEN cDNA 2310008H04 gene	224008	0.79	0.69	1.07	0.73	-0.43	ns
Spcs3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	76687	2.55	2.55	2.62	0.97	0.34	ns
D430028G21Rik	RIKEN cDNA D430028G21 gene	228607	0.64	0.52	0.63	1.01	-0.31	ns
Dnajb4	DnaJ (Hsp40) homolog, subfamily B, member 4	67035	1.19	1.06	0.62	1.91	0.18	ns
Mrpl53	mitochondrial ribosomal protein L53	68499	1.40	1.47	1.97	0.71	-0.76	ns
Tmem121	transmembrane protein 121	69195	0.27	0.33	0.50	0.55	-0.40	ns
Ankrd54	ankyrin repeat domain 54	223690	1.01	0.94	1.07	0.93	-0.12	ns
EG627828		627828	6.39	6.80	5.63	1.13	0.56	ns
0610037P05Rik	RIKEN cDNA 0610037P05 gene	66086	2.13	1.89	2.11	1.01	-0.24	ns
Wdr26	WD repeat domain 26	226757	3.30	3.44	2.85	1.15	-0.22	ns
Zswim1	zinc finger, SWIM domain containing 1	71971	0.54	0.51	0.53	1.00	-0.44	ns
Sbk1	SH3-binding kinase 1	104175	0.57	0.45	0.60	0.95	-0.28	ns
Crabp2	cellular retinoic acid binding protein II	12904	1.14	1.21	0.27	4.25	0.60	ns
Ttc4	tetratricopeptide repeat domain 4	72354	0.54	0.46	0.51	1.05	-0.06	ns
Ypel5	yippee-like 5 (Drosophila)	383295	0.80	0.62	0.36	2.24	0.85	*
Qtrtd1	queuine tRNA-ribosyltransferase domain containing 1	106248	0.58	0.65	0.72	0.79	-0.93	**
Rnh1	ribonuclease/angiogenin inhibitor 1	107702	2.02	1.97	2.07	0.97	0.11	ns
C330007P06Rik	RIKEN cDNA C330007P06 gene	77644	1.08	1.09	1.30	0.83	-0.45	ns
Mb	myoglobin	17189	0.07	0.11	0.41	0.16	-0.68	ns
Psmb4	proteasome (prosome, macropain) subunit, beta type 4	19172	8.92	9.33	7.83	1.13	0.65	ns
Cbara1	calcium binding atopy-related autoantigen 1	216001	1.01	0.80	0.67	1.51	0.28	ns
Lass5	longevity assurance homolog 5 (S. cerevisiae)	71949	5.94	6.22	5.86	1.01	-0.24	ns
Ppap2c	phosphatidic acid phosphatase type 2c	50784	6.66	6.27	5.34	1.24	-0.07	ns
Kbtbd2	kelch repeat and BTB (POZ) domain containing 2	210973	1.64	1.64	2.13	0.77	-0.83	*
Zfp330	zinc finger protein 330	30932	0.93	1.08	1.17	0.79	-0.11	ns
Immp1l	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	66541	1.62	1.29	1.23	1.31	0.54	ns
Edem1	ER degradation enhancer, mannosidase alpha-like 1	192193	0.45	0.46	0.60	0.76	-0.41	ns
Ormdl1	ORM1-like 1 (S. cerevisiae)	227102	1.50	1.57	1.31	1.14	0.40	ns
Wdr20a	WD repeat domain 20a	69641	1.83	1.96	1.71	1.06	-0.44	ns

Btf3l4	basic transcription factor 3-like 4	70533	0.75	0.99	0.99	0.76	-0.83	*
Scamp5	secretory carrier membrane protein 5	56807	0.95	0.80	0.25	3.73	0.61	ns
Ptpn11	protein tyrosine phosphatase, non-receptor type 11	19247	3.14	3.40	4.10	0.76	-0.33	ns
Hdac11	histone deacetylase 11	232232	0.61	0.43	0.36	1.69	0.14	ns
Wbp5	WW domain binding protein 5	22381	16.64	16.07	15.67	1.06	0.55	ns
Cul2	cullin 2	71745	0.98	0.98	1.14	0.86	0.22	ns
Traf2	Tnf receptor-associated factor 2	22030	0.42	0.39	0.46	0.92	-0.62	ns
BC021381	cDNA sequence BC021381	212483	0.84	0.84	0.89	0.94	0.24	ns
Rbm7	RNA binding motif protein 7	67010	3.78	3.13	3.08	1.22	0.79	ns
Rnpep	arginyl aminopeptidase (aminopeptidase B)	215615	0.65	0.64	0.51	1.28	-0.05	ns
Zfp422	zinc finger protein 422	67255	0.57	0.65	0.53	1.07	-0.03	ns
Mfsd1	major facilitator superfamily domain containing 1	66868	2.22	2.10	1.37	1.61	0.17	ns
Prmt7	protein arginine N-methyltransferase 7	214572	0.60	0.58	0.54	1.10	0.71	ns
Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	66884	2.69	2.79	2.94	0.91	-0.65	ns
Irf2bp1	interferon regulatory factor 2 binding protein 1	272359	0.81	0.77	0.71	1.14	0.13	ns
Pxk	PX domain containing serine/threonine kinase	218699	0.60	0.53	0.82	0.72	-0.57	ns
Ikbkap	inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	230233	1.04	1.28	1.39	0.74	-0.81	*
Lsr	lipolysis stimulated lipoprotein receptor	54135	0.96	1.06	1.02	0.94	0.29	ns
Rexo2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	104444	1.50	1.23	0.86	1.74	0.85	*
Frmd6	FERM domain containing 6	319710	0.88	0.99	1.16	0.76	0.01	ns
Ccdc115	coiled-coil domain containing 115	69668	0.48	0.50	0.36	1.33	0.50	ns
Pdzd11	PDZ domain containing 11	72621	0.42	0.35	0.73	0.57	-0.59	ns
Ogdh	oxoglutarate dehydrogenase (lipoamide)	18293	1.26	1.27	1.43	0.88	-0.75	ns
Zadh2	zinc binding alcohol dehydrogenase, domain containing 2	225791	0.72	0.80	0.69	1.04	0.50	ns
Yipf3	Yip1 domain family, member 3	28064	0.64	0.69	0.53	1.21	0.56	ns
Fus	fusion, derived from t(12;16) malignant liposarcoma (human)	233908	3.26	3.82	3.14	1.03	0.48	ns
Obfc2b	oligonucleotide/oligosaccharide-binding fold containing 2B	69917	1.06	0.87	0.79	1.33	0.23	ns
Zfp212	Zinc finger protein 212	232784	0.69	0.80	0.66	1.04	0.35	ns
Snrpe	small nuclear ribonucleoprotein E	20643	10.82	10.99	9.63	1.12	0.38	ns
Chd4	chromodomain helicase DNA binding protein 4	107932	2.38	2.33	2.37	1.00	0.00	ns
Pabpc4		230721	1.92	1.80	1.40	1.36	0.77	ns
Chmp7	CHMP family, member 7	105513	0.69	0.68	0.61	1.13	0.86	*
1110012L19Rik	RIKEN cDNA 1110012L19 gene	68618	0.37	0.38	0.64	0.58	-0.68	ns
BC002230	cDNA sequence BC002230	217827	0.83	0.80	0.74	1.12	0.07	ns
Cdca7l	cell division cycle associated 7 like	217946	1.93	1.95	1.77	1.09	-0.04	ns
Mrpl14	mitochondrial ribosomal protein L14	68463	1.58	1.23	1.09	1.44	0.93	**
Arhgap1	Rho GTPase activating protein 1	228359	1.20	0.90	0.62	1.95	0.50	ns
Ctsl	cathepsin L	13039	2.44	4.02	6.76	0.36	-0.77	ns
Tmem101	transmembrane protein 101	76547	0.50	0.46	0.48	1.04	0.60	ns
Picalm	phosphatidylinositol binding clathrin assembly protein	233489	3.86	3.62	3.61	1.06	0.22	ns
Ythdf2	YTH domain family 2	213541	1.48	1.57	1.59	0.93	-0.71	ns
Senp1	SUMO1/sentrin specific peptidase 1	223870	0.88	0.93	1.09	0.80	-0.70	ns
Rbm43	RNA binding motif protein 43	71684	0.52	0.54	0.56	0.93	0.15	ns
Zfp7	zinc finger protein 7	223669	1.23	1.07	1.11	1.10	-0.14	ns
Abhd14b	abhydrolase domain containing 14b	76491	1.37	1.01	0.54	2.55	0.61	ns
Tmed1	transmembrane emp24 domain containing 1	17083	0.72	0.65	0.67	1.07	0.38	ns
Pcnxl3	pecanex-like 3 (Drosophila)	104401	1.85	1.73	1.29	1.43	0.87	*
Inpp5b	inositol polyphosphate-5-phosphatase B	16330	0.73	0.63	0.73	0.99	-0.10	ns
1810009O10Rik	RIKEN cDNA 1810009O10 gene	69109	0.30	0.34	0.30	1.01	-0.41	ns
Plac8	placenta-specific 8	231507	2.10	2.63	5.61	0.37	-0.85	*
Psmf1	proteasome (prosome, macropain) inhibitor subunit 1	228769	0.75	0.69	0.98	0.77	-0.61	ns
Suox	sulfite oxidase	211389	0.28	0.27	0.29	0.95	-0.15	ns
Vps36	vacuolar protein sorting 36 (yeast)	70160	0.80	0.80	1.12	0.71	-0.67	ns
Mta3	metastasis associated 3	116871	1.03	0.80	0.80	1.29	0.71	ns
Anp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	66471	4.57	4.83	4.39	1.04	0.47	ns
Mpnd	MPN domain containing	68047	2.20	1.99	1.40	1.56	0.85	*
Racgap1	Rac GTPase-activating protein 1	26934	2.01	1.91	2.55	0.78	0.00	ns
Dennd2d	DENN/MADD domain containing 2D	72121	0.33	0.51	0.26	1.28	0.12	ns
Polr3gl	polymerase (RNA) III (DNA directed) polypeptide G like	69870	0.82	0.77	0.60	1.36	0.60	ns
Rbm19	RNA binding motif protein 19	74111	0.43	0.54	0.44	0.97	0.23	ns
Cops6	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana)	26893	3.42	3.60	4.09	0.83	-0.52	ns
Alg1	asparagine-linked glycosylation 1 homolog (yeast, beta-1,4-mannosyltransferase)	208211	0.47	0.46	0.69	0.68	-0.66	ns
Commd5	COMM domain containing 5	66398	0.69	0.68	0.70	0.98	-0.41	ns
Ehf	ets homologous factor	13661	2.59	2.23	2.40	1.07	-0.42	ns
Aaas	achalasia, adrenocortical insufficiency, alacrimia	223921	1.26	1.26	1.93	0.65	-0.84	*
Zfyve19	zinc finger, FYVE domain containing 19	72008	0.65	0.61	0.61	1.07	-0.01	ns
Chac1	ChaC, cation transport regulator-like 1 (E. coli)	69065	1.89	1.53	1.04	1.81	0.61	ns
2310056P07Rik	RIKEN cDNA 2310056P07 gene	70186	6.52	6.47	9.57	0.68	-0.52	ns
Blvrb	biliverdin reductase B (flavin reductase (NADPH))	233016	0.41	0.41	0.45	0.92	-0.04	ns
Cuta	cutA divalent cation tolerance homolog (E. coli)	67675	1.90	1.57	1.07	1.77	0.99	***
Atp11b	ATPase, Class VI, type 11B	76295	2.16	2.28	2.78	0.77	-0.87	*
Zfand2b	zinc finger, AN1 type domain 2B	68818	0.39	0.39	0.38	1.02	-0.49	ns
2700050L05Rik	RIKEN cDNA 2700050L05 gene	214764	0.31	0.37	0.38	0.82	-0.84	*
Pex26	peroxisome biogenesis factor 26	74043	0.46	0.51	0.55	0.84	-0.36	ns
Cbr4	carbonyl reductase 4	234309	0.83	0.98	1.28	0.64	-0.86	*
Pnkd	paroxysmal nonkinesiogenic dyskinesia	56695	0.92	0.86	0.69	1.32	0.69	ns
Ecd	ecdysoneless homolog (Drosophila)	70601	1.27	1.20	1.02	1.23	-0.07	ns
Pcca	propionyl-Coenzyme A carboxylase, alpha polypeptide	110821	0.76	0.66	0.47	1.60	0.77	ns
Ift20	intraflagellar transport 20 homolog (Chlamydomonas)	55978	0.58	0.56	0.52	1.11	0.53	ns
Cast	calpastatin	12380	1.52	2.01	2.52	0.60	-0.30	ns
Tgm1	transglutaminase 1, K polypeptide	21816	0.17	0.37	0.93	0.18	-0.75	ns
Spsb4	splA/ryanodine receptor domain and SOCS box containing 4	211949	0.56	0.62	0.68	0.81	-0.07	ns
Rogdi	rogdi homolog (Drosophila)	66049	1.49	1.25	1.24	1.19	-0.20	ns
Myo18a	myosin XVIIIa	360013	1.88	2.15	1.24	1.51	0.27	ns

Egfl7	EGF-like domain 7	353156	0.28	0.39	0.35	0.80	-0.71	ns
Gfod2	glucose-fructose oxidoreductase domain containing 2	70575	0.32	0.34	0.27	1.17	0.04	ns
Dbndd2	dysbindin (dystrobrevin binding protein 1) domain containing 2	52840	1.93	2.24	2.59	0.74	-0.23	ns
Zdhhc20	zinc finger, DHHC domain containing 20	75965	0.74	0.82	1.22	0.60	-0.79	ns
BC027231	cDNA sequence BC027231	212547	0.38	0.42	0.42	0.90	-0.54	ns
Ccdc104	coiled-coil domain containing 104	216618	0.94	1.02	1.07	0.87	-0.48	ns
1110005A03Rik	RIKEN cDNA 1110005A03 gene	74319	0.68	0.62	0.66	1.03	0.43	ns
4933407N01Rik	RIKEN cDNA 4933407N01 gene	66753	0.80	0.80	0.96	0.83	-0.32	ns
Sc5d	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	235293	1.56	1.26	1.47	1.06	0.50	ns
Aldoc	aldolase 3, C isoform	11676	2.26	2.36	3.14	0.72	-0.37	ns
Ifnar2	interferon (alpha and beta) receptor 2	15976	0.85	0.99	1.20	0.70	-0.98	***
Ubl7	ubiquitin-like 7 (bone marrow stromal cell-derived)	69459	0.97	0.78	0.86	1.12	0.61	ns
Gtpbp5	GTP binding protein 5	52856	0.30	0.30	0.38	0.79	-0.50	ns
Eif5a	eukaryotic translation initiation factor 5A	276770	13.90	14.28	14.76	0.94	-0.63	ns
Cryzl1	crystallin, zeta (quinone reductase)-like 1	66609	1.73	1.68	1.79	0.96	-0.24	ns
Parp8	poly (ADP-ribose) polymerase family, member 8	52552	0.30	0.49	0.52	0.57	-0.81	*
Plxnd1	plexin D1	67784	0.15	0.23	0.49	0.30	-0.84	*
Zdhhc8	zinc finger, DHHC domain containing 8	27801	0.85	0.71	0.77	1.10	0.61	ns
E2f4	E2F transcription factor 4	104394	0.31	0.31	0.25	1.22	0.68	ns
Rabepk	Rab9 effector protein with kelch motifs	227746	0.46	0.36	0.30	1.54	0.46	ns
Lyplal1	lysophospholipase-like 1	226791	0.62	0.75	0.51	1.21	0.08	ns
Wac	WW domain containing adaptor with coiled-coil	225131	1.99	2.79	2.10	0.94	0.22	ns
Chchd3	coiled-coil-helix-coiled-coil-helix domain containing 3	66075	1.36	1.24	1.40	0.96	-0.56	ns
Chchd5	coiled-coil-helix-coiled-coil-helix domain containing 5	66170	0.58	0.63	0.84	0.68	-0.78	ns
Larp2	La ribonucleoprotein domain family, member 2	214048	0.35	0.44	0.33	1.05	0.29	ns
Hibch	3-hydroxyisobutyryl-Coenzyme A hydrolase	227095	0.35	0.39	0.23	1.50	0.09	ns
Rhebl1	Ras homolog enriched in brain like 1	69159	0.49	0.56	0.63	0.77	-0.26	ns
Spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	229285	1.38	1.22	0.99	1.38	0.79	ns
Lrch4	leucine-rich repeats and calponin homology (CH) domain containing 4	231798	0.63	0.51	0.45	1.40	0.21	ns
Mif4gd	MIF4G domain containing	69674	0.57	0.52	0.83	0.68	-0.76	ns
Arhgap12	Rho GTPase activating protein 12	75415	0.51	0.52	0.67	0.76	-0.35	ns
Steap1	six transmembrane epithelial antigen of the prostate 1	70358	0.74	0.94	0.96	0.77	-0.77	ns
Mtfr1	mitochondrial fission regulator 1	67472	1.28	1.48	1.32	0.97	-0.54	ns
Bcs1l	BCS1-like (yeast)	66821	0.53	0.57	0.41	1.29	-0.17	ns
Tdrd3	tudor domain containing 3	219249	0.85	0.79	0.90	0.94	0.21	ns
Ephb3	Eph receptor B3	13845	0.50	0.42	0.65	0.76	-0.51	ns
Nln	neurolysin (metallopeptidase M3 family)	75805	0.37	0.46	0.35	1.05	-0.40	ns
Fbxw7	F-box and WD-40 domain protein 7, archipelago homolog (Drosophila)	50754	0.76	0.71	0.49	1.54	0.67	ns
Dhrs4	dehydrogenase/reductase (SDR family) member 4	28200	1.02	0.85	0.84	1.20	0.17	ns
Parp14	poly (ADP-ribose) polymerase family, member 14	547253	0.08	0.11	0.61	0.12	-0.70	ns
Zfp810	zinc finger protein 810	235050	0.56	0.36	0.35	1.60	0.86	*
Ifi203	interferon activated gene 203	15950	0.04	0.07	0.44	0.08	-0.59	ns
6720467C03Rik	RIKEN cDNA 6720467C03 gene	68099	1.15	1.29	1.37	0.84	-0.53	ns
LOC637796		637796	0.83	0.82	0.72	1.15	0.00	ns
Stx4a	syntaxin 4A (placental)	20909	0.65	0.75	0.93	0.70	-0.94	**
Bcl9	B-cell CLL/lymphoma 9	77578	0.44	0.41	0.39	1.11	-0.33	ns
Nudt3	nudix (nucleotide diphosphate linked moiety X)-type motif 3	56409	1.48	1.06	0.95	1.54	0.86	*
Prkdc	protein kinase, DNA activated, catalytic polypeptide	19090	0.68	0.61	0.67	1.02	-0.09	ns
BC025076	cDNA sequence BC025076	216829	0.73	0.63	0.67	1.09	0.14	ns
Tiprl	TIP41, TOR signalling pathway regulator-like (S. cerevisiae)	226591	1.04	0.97	0.93	1.11	0.22	ns
Gats	opposite strand transcription unit to Stag3	80909	0.33	0.40	0.36	0.91	-0.63	ns
Sphk1	sphingosine kinase 1	20698	0.94	0.88	0.71	1.30	-0.33	ns
Lmbrd1	LMBR1 domain containing 1	68421	1.26	1.16	0.99	1.26	0.90	*
Pkd1l2	Polycystic kidney disease 1 like 2	76645	0.73	0.62	0.67	1.09	-0.37	ns
C730048C13Rik		319800	0.74	0.18	0.01	78.20	0.93	**
D630002G06Rik		236293	0.74	0.18	0.01	78.20	0.93	**
Armc1		74252	1.49	1.40	1.30	1.14	0.21	ns
LOC634390		634390	1.49	1.40	1.30	1.14	0.21	ns
Dbr1	debranching enzyme homolog 1 (S. cerevisiae)	83703	0.56	0.76	0.59	0.94	0.41	ns
Rab4b	RAB4B, member RAS oncogene family	19342	0.36	0.36	0.55	0.65	-0.89	*
Wdr75	WD repeat domain 75	73674	0.67	0.77	0.78	0.85	-0.52	ns
Hoxb6	homeo box B6	15414	1.12	0.90	0.99	1.12	-0.01	ns
Trim3	tripartite motif protein 3	55992	0.66	0.48	0.44	1.47	0.13	ns
Ap4s1	adaptor-related protein complex AP-4, sigma 1	11782	0.71	0.76	0.77	0.92	-0.39	ns
Acly	ATP citrate lyase	104112	4.76	4.42	5.39	0.88	-0.09	ns
C530043G21Rik	RIKEN cDNA C530043G21 gene	215015	1.99	2.19	2.15	0.92	-0.57	ns
Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform	19043	2.21	2.06	1.87	1.18	0.85	*
Drap1	Dr1 associated protein 1 (negative cofactor 2 alpha)	66556	2.81	2.67	2.04	1.37	0.94	**
Narf	nuclear prelamin A recognition factor	67608	1.09	0.92	0.59	1.85	0.77	ns
Tmco6	transmembrane and coiled-coil domains 6	71983	0.48	0.46	0.38	1.24	0.63	ns
Gpx4	glutathione peroxidase 4	625249	6.81	6.44	5.71	1.19	0.19	ns
1110007L15Rik	RIKEN cDNA 1110007L15 gene	67604	1.56	1.52	1.69	0.92	-0.36	ns
Aprt	adenine phosphoribosyl transferase	11821	2.95	3.39	2.44	1.20	0.41	ns
Map2k3	mitogen activated protein kinase kinase 3	26397	1.52	1.44	1.40	1.08	-0.20	ns
Vps39	vacuolar protein sorting 39 (yeast)	269338	0.48	0.42	0.36	1.32	0.63	ns
Smyd5	SET and MYND domain containing 5	232187	0.41	0.45	0.37	1.11	0.41	ns
Slu7	SLU7 splicing factor homolog (S. cerevisiae)	193116	1.02	1.09	1.36	0.75	-0.76	ns
Wdr13	WD repeat domain 13	73447	0.34	0.46	0.63	0.54	-0.65	ns
Zfp62	zinc finger protein 62	22720	0.30	0.41	0.36	0.83	-0.13	ns
Abca3	ATP-binding cassette, sub-family A (ABC1), member 3	27410	1.12	1.33	0.78	1.42	0.57	ns
Map2k7	mitogen activated protein kinase kinase 7	26400	1.89	2.32	2.69	0.70	-0.91	*
Paip1	polyadenylate binding protein-interacting protein 1	218693	1.12	1.52	1.75	0.64	-0.67	ns
Cdk7	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	12572	0.54	0.66	0.78	0.69	-0.97	**
Ugp2	UDP-glucose pyrophosphorylase 2	216558	1.86	1.58	1.94	0.95	0.17	ns

Znhit1	zinc finger, HIT domain containing 1	70103	3.19	3.11	2.92	1.09	0.44	ns
Atg12	autophagy-related 12 (yeast)	67526	0.59	0.51	0.49	1.21	0.64	ns
Setd3	SET domain containing 3	52690	1.45	1.41	1.62	0.89	-0.55	ns
Dhx9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	13211	3.29	3.65	3.24	1.01	0.01	ns
Blnk	B-cell linker	17060	2.74	3.19	1.89	1.44	0.62	ns
Kifap3	kinesin-associated protein 3	16579	1.17	1.16	0.94	1.24	0.51	ns
Muc20	mucin 20	224116	0.40	1.03	0.37	1.08	0.21	ns
Ryk	receptor-like tyrosine kinase	20187	1.17	1.17	1.06	1.10	0.53	ns
Il1rn	interleukin 1 receptor antagonist	16181	0.08	0.14	0.44	0.19	-0.54	ns
Vegfb	vascular endothelial growth factor B	22340	1.17	1.10	0.85	1.37	0.84	*
Htatip2	HIV-1 tat interactive protein 2, homolog (human)	53415	0.37	0.57	0.47	0.80	0.01	ns
Scrn2	secernin 2	217140	0.36	0.37	0.35	1.00	-0.12	ns
Copz1	coatomer protein complex, subunit zeta 1	56447	1.98	1.83	2.03	0.97	0.24	ns
Nox4	NADPH oxidase 4	50490	0.63	0.41	0.37	1.68	0.72	ns
Setdb1	SET domain, bifurcated 1	84505	0.91	0.80	0.80	1.13	-0.14	ns
Ptrh2	peptidyl-tRNA hydrolase 2	217057	1.60	1.46	1.17	1.36	0.45	ns
Lsm2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	27756	1.61	1.13	1.13	1.42	0.71	ns
Dhcr24	24-dehydrocholesterol reductase	74754	0.97	0.89	0.85	1.14	0.53	ns
Gtf2ird1	general transcription factor II I repeat domain-containing 1	57080	1.00	0.93	1.00	1.00	0.10	ns
Zfp758	zinc finger protein 758	224598	0.40	0.38	0.24	1.67	0.80	ns
Edn1	endothelin 1	13614	0.24	0.38	0.38	0.62	-0.71	ns
Adamtsl4	ADAMTS-like 4	229595	0.36	0.37	0.45	0.78	-0.08	ns
Xrcc5	X-ray repair complementing defective repair in Chinese hamster cells 5	22596	0.42	0.43	0.22	1.87	0.40	ns
Parp3	poly (ADP-ribose) polymerase family, member 3	235587	0.28	0.25	0.34	0.81	-0.74	ns
Cul4a	cullin 4A	99375	0.70	0.59	0.97	0.72	-0.69	ns
Osbpl2	oxysterol binding protein-like 2	228983	0.90	0.91	0.96	0.94	-0.54	ns
Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	16653	1.88	1.97	2.19	0.85	-0.70	ns
Casd1	CAS1 domain containing 1	213819	0.89	0.92	0.93	0.96	-0.57	ns
Gtrgeo22	gene trap ROSA b-geo 22	110012	0.53	0.43	0.43	1.23	0.79	ns
Map2k4	mitogen activated protein kinase kinase 4	26398	0.71	0.62	0.70	1.01	-0.34	ns
Lrrk1	leucine-rich repeat kinase 1	233328	1.16	0.87	0.90	1.28	0.57	ns
Chmp4b	chromatin modifying protein 4B	75608	7.10	7.13	8.26	0.86	-0.83	*
Adrbk1	adrenergic receptor kinase, beta 1	110355	1.00	0.92	1.01	0.99	0.35	ns
9130404D08Rik	RIKEN cDNA 9130404D08 gene	74549	0.41	0.53	0.49	0.83	-0.59	ns
3930401K13Rik	RIKEN cDNA 3930401K13 gene	74022	2.99	2.34	2.87	1.03	-0.10	ns
Taf11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor	68776	0.38	0.39	0.27	1.42	0.91	*
Zfp426	zinc finger protein 426	235028	0.48	0.39	0.31	1.56	0.94	**
Uxs1	UDP-glucuronate decarboxylase 1	67883	0.59	0.65	0.60	0.97	-0.20	ns
Exosc1	exosome component 1	66583	1.29	1.39	1.06	1.21	0.73	ns
Siva1	SIVA1, apoptosis-inducing factor	30954	4.09	4.33	4.20	0.97	-0.18	ns
Ldb1	LIM domain binding 1	16825	1.22	1.12	0.94	1.30	0.79	ns
Pla2g12a	phospholipase A2, group XIIA	66350	0.40	0.50	0.54	0.74	-0.66	ns
Prkar1a	protein kinase, cAMP dependent regulatory, type I, alpha	19084	4.76	4.68	4.69	1.01	0.52	ns
Col4a1	procollagen, type IV, alpha 1	12826	2.21	2.07	0.87	2.52	0.59	ns
Tmpo	thymopoietin	21917	6.68	6.46	5.68	1.17	0.42	ns
Mgat2	mannoside acetylglucosaminyltransferase 2	217664	1.45	1.45	1.49	0.97	-0.53	ns
Bap1	Brca1 associated protein 1	104416	1.43	1.49	1.54	0.92	-0.19	ns
Cdca3	cell division cycle associated 3	14793	1.81	1.74	2.47	0.73	-0.26	ns
Klhl26	kelch-like 26 (Drosophila)	234378	0.86	0.76	0.91	0.94	0.19	ns
2310011J03Rik	RIKEN cDNA 2310011J03 gene	66374	0.82	0.66	0.63	1.29	0.44	ns
Arpc5l	actin related protein 2/3 complex, subunit 5-like	74192	2.28	2.28	1.97	1.15	0.16	ns
Zfp281	zinc finger protein 281	226442	0.97	0.88	0.77	1.24	0.58	ns
Cacybp	calcyclin binding protein	12301	1.83	1.88	1.61	1.13	-0.26	ns
Mrpl12	mitochondrial ribosomal protein L12	56282	2.52	2.44	2.69	0.93	-0.20	ns
Rpl7l1	ribosomal protein L7-like 1	66229	1.89	1.61	1.04	1.81	0.99	***
Ctdsp1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	227292	1.59	1.79	1.12	1.42	0.50	ns
Rnf11	ring finger protein 11	29864	2.00	1.91	2.06	0.97	-0.35	ns
Slc35f5	solute carrier family 35, member F5	74150	0.71	0.76	1.03	0.69	-0.88	*
Limk2	LIM motif-containing protein kinase 2	16886	0.60	0.81	0.71	0.84	-0.53	ns
Strbp	spermatid perinuclear RNA binding protein	20744	1.92	1.42	1.34	1.43	0.58	ns
Prpsap2	phosphoribosyl pyrophosphate synthetase-associated protein 2	212627	0.74	0.62	0.58	1.28	0.75	ns
Ndfip2	Nedd4 family interacting protein 2	76273	1.58	1.45	1.97	0.80	-0.52	ns
Thap7	THAP domain containing 7	69009	1.03	1.13	1.10	0.94	-0.11	ns
6720460F02Rik	RIKEN cDNA 6720460F02 gene	109212	0.60	0.66	0.69	0.87	0.29	ns
Spryd4	SPRY domain containing 4	66701	0.46	0.39	0.37	1.23	0.54	ns
Zcchc17	zinc finger, CCHC domain containing 17	619605	0.49	0.59	0.50	0.98	0.36	ns
Gatad1	GATA zinc finger domain containing 1	67210	1.17	0.97	1.09	1.07	0.13	ns
Trmt5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	76357	0.36	0.46	0.41	0.87	-0.18	ns
Rbm28	RNA binding motif protein 28	68272	1.07	1.15	1.02	1.04	0.55	ns
Tmem185b	transmembrane protein 185B	226351	0.92	1.01	0.83	1.10	0.33	ns
P4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	18451	1.66	1.87	1.88	0.88	0.20	ns
D230025D16Rik	RIKEN cDNA D230025D16 gene	234678	0.60	0.66	0.56	1.07	0.57	ns
Chtf18	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	214901	0.47	0.49	0.25	1.84	0.81	ns
AA408296	expressed sequence AA408296	215193	0.33	0.36	0.31	1.06	0.00	ns
Dullard	Dullard homolog (Xenopus laevis)	67181	1.60	1.62	1.90	0.84	-0.47	ns
Tsc2	tuberous sclerosis 2	22084	0.99	0.75	0.53	1.87	0.95	**
Npnt	nephronectin	114249	7.80	8.32	2.92	2.66	0.39	ns
Mtrr	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	210009	0.21	0.31	0.37	0.58	-0.28	ns
Mrps35	mitochondrial ribosomal protein S35	232536	0.77	0.80	0.72	1.07	0.62	ns
Rab23	RAB23, member RAS oncogene family	19335	0.31	0.38	0.37	0.82	-0.57	ns
Nat11	N-acetyltransferase 11	70999	1.73	1.48	1.39	1.24	0.94	**
AI314180	expressed sequence AI314180	230249	0.80	0.76	0.86	0.93	-0.66	ns
Ank3	ankyrin 3, epithelial	11735	1.92	1.33	1.75	1.09	-0.31	ns
Zfp160	zinc finger protein 160	224585	0.61	0.47	0.43	1.42	0.81	ns

Ptpn13	protein tyrosine phosphatase, non-receptor type 13	19249	1.74	1.91	1.91	0.91	-0.10	ns
Brcc3	BRCA1/BRCA2-containing complex, subunit 3	210766	0.63	0.52	0.91	0.68	-0.43	ns
Tlcd1	TLC domain containing 1	68385	0.91	0.80	0.48	1.88	0.09	ns
Slc35c1	solute carrier family 35, member C1	228368	0.29	0.29	0.30	0.96	-0.05	ns
Spnb2	spectrin beta 2	20742	7.66	6.44	7.27	1.05	0.36	ns
Mrpl44	mitochondrial ribosomal protein L44	69163	1.37	1.17	0.80	1.71	0.78	ns
H6pd	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	100198	0.95	1.09	1.31	0.72	-0.90	*
Sec24c	SEC24 related gene family, member C (S. cerevisiae)	218811	2.13	2.30	2.08	1.02	0.49	ns
Ube3b	ubiquitin protein ligase E3B	117146	0.88	0.85	0.84	1.04	0.74	ns
AU040320	expressed sequence AU040320	100317	0.82	0.86	0.89	0.91	-0.30	ns
Clint1	clathrin interactor 1	216705	2.61	2.63	3.18	0.82	-0.81	ns
Fbxo18	F-box protein 18	50755	0.88	0.82	0.61	1.45	0.85	*
Nisch	nischarin	64652	5.26	4.13	3.58	1.46	0.82	*
Eprs		107508	2.26	2.39	1.85	1.21	0.52	ns
LOC633677		633677	2.26	2.39	1.85	1.21	0.52	ns
2310001A20Rik	RIKEN cDNA 2310001A20 gene	71881	0.80	0.96	0.90	0.88	0.05	ns
Ets1	E26 avian leukemia oncogene 1, 5' domain	23871	1.63	1.41	1.03	1.57	0.99	***
2810407C02Rik	RIKEN cDNA 2810407C02 gene	69227	6.79	6.17	5.60	1.21	0.53	ns
Gspt1	G1 to S phase transition 1	14852	2.84	2.96	3.61	0.78	-0.83	*
Dgkz	diacylglycerol kinase zeta	104418	1.50	1.25	1.41	1.06	0.25	ns
Grwd1	glutamate-rich WD repeat containing 1	101612	0.58	0.74	0.61	0.95	-0.16	ns
Hadha	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	97212	1.93	1.75	1.67	1.15	0.50	ns
Srebf2	sterol regulatory element binding factor 2	20788	1.73	1.49	2.46	0.70	-0.57	ns
Nup153	nucleoporin 153	218210	2.96	2.89	2.98	0.99	0.42	ns
LOC671535		671535	0.33	0.44	0.73	0.45	-0.75	ns
Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	108148	2.16	2.38	1.22	1.76	0.57	ns
Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	66218	6.71	6.20	6.53	1.02	0.17	ns
Rbm5	RNA binding motif protein 5	83486	2.83	2.59	2.26	1.25	0.97	**
Wdr82	WD repeat domain containing 82	77305	1.00	1.06	1.07	0.93	0.16	ns
Wasl	Wiskott-Aldrich syndrome-like (human)	73178	4.81	6.07	4.43	1.08	0.12	ns
Tbcd	tubulin-specific chaperone d	108903	1.28	1.20	1.20	1.06	0.46	ns
Nckap1	NCK-associated protein 1	50884	6.02	5.43	4.70	1.28	0.60	ns
Smc4	structural maintenance of chromosomes 4	70099	10.07	9.51	8.24	1.22	0.87	*
Obfc2a	oligonucleotide/oligosaccharide-binding fold containing 2A	109019	0.49	0.51	0.47	1.04	-0.42	ns
Anks1	ankyrin repeat and SAM domain containing 1	224650	0.33	0.39	0.32	1.03	-0.04	ns
Sucla2	succinate-Coenzyme A ligase, ADP-forming, beta subunit	20916	2.50	2.29	3.13	0.79	-0.45	ns
Cited2		17684	4.49	4.02	4.20	1.06	-0.27	ns
Prdm4	PR domain containing 4	72843	0.85	0.66	0.57	1.48	0.85	*
Pkp4	plakophilin 4	227937	2.11	2.18	1.71	1.23	-0.17	ns
Tex2	testis expressed gene 2	21763	0.49	0.50	0.82	0.60	-0.31	ns
Skil	SKI-like	20482	3.59	3.81	2.57	1.39	0.79	ns
9130401M01Rik	RIKEN cDNA 9130401M01 gene	75758	0.69	0.83	1.06	0.65	-0.45	ns
Mcat	malonyl CoA:ACP acyltransferase (mitochondrial)	223722	0.38	0.39	0.51	0.74	-0.76	ns
Ahnak	AHNAK nucleoprotein (desmoyokin)	66395	10.07	10.56	6.61	1.52	0.66	ns
Tmem63b	transmembrane protein 63b	224807	0.56	0.53	0.38	1.46	0.33	ns
Dock1	dedicator of cyto-kinesis 1	330662	0.86	0.88	0.61	1.40	0.11	ns
Cxxc1	CXXC finger 1 (PHD domain)	74322	0.62	0.64	0.67	0.92	-0.05	ns
Utrn	utrophin	22288	2.24	1.70	1.98	1.13	-0.03	ns
Gcap14	granule cell antiserum positive 14	72972	0.54	0.50	0.47	1.14	-0.21	ns
2010106G01Rik	RIKEN cDNA 2010106G01 gene	66552	1.84	1.56	2.04	0.90	-0.36	ns
Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7	108150	0.23	0.36	0.28	0.81	0.07	ns
Abcc1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	17250	3.89	3.83	5.07	0.76	-0.79	ns
Man1b1	mannosidase, alpha, class 1B, member 1	227619	0.41	0.50	0.34	1.21	0.50	ns
Topbp1	topoisomerase (DNA) II beta binding protein	235559	3.10	2.93	3.12	0.99	0.49	ns
Cep55	centrosomal protein 55	74107	2.57	2.78	2.73	0.94	0.47	ns
Ostf1	osteoclast stimulating factor 1	20409	1.67	1.68	1.52	1.09	0.17	ns
Plekhg5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	269608	0.35	0.44	0.32	1.09	0.35	ns
Nbea	neurobeachin	26422	1.75	1.09	0.56	3.08	0.65	ns
Utp20	UTP20, small subunit (SSU) processome component, homolog (yeast)	70683	0.99	1.00	0.71	1.39	0.49	ns
Fbxo38	F-box protein 38	107035	0.54	0.57	0.59	0.90	0.07	ns
1110002N22Rik	RIKEN cDNA 1110002N22 gene	68550	0.35	0.38	0.32	1.09	0.08	ns
Shprh	SNF2 histone linker PHD RING helicase	268281	0.39	0.35	0.41	0.95	-0.52	ns
Grpel2	GrpE-like 2, mitochondrial	17714	0.63	0.71	0.88	0.71	-0.47	ns
Tenc1	tensin like C1 domain-containing phosphatase	209039	0.46	0.36	0.23	2.03	0.84	*
Clasp1	CLIP associating protein 1	76707	1.82	1.72	1.32	1.37	0.44	ns
Las1l	LAS1-like (S. cerevisiae)	76130	0.47	0.53	0.57	0.82	-0.10	ns
Spnb3	spectrin beta 3	20743	1.84	1.45	0.83	2.21	0.07	ns
Gfer	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	11692	1.08	1.25	0.94	1.14	0.60	ns
AA409316	expressed sequence AA409316	105732	1.30	1.40	1.62	0.80	-0.78	ns
Smarcad1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1`	13990	1.16	1.00	1.24	0.93	-0.56	ns
Farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived)	223254	0.81	0.74	0.95	0.85	-0.20	ns
Sos2	Son of sevenless homolog 2 (Drosophila)	20663	0.97	1.05	1.34	0.72	-0.97	**
Rassf8	Ras association (RalGDS/AF-6) domain family 8	71323	0.69	0.69	0.92	0.75	-0.40	ns
Slain2	SLAIN motif family, member 2	75991	0.93	0.77	0.92	1.01	0.10	ns
Ap2b1	adaptor-related protein complex 2, beta 1 subunit	71770	2.58	2.39	2.91	0.88	-0.44	ns
Pcdh1	protocadherin 1	75599	0.22	0.33	0.35	0.62	-0.27	ns
Myo5b	myosin Vb	17919	0.32	0.52	0.59	0.53	-0.57	ns
Wwp1	WW domain containing E3 ubiquitin protein ligase 1	107568	0.59	0.55	0.49	1.19	0.08	ns
Aldh3b1	aldehyde dehydrogenase 3 family, member B1	67689	0.37	0.23	0.23	1.64	0.19	ns
Arhgef10	Rho guanine nucleotide exchange factor (GEF) 10	234094	0.34	0.38	0.22	1.55	0.64	ns

Arhgef5	Rho guanine nucleotide exchange factor (GEF) 5	54324	2.12	2.11	2.06	1.03	0.40	ns
Zfyve26	zinc finger, FYVE domain containing 26	211978	0.70	0.62	0.85	0.82	-0.55	ns
Cables2	Cdk5 and Abl enzyme substrate 2	252966	0.38	0.39	0.57	0.67	-0.72	ns
Cgnl1		68178	1.95	1.69	1.65	1.17	0.70	ns
LOC677485		677485	1.95	1.69	1.65	1.17	0.70	ns
Tada2l	transcriptional adaptor 2 (ADA2 homolog, yeast)-like	217031	0.67	0.71	0.75	0.88	-0.58	ns
5930416I19Rik	RIKEN cDNA 5930416I19 gene	72440	0.89	1.05	1.20	0.73	-0.31	ns
Hoxb9	homeo box B9	15417	2.10	1.65	1.43	1.46	0.86	*
Hspa1b	heat shock protein 1B	15511	9.41	10.34	9.68	0.97	-0.44	ns
Brwd1	bromodomain and WD repeat domain containing 1	93871	0.87	1.08	0.88	0.99	0.05	ns
Iqsec1	IQ motif and Sec7 domain 1	232227	0.98	1.10	0.71	1.38	0.67	ns
Qser1	glutamine and serine rich 1	99003	0.94	0.62	0.52	1.77	0.86	*
Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	93747	1.14	1.16	1.28	0.88	-0.49	ns
B3gnt1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	108902	0.98	0.90	0.60	1.64	0.83	*
Parp4		328417	0.47	0.41	0.41	1.14	0.84	*
Sept5		18951	0.47	0.92	0.94	0.50	-0.87	*
Gp1bb		14724	0.47	0.92	0.94	0.50	-0.87	*
Trim16	tripartite motif protein 16	94092	0.33	0.37	0.37	0.89	-0.03	ns
Coro2a	coronin, actin binding protein 2A	107684	0.57	0.71	0.74	0.76	-0.65	ns
Sfrs11	splicing factor, arginine/serine-rich 11	69207	5.55	5.36	4.62	1.20	0.16	ns
1700081L11Rik	RIKEN cDNA 1700081L11 gene	76719	1.40	1.19	0.94	1.49	0.77	ns
Zfp322a	zinc finger protein 322a	218100	0.39	0.33	0.44	0.90	-0.65	ns
Creb3l2	cAMP responsive element binding protein 3-like 2	208647	1.16	0.88	0.62	1.87	0.78	ns
Usp53	ubiquitin specific peptidase 53	99526	0.33	0.38	0.80	0.41	-0.90	*
Amotl2	angiomotin like 2	56332	1.71	1.75	1.42	1.20	0.16	ns
Cars	cysteinyl-tRNA synthetase	27267	0.65	0.68	0.80	0.82	-0.63	ns
Med19	mediator of RNA polymerase II transcription, subunit 19 homolog (yeast)	381379	1.13	0.92	0.89	1.26	0.68	ns
Wtap	Wilms' tumour 1-associating protein	60532	4.49	4.17	2.81	1.59	0.93	**
Phactr2	phosphatase and actin regulator 2	215789	0.46	0.28	0.24	1.93	0.07	ns
Erdr1	erythroid differentiation regulator 1	170942	2.29	2.45	3.63	0.63	-0.18	ns
Lrrc1	leucine rich repeat containing 1	214345	0.51	0.48	0.35	1.44	0.21	ns
Ccdc86	coiled-coil domain containing 86	108673	0.58	0.77	0.41	1.41	0.41	ns
Zfp236	Zinc finger protein 236	329002	0.85	0.79	0.75	1.13	-0.30	ns
Dgcr6	DiGeorge syndrome critical region gene 6	13353	0.55	0.73	0.75	0.73	-0.38	ns
Taf4a	TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor	228980	0.60	0.61	0.89	0.67	-0.79	ns
Helz	helicase with zinc finger domain	78455	1.30	1.08	1.02	1.26	0.90	*
Ppil5	peptidylprolyl isomerase (cyclophilin) like 5	69706	1.05	1.30	1.63	0.64	-0.48	ns
Banp	Btg3 associated nuclear protein	53325	0.41	0.38	0.39	1.05	-0.16	ns
Metapl1	methionine aminopeptidase-like 1	66559	0.55	0.54	0.25	2.22	0.78	ns
Rbm6	RNA binding motif protein 6	19654	0.74	0.88	0.60	1.23	0.70	ns
Smtn	smoothelin	29856	1.03	1.09	1.41	0.73	-0.78	ns
Hoxb8	homeo box B8	15416	0.96	0.55	0.45	2.12	0.42	ns
Ilkap	integrin-linked kinase-associated serine/threonine phosphatase 2C	67444	0.97	1.03	0.91	1.05	0.56	ns
Zfp36	zinc finger protein 36	22695	0.49	0.46	0.44	1.12	-0.44	ns
Plaur	plasminogen activator, urokinase receptor	18793	0.53	0.75	1.29	0.41	-0.84	*
Hmgb2		97165	6.21	7.21	7.80	0.79	-0.01	ns
Hist1h2be		319179	1.31	0.94	0.81	1.61	0.80	ns
Hist1h2bl		319185	1.31	0.94	0.81	1.61	0.80	ns
Hist1h2bm		319186	1.31	0.94	0.81	1.61	0.80	ns
Hist1h2bp		319188	1.31	0.94	0.81	1.61	0.80	ns
LOC665622		665622	1.31	0.94	0.81	1.61	0.80	ns
Nfya	nuclear transcription factor-Y alpha	18044	1.44	1.35	1.07	1.34	0.37	ns
Iscu	IscU iron-sulfur cluster scaffold homolog (E. coli)	66383	2.63	2.26	1.75	1.50	0.81	ns
Mrpl21	mitochondrial ribosomal protein L21	353242	1.68	1.48	1.02	1.64	0.83	*
1500032L24Rik	RIKEN cDNA 1500032L24 gene	69029	3.27	3.31	3.16	1.03	0.21	ns
Mrps28	mitochondrial ribosomal protein S28	66230	0.87	1.14	0.93	0.93	-0.53	ns
Anapc13	anaphase promoting complex subunit 13	69010	1.98	2.21	1.85	1.06	0.45	ns
Actr2	ARP2 actin-related protein 2 homolog (yeast)	66713	4.82	4.81	6.30	0.76	-0.75	ns
Ptk7	PTK7 protein tyrosine kinase 7	71461	0.37	0.43	0.43	0.86	-0.23	ns
Polr2k	polymerase (RNA) II (DNA directed) polypeptide K	17749	5.58	5.29	6.91	0.80	-0.33	ns
2310061C15Rik	RIKEN cDNA 2310061C15 gene	66531	0.84	0.86	0.86	0.97	0.50	ns
Gins1	GINS complex subunit 1 (Psf1 homolog)	69270	0.91	1.02	1.08	0.84	-0.26	ns
Taf6l	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor	225895	1.03	0.64	0.52	1.97	0.78	ns
5330431N19Rik	RIKEN cDNA 5330431N19 gene	226162	1.23	1.35	1.02	1.20	0.64	ns
Stard13	serologically defined colon cancer antigen 13	243362	0.34	0.29	0.24	1.40	0.34	ns
Thnsl1	threonine synthase-like 1 (bacterial)	208967	0.31	0.34	0.32	0.96	-0.23	ns
Mycbp	c-myc binding protein	56309	0.77	0.75	0.90	0.85	-0.77	ns
Pcbd2	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	72562	0.93	1.04	0.80	1.15	0.61	ns
Tradd	TNFRSF1A-associated via death domain	71609	0.54	0.52	0.62	0.86	-0.13	ns
Kctd2	potassium channel tetramerisation domain containing 2	70382	1.07	0.96	1.05	1.01	0.32	ns
1810014F10Rik	RIKEN cDNA 1810014F10 gene	69064	0.19	0.30	0.52	0.37	-0.80	ns
Senp6	SUMO/sentrin specific peptidase 6	215351	1.86	1.60	1.19	1.55	0.95	**
Bag5	BCL2-associated athanogene 5	70369	0.87	0.83	0.92	0.94	0.26	ns
Bola1	bolA-like 1 (E. coli)	69168	0.59	0.64	0.60	0.99	-0.43	ns
Trp53inp2	transformation related protein 53 inducible nuclear protein 2	68728	0.75	0.69	0.99	0.75	-0.51	ns
Tbrg1	transforming growth factor beta regulated gene 1	21376	3.00	2.46	2.38	1.26	0.88	*
Rtn4	reticulon 4	68585	10.10	9.47	9.47	1.06	0.18	ns
Zdhhc2	zinc finger, DHHC domain containing 2	70546	0.77	0.79	0.18	4.38	0.63	ns
Zdhhc2	zinc finger, DHHC domain containing 2	70546	0.23	0.30	0.05	4.51	0.66	ns
Dek	DEK oncogene (DNA binding)	110052	9.03	8.82	9.63	0.93	0.24	ns
Klhl7	kelch-like 7 (Drosophila)	52323	0.29	0.30	0.35	0.84	-0.57	ns
Tfrc	transferrin receptor	22042	4.74	5.95	6.80	0.69	-0.66	ns
Eif2s1	eukaryotic translation initiation factor 2, subunit 1 alpha	13665	5.12	5.13	5.40	0.94	-0.06	ns
Tm7sf3	transmembrane 7 superfamily member 3	67623	0.41	0.41	0.40	1.03	-0.45	ns

Ttc27	tetratricopeptide repeat domain 27	74196	0.36	0.42	0.27	1.35	0.63	ns
2810012G03Rik	RIKEN cDNA 2810012G03 gene	66306	0.88	0.92	0.93	0.95	0.42	ns
Lman1	lectin, mannose-binding, 1	70361	1.24	1.24	1.33	0.93	0.28	ns
Thoc5	THO complex 5	107829	0.63	0.61	0.71	0.89	-0.02	ns
Ranbp3	RAN binding protein 3	71810	0.84	0.82	0.60	1.39	0.91	*
Rbm22	RNA binding motif protein 22	66810	0.97	1.12	1.16	0.84	0.22	ns
Pnpt1	polyribonucleotide nucleotidyltransferase 1	71701	0.48	0.61	0.69	0.70	-0.97	**
Snrpd2	small nuclear ribonucleoprotein D2	107686	5.19	4.85	5.05	1.02	0.37	ns
Dnajc8		68598	3.53	3.46	3.25	1.08	0.65	ns
0610009O20Rik	RIKEN cDNA 0610009O20 gene	66839	0.49	0.48	0.47	1.03	0.58	ns
Zfp512	zinc finger protein 512	269639	1.21	1.16	1.13	1.07	0.83	*
Rbm17	RNA binding motif protein 17	76938	2.60	2.75	2.17	1.19	0.66	ns
Dhx35	DEAH (Asp-Glu-Ala-His) box polypeptide 35	71715	0.60	0.56	0.62	0.97	-0.38	ns
Ihpk1	inositol hexaphosphate kinase 1	27399	1.11	0.92	0.83	1.34	0.94	**
Ctdp1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	67655	0.49	0.57	0.52	0.94	0.46	ns
Tsfm	Ts translation elongation factor, mitochondrial	66399	0.72	0.57	0.59	1.21	0.55	ns
Mett11d1	methyltransferase 11 domain containing 1	52535	0.40	0.37	0.40	0.99	0.02	ns
Kbtbd7	kelch repeat and BTB (POZ) domain containing 7	211255	0.78	0.82	0.90	0.85	-0.68	ns
Clcn7	chloride channel 7	26373	0.47	0.47	0.36	1.27	0.58	ns
Wdr57	WD repeat domain 57 (U5 snRNP specific)	66585	1.36	1.21	2.06	0.65	-0.66	ns
Tanc1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	66860	1.58	1.23	0.88	1.79	0.34	ns
5730469M10Rik	RIKEN cDNA 5730469M10 gene	70564	2.24	2.65	6.61	0.34	-0.75	ns
Slc25a24	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	229731	4.15	4.40	3.19	1.30	0.68	ns
Zdhhc24	zinc finger, DHHC domain containing 24	70605	0.46	0.34	0.35	1.32	0.29	ns
Ccdc53	coiled-coil domain containing 53	67282	1.04	1.06	1.03	1.00	-0.47	ns
Rnaseh2a	ribonuclease H2, large subunit	69724	1.39	1.53	1.53	0.91	-0.12	ns
Pih1d1	PIH1 domain containing 1	68845	0.55	0.77	0.84	0.66	-0.60	ns
R3hdm2	R3H domain containing 2	71750	1.44	1.15	1.25	1.15	0.19	ns
Rnaset2a		#######	5.78	5.56	6.47	0.89	-0.65	ns
Rnaset2b		68195	5.78	5.56	6.47	0.89	-0.65	ns
R3hcc1	R3H domain and coiled-coil containing 1	71843	0.48	0.48	0.48	0.99	0.13	ns
2810008M24Rik	RIKEN cDNA 2810008M24 gene	75616	1.60	2.43	2.64	0.60	-0.91	*
Fbxo7	F-box protein 7	69754	0.76	0.56	0.56	1.33	0.47	ns
Myh10	myosin, heavy polypeptide 10, non-muscle	77579	3.58	3.70	3.34	1.07	0.72	ns
Pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)	59001	1.12	0.97	0.95	1.17	0.14	ns
Atp13a2	ATPase type 13A2	74772	0.52	0.43	0.54	0.96	-0.43	ns
Papd1	PAP associated domain containing 1	67440	0.73	0.75	0.81	0.90	0.16	ns
Creld2	cysteine-rich with EGF-like domains 2	76737	1.21	1.36	1.06	1.14	0.33	ns
Eif4g2	eukaryotic translation initiation factor 4, gamma 2	13690	11.18	11.08	11.88	0.94	-0.67	ns
Ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	67533	0.88	0.88	0.76	1.15	0.08	ns
2510012J08Rik	RIKEN cDNA 2510012J08 gene	70312	1.62	1.46	1.58	1.02	-0.04	ns
Rrbp1	ribosome binding protein 1	81910	1.03	1.33	1.60	0.64	-0.37	ns
Vkorc1	vitamin K epoxide reductase complex, subunit 1	27973	0.96	1.05	1.12	0.85	-0.31	ns
Acsl3	acyl-CoA synthetase long-chain family member 3	74205	1.26	0.98	1.08	1.16	-0.10	ns
5730494N06Rik	RIKEN cDNA 5730494N06 gene	70612	1.86	1.81	1.95	0.95	-0.16	ns
Nub1	negative regulator of ubiquitin-like proteins 1	53312	0.68	0.73	0.87	0.78	-0.93	**
Gtf3c2	general transcription factor IIIC, polypeptide 2, beta	71752	1.26	1.42	1.58	0.79	-0.92	**
Itgav	integrin alpha V	16410	5.07	5.26	4.06	1.24	0.25	ns
1700034H14Rik	RIKEN cDNA 1700034H14 gene	67105	0.31	0.40	0.31	1.01	0.25	ns
Prmt1	protein arginine N-methyltransferase 1	15469	2.97	3.16	3.33	0.89	-0.59	ns
Snn	stannin	20621	1.00	0.81	0.66	1.50	0.22	ns
Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	66091	4.16	4.43	5.67	0.73	-0.56	ns
Coq2	coenzyme Q2 homolog, prenyltransferase (yeast)	71883	0.97	1.27	1.71	0.56	-0.82	*
Fcf1	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	73736	2.73	3.09	3.62	0.75	-0.69	ns
Fastkd3	FAST kinase domains 3	69577	0.47	0.67	0.85	0.55	-0.85	*
Apoo		68316	0.74	0.58	0.98	0.75	-0.37	ns
D11Wsu47e	DNA segment, Chr 11, Wayne State University 47, expressed	276852	0.41	0.31	0.29	1.43	0.86	*
Snupn	snurportin 1	66069	0.33	0.36	0.34	0.97	0.38	ns
Ints10		70885	0.49	0.67	0.61	0.81	-0.36	ns
LOC674888		674888	0.49	0.67	0.61	0.81	-0.36	ns
Brwd2	bromodomain and WD repeat domain containing 2	207425	1.20	1.15	1.32	0.90	-0.43	ns
Gstk1	glutathione S-transferase kappa 1	76263	0.30	0.47	0.83	0.36	-0.85	*
Fbxo21	F-box protein 21	231670	0.56	0.47	0.57	0.97	-0.21	ns
Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	69719	0.75	0.87	0.74	1.01	-0.18	ns
Ppat	phosphoribosyl pyrophosphate amidotransferase	231327	1.06	1.01	1.16	0.90	-0.73	ns
Rapgef2	Rap guanine nucleotide exchange factor (GEF) 2	76089	1.92	1.91	1.78	1.07	-0.42	ns
Lpin2	lipin 2	64898	0.98	0.83	0.76	1.29	0.52	ns
Ddx10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	77591	0.98	0.89	0.83	1.17	0.80	ns
Dph5	DPH5 homolog (S. cerevisiae)	69740	0.51	0.59	0.49	1.02	0.31	ns
Pou6f1	POU domain, class 6, transcription factor 1	19009	0.72	0.56	0.72	0.99	-0.10	ns
2410008K03Rik	RIKEN cDNA 2410008K03 gene	71962	0.37	0.32	0.27	1.39	0.16	ns
Tmem181	transmembrane protein 181	77106	0.93	0.92	0.62	1.49	0.83	*
Brms1l	breast cancer metastasis-suppressor 1-like	52592	1.48	1.48	1.30	1.14	0.71	ns
Twistnb	TWIST neighbor	28071	1.10	1.16	1.27	0.86	-0.45	ns
Sec63	SEC63-like (S. cerevisiae)	140740	0.91	0.64	0.54	1.70	0.65	ns
Crebzf	CREB/ATF bZIP transcription factor	233490	0.85	0.82	0.74	1.14	0.09	ns
Fbxl17	F-box and leucine-rich repeat protein 17	50758	0.61	0.54	0.40	1.52	0.62	ns
2010300C02Rik		72097	0.73	0.82	0.84	0.87	-0.46	ns
Nars	asparaginyl-tRNA synthetase	70223	4.06	4.54	4.12	0.98	0.35	ns
Col4a3bp	procollagen, type IV, alpha 3 (Goodpasture antigen) binding protein	68018	1.34	1.52	1.64	0.81	-0.37	ns
Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	66921	1.45	1.43	1.14	1.26	0.51	ns
Apaf1	apoptotic peptidase activating factor 1	11783	0.55	0.53	0.54	1.02	-0.36	ns
2510003E04Rik	RIKEN cDNA 2510003E04 gene	72320	2.50	2.29	2.03	1.23	0.80	ns
2700029M09Rik	RIKEN cDNA 2700029M09 gene	72612	3.17	2.98	3.37	0.93	0.24	ns

Znhit3	zinc finger, HIT type 3	448850	0.46	0.48	0.78	0.59	-0.86	*
Sfrs2ip	splicing factor, arginine/serine-rich 2, interacting protein	72193	2.46	2.28	2.78	0.88	-0.61	ns
Ttll5	tubulin tyrosine ligase-like family, member 5	320244	0.63	0.53	0.51	1.23	0.26	ns
Fbxo45	F-box protein 45	268882	1.08	1.08	1.30	0.83	-0.25	ns
Cdc2l5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	69562	1.08	1.00	1.16	0.92	-0.42	ns
Vps36	vacuolar protein sorting 36 (yeast)	70160	0.64	0.76	0.62	1.02	0.22	ns
Creb1	cAMP responsive element binding protein 1	12912	1.72	1.80	1.42	1.20	0.54	ns
Dhrs13	dehydrogenase/reductase (SDR family) member 13	70451	0.83	0.82	0.67	1.24	-0.13	ns
Galc	galactosylceramidase	14420	0.32	0.34	0.38	0.85	-0.73	ns
Dip2a	DIP2 disco-interacting protein 2 homolog A (Drosophila)	64451	1.25	1.09	1.07	1.16	0.28	ns
Prkar2a	protein kinase, cAMP dependent regulatory, type II alpha	19087	1.76	1.69	1.54	1.13	0.72	ns
Wbp7	WW domain binding protein 7	75410	0.93	0.96	1.15	0.80	-0.87	*
Rfc5	replication factor C (activator 1) 5	72151	2.33	2.38	2.83	0.82	-0.45	ns
D19Ertd737e	DNA segment, Chr 19, ERATO Doi 737, expressed	76539	2.02	1.89	1.20	1.67	0.96	**
Ppil2	peptidylprolyl isomerase (cyclophilin)-like 2	66053	1.50	1.51	1.79	0.84	-0.56	ns
2310007D09Rik	RIKEN cDNA 2310007D09 gene	71878	0.61	0.69	0.76	0.80	0.14	ns
Clip1	CAP-GLY domain containing linker protein 1	56430	1.00	0.86	0.94	1.06	0.21	ns
Tmem65	transmembrane protein 65	74868	1.10	0.86	0.81	1.34	0.77	ns
Ube2c	ubiquitin-conjugating enzyme E2C	68612	7.90	7.61	8.46	0.93	0.31	ns
D12Ertd647e	DNA segment, Chr 12, ERATO Doi 647, expressed	52668	0.18	0.06	3.00	0.06	-0.55	ns
Scyl3	SCY1-like 3 (S. cerevisiae)	240880	0.59	0.62	0.55	1.06	0.07	ns
Zmym2	zinc finger, MYM-type 2	76007	1.38	1.27	1.16	1.19	-0.02	ns
Upf3a	UPF3 regulator of nonsense transcripts homolog A (yeast)	67031	0.65	0.97	0.90	0.72	-0.23	ns
Ttc32	tetratricopeptide repeat domain 32	75516	0.32	0.44	0.39	0.82	-0.39	ns
Zhx3	zinc fingers and homeoboxes 3	320799	0.44	0.36	0.28	1.57	0.53	ns
Igf1r	insulin-like growth factor I receptor	16001	2.84	2.56	1.99	1.42	0.15	ns
Uaca	uveal autoantigen with coiled-coil domains and ankyrin repeats	72565	0.28	0.30	0.32	0.86	0.39	ns
6820431F20Rik	RIKEN cDNA 6820431F20 gene	381598	5.32	4.85	4.91	1.08	0.33	ns
Smndc1	survival motor neuron domain containing 1	76479	1.32	1.43	1.26	1.05	0.22	ns
Rnaseh2b	ribonuclease H2, subunit B	67153	1.16	1.17	0.92	1.26	0.67	ns
3110082I17Rik	RIKEN cDNA 3110082I17 gene	73212	0.52	0.53	0.42	1.23	0.65	ns
Iws1	IWS1 homolog (S. cerevisiae)	73473	0.42	0.57	0.52	0.81	0.21	ns
Zfp740	zinc finger protein 740	68744	1.40	1.33	1.63	0.86	-0.79	ns
Sec31a	SEC31 homolog A (S. cerevisiae)	69162	0.95	0.92	0.91	1.04	-0.06	ns
Nvl	nuclear VCP-like	67459	0.35	0.44	0.26	1.37	-0.09	ns
1810048J11Rik	RIKEN cDNA 1810048J11 gene	67708	0.41	0.44	0.37	1.12	0.07	ns
Ankhd1	ankyrin repeat and KH domain containing 1	108857	0.88	1.01	0.94	0.93	0.27	ns
4631424J17Rik	RIKEN cDNA 4631424J17 gene	70802	0.74	0.55	0.57	1.30	-0.07	ns
Zfp251	zinc finger protein 251	71591	0.47	0.41	0.49	0.96	0.34	ns
Lnp	limb and neural patterns	69605	0.55	0.47	0.46	1.19	0.61	ns
4930422G04Rik	RIKEN cDNA 4930422G04 gene	71643	0.57	0.63	0.61	0.93	0.17	ns
Zfp335	zinc finger protein 335	329559	0.60	0.56	0.54	1.10	0.04	ns
Cltb	clathrin, light polypeptide (Lcb)	74325	0.70	0.80	1.29	0.54	-0.53	ns
Etaa1	Ewing's tumor-associated antigen 1	68145	0.42	0.45	0.70	0.60	-0.67	ns
Kdelc2	KDEL (Lys-Asp-Glu-Leu) containing 2	68304	0.44	0.39	0.21	2.08	0.67	ns
Gpr160	G protein-coupled receptor 160	71862	0.84	0.83	0.44	1.88	0.51	ns
Rab10	RAB10, member RAS oncogene family	19325	5.51	5.51	5.37	1.02	-0.22	ns
EG622236		622236	6.66	8.31	8.09	0.82	-0.71	ns
Ubtf	upstream binding transcription factor, RNA polymerase I	21429	1.44	1.35	1.01	1.41	0.83	*
Csnk2a2	casein kinase 2, alpha prime polypeptide	13000	1.66	1.98	1.85	0.89	-0.20	ns
Rnmt	RNA (guanine-7-) methyltransferase	67897	0.59	0.62	0.66	0.90	0.26	ns
4933413G19Rik		71149	1.17	1.30	1.69	0.69	-0.12	ns
Foxm1		14235	1.17	1.30	1.69	0.69	-0.12	ns
Arsk	arylsulfatase K	77041	0.24	0.29	0.29	0.82	-0.58	ns
Wdsub1	WD repeat, SAM and U-box domain containing 1	72137	0.36	0.32	0.33	1.09	-0.44	ns
Rpl22	ribosomal protein L22	19934	16.33	15.39	15.20	1.07	0.86	*
Txndc13	thioredoxin domain containing 13	52837	1.30	1.18	1.06	1.22	0.38	ns
Rgs12	regulator of G-protein signaling 12	71729	0.31	0.38	0.36	0.84	-0.19	ns
Fbxo30	F-box protein 30	71865	0.72	0.64	0.56	1.27	0.69	ns
Nudt12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	67993	0.45	0.68	0.38	1.18	0.35	ns
Tmem50a	transmembrane protein 50A	71817	1.00	1.01	1.40	0.71	-0.66	ns
Ccdc109a	coiled-coil domain containing 109A	215999	1.05	0.99	0.77	1.36	0.12	ns
Gtf2h1	general transcription factor II H, polypeptide 1	14884	0.51	0.49	0.51	0.98	-0.37	ns
2310005E10Rik	RIKEN cDNA 2310005E10 gene	67861	0.32	0.21	0.44	0.72	-0.55	ns
Plscr1	phospholipid scramblase 1	22038	0.99	1.12	1.19	0.83	-0.40	ns
Smpd4	sphingomyelin phosphodiesterase 4	77626	0.71	0.69	0.94	0.75	-0.50	ns
1110034A24Rik	RIKEN cDNA 1110034A24 gene	109065	0.67	0.66	0.82	0.81	-0.02	ns
Acbd6	acyl-Coenzyme A binding domain containing 6	72482	0.66	0.58	0.43	1.53	0.75	ns
Rai1	retinoic acid induced 1	19377	0.78	0.83	0.76	1.02	0.04	ns
Acad9	acyl-Coenzyme A dehydrogenase family, member 9	229211	0.54	0.61	0.47	1.14	0.27	ns
2700089E24Rik	RIKEN cDNA 2700089E24 gene	381820	1.55	1.54	0.96	1.60	0.87	*
Brf1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	72308	0.44	0.46	0.44	0.99	0.46	ns
3000004C01Rik	RIKEN cDNA 3000004C01 gene	70218	0.71	0.82	0.92	0.77	0.10	ns
Uqcrh	ubiquinol-cytochrome c reductase hinge protein	66576	4.79	4.81	4.97	0.96	-0.13	ns
Cdkl1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	71091	1.78	2.22	1.28	1.38	-0.14	ns
Zfp618	zinc fingerprotein 618	72701	0.59	0.50	0.30	1.99	0.64	ns
Rpusd1	RNA pseudouridylate synthase domain containing 1	106707	0.47	0.37	0.25	1.90	0.83	*
Polr3c	polymerase (RNA) III (DNA directed) polypeptide C	74414	1.05	1.25	1.19	0.88	-0.72	ns
Agpat5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	52123	1.36	1.20	1.77	0.76	-0.08	ns
Marveld3	MARVEL (membrane-associating) domain containing 3	73608	0.67	0.67	0.41	1.62	0.46	ns
Phf14	PHD finger protein 14	75725	1.40	1.67	1.47	0.95	-0.55	ns
Cxadr	coxsackievirus and adenovirus receptor	13052	2.72	2.47	2.36	1.15	-0.16	ns
Pgm1	phosphoglucomutase 1	66681	0.33	0.37	0.40	0.82	0.06	ns
Plxna2	plexin A2	18845	0.25	0.39	0.35	0.72	0.19	ns
Ly6e	lymphocyte antigen 6 complex, locus E	17069	0.64	1.57	11.70	0.05	-0.67	ns

Iqwd1	IQ motif and WD repeats 1	74106	0.50	0.55	0.45	1.10	-0.30	ns
2610039C10Rik	RIKEN cDNA 2610039C10 gene	66578	2.18	2.11	3.05	0.71	-0.50	ns
Cdc40	cell division cycle 40 homolog (yeast)	71713	1.01	0.93	0.91	1.10	0.53	ns
Vrk2	vaccinia related kinase 2	69922	0.27	0.34	0.49	0.56	-0.59	ns
Npal1	NIPA-like domain containing 1	70701	0.70	0.85	0.69	1.00	-0.53	ns
Tex9	testis expressed gene 9	21778	0.37	0.32	0.20	1.83	0.85	*
Sh2d4a	SH2 domain containing 4A	72281	1.59	2.04	1.78	0.89	-0.59	ns
Dennd1b	DENN/MADD domain containing 1B	329260	0.42	0.43	0.21	2.00	0.57	ns
Ccnt2	Cyclin T2	72949	0.99	0.90	0.74	1.34	0.24	ns
Sec14l1	SEC14-like 1 (S. cerevisiae)	74136	0.90	0.92	0.95	0.94	-0.46	ns
Gas2l3	growth arrest-specific 2 like 3	237436	1.33	1.33	1.07	1.24	0.66	ns
Rps15a	ribosomal protein S15a	267019	14.65	14.90	14.48	1.01	-0.44	ns
D630002J15Rik	RIKEN cDNA D630002J15 gene	77522	0.78	0.69	0.45	1.70	-0.34	ns
Depdc6	DEP domain containing 6	97998	0.34	0.26	0.25	1.37	0.13	ns
Plp2	proteolipid protein 2	18824	5.27	5.19	6.50	0.81	0.11	ns
Ccdc18	coiled-coil domain containing 18	73254	0.23	0.27	0.38	0.60	-0.73	ns
Erp29	endoplasmic reticulum protein 29	67397	1.21	1.51	1.59	0.76	-0.64	ns
Brp44l	brain protein 44-like	55951	1.13	1.00	0.60	1.88	0.74	ns
Nphp1	nephronophthisis 1 (juvenile) homolog (human)	53885	0.52	0.74	0.65	0.79	-0.65	ns
Mrps7	mitochondrial ribosomal protein S7	50529	1.37	1.33	1.45	0.94	0.00	ns
Mrps17	mitochondrial ribosomal protein S17	66258	1.57	1.62	1.76	0.89	-0.25	ns
Tmem77	transmembrane protein 77	67171	1.52	1.47	1.37	1.11	0.62	ns
Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	22589	0.23	0.24	0.65	0.36	-0.79	ns
Nt5m	5',3'-nucleotidase, mitochondrial	103850	0.42	0.36	0.37	1.13	0.33	ns
Orc4l	origin recognition complex, subunit 4-like (S. cerevisiae)	26428	1.01	0.84	0.71	1.41	0.83	*
N6amt1	N-6 adenine-specific DNA methyltransferase 1 (putative)	67768	0.31	0.36	0.21	1.45	0.15	ns
Rnaseh1	ribonuclease H1	19819	0.28	0.39	0.41	0.69	-0.46	ns
Zbed3	zinc finger, BED domain containing 3	72114	0.42	0.44	0.35	1.22	0.65	ns
Otud5	OTU domain containing 5	54644	0.61	0.72	0.72	0.85	0.30	ns
Slc37a3	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	72144	0.66	0.74	0.80	0.81	-0.74	ns
Ssb	Sjogren syndrome antigen B	20823	2.17	1.99	1.54	1.40	0.20	ns
Mett10d	methyltransferase 10 domain containing	67493	0.41	0.43	0.49	0.84	-0.98	***
Exosc10	exosome component 10	50912	1.36	1.36	1.53	0.89	0.01	ns
Usp21	ubiquitin specific peptidase 21	30941	0.89	0.74	0.60	1.47	0.67	ns
Usp15	ubiquitin specific peptidase 15	14479	0.92	0.84	0.74	1.23	0.29	ns
Pex3	peroxisomal biogenesis factor 3	56535	0.85	0.70	0.51	1.66	0.56	ns
Pgs1	phosphatidylglycerophosphate synthase 1	74451	0.63	0.58	0.77	0.82	-0.29	ns
2410017P07Rik	RIKEN cDNA 2410017P07 gene	103268	0.70	0.64	0.58	1.21	0.61	ns
Rnf138	ring finger protein 138	56515	0.68	0.85	0.84	0.80	-0.21	ns
Rsrc2	arginine/serine-rich coiled-coil 2	208606	2.78	2.72	2.92	0.95	-0.51	ns
Gal3st1	galactose-3-O-sulfotransferase 1	53897	0.59	0.51	0.46	1.27	0.48	ns
Gtf2h3	general transcription factor IIH, polypeptide 3	209357	0.53	0.47	0.48	1.10	0.66	ns
Jmjd6	jumonji domain containing 6	107817	0.52	0.61	1.11	0.47	-0.64	ns
Mterfd1	MTERF domain containing 1	66410	0.78	1.20	1.44	0.54	-0.92	**
4921524J17Rik	RIKEN cDNA 4921524J17 gene	66714	0.92	0.96	1.15	0.80	-0.46	ns
0610007P14Rik	RIKEN cDNA 0610007P14 gene	58520	2.16	1.98	2.53	0.85	-0.48	ns
Cyba	cytochrome b-245, alpha polypeptide	13057	1.16	1.16	0.50	2.32	0.47	ns
Intu	inturned planar cell polarity effector homolog (Drosophila)	380614	0.50	0.38	0.41	1.22	0.69	ns
Tspan12	tetraspanin 12	269831	0.66	1.07	1.57	0.42	-0.83	*
Pi4k2a	phosphatidylinositol 4-kinase type 2 alpha	84095	0.60	0.73	0.56	1.08	0.22	ns
4933426M11Rik	RIKEN cDNA 4933426M11 gene	217684	0.52	0.49	0.90	0.58	-0.84	*
6430527G18Rik	RIKEN cDNA 6430527G18 gene	238330	9.75	9.05	8.65	1.12	0.05	ns
Sept7	septin 7	235072	6.75	5.42	4.12	1.63	0.96	**
1810013D10Rik	RIKEN cDNA 1810013D10 gene	66278	0.55	0.54	0.49	1.10	0.22	ns
Arrdc3	arrestin domain containing 3	105171	1.28	1.48	2.38	0.54	-0.94	**
LOC639593		639593	19.77	18.50	16.22	1.21	0.93	**
Phf6	PHD finger protein 6	70998	0.37	0.59	0.65	0.56	-0.58	ns
Cltc	clathrin, heavy polypeptide (Hc)	67300	6.38	6.57	7.84	0.81	-0.92	**
EG666642		666642	20.13	20.70	17.09	1.17	0.87	*
LOC433941		433941	20.13	20.70	17.09	1.17	0.87	*
LOC622707		622707	20.13	20.70	17.09	1.17	0.87	*
LOC665032		665032	20.13	20.70	17.09	1.17	0.87	*
LOC669999		669999	20.13	20.70	17.09	1.17	0.87	*
Rpl29		19944	20.13	20.70	17.09	1.17	0.87	*
Samd14	sterile alpha motif domain containing 14	217125	0.47	0.42	0.41	1.14	0.79	ns
Gtf2a1	General transcription factor II A, 1	83602	1.18	1.23	1.21	0.97	-0.41	ns
Fbxl3	F-box and leucine-rich repeat protein 3	50789	1.07	0.92	1.09	0.98	-0.33	ns
Cbx5	chromobox homolog 5 (Drosophila HP1a)	12419	5.04	5.18	4.60	1.09	0.47	ns
Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7	66433	0.30	0.39	0.11	2.72	0.71	ns
Cggbp1	CGG triplet repeat binding protein 1	106143	6.69	6.50	6.38	1.04	-0.30	ns
6330569M22Rik	RIKEN cDNA 6330569M22 gene	229707	0.79	0.89	0.78	1.01	-0.24	ns
Mgrn1	mahogunin, ring finger 1	17237	1.10	0.84	1.26	0.87	-0.61	ns
Acad11	acyl-Coenzyme A dehydrogenase family, member 11	102632	0.64	0.48	0.42	1.54	0.88	*
D10Wsu102e	DNA segment, Chr 10, Wayne State University 102, expressed	28109	1.26	1.16	0.94	1.33	0.45	ns
Srd5a1	steroid 5 alpha-reductase 1	78925	1.53	2.10	2.72	0.56	-0.89	*
Zranb2	zinc finger, RAN-binding domain containing 2	53861	3.31	3.34	3.21	1.02	-0.22	ns
Dirc2	disrupted in renal carcinoma 2 (human)	224132	0.36	0.39	0.46	0.79	-0.80	ns
Spata13	spermatogenesis associated 13	219140	0.48	0.46	0.14	3.45	-0.01	ns
Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	78689	2.03	2.08	2.06	0.98	0.23	ns
Ilvbl	ilvB (bacterial acetolactate synthase)-like	216136	0.87	0.75	0.42	2.04	0.65	ns
Dctd	dCMP deaminase	320685	0.44	0.49	0.31	1.42	0.06	ns
Atp5g3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 3	228033	14.45	12.31	9.73	1.48	0.62	ns
Klf3	Kruppel-like factor 3 (basic)	16599	2.14	2.50	2.13	1.00	-0.06	ns
Snx8	sorting nexin 8	231834	0.39	0.39	0.41	0.94	-0.39	ns
Zubr1	zinc finger, UBR1 type 1	69116	1.15	1.26	1.56	0.74	-0.81	ns

Tmem11	transmembrane protein 11	216821	0.85	0.77	0.92	0.92	-0.63	ns
Rere	arginine glutamic acid dipeptide (RE) repeats	68703	1.40	1.25	1.17	1.19	0.65	ns
Insig1	insulin induced gene 1	231070	1.35	1.42	1.76	0.76	-0.73	ns
Wasf2	WAS protein family, member 2	242687	2.83	2.60	3.21	0.88	-0.51	ns
Thra	thyroid hormone receptor alpha	21833	0.69	0.58	0.66	1.05	0.25	ns
Timp2	tissue inhibitor of metalloproteinase 2	21858	4.13	3.79	3.11	1.32	0.70	ns
A130022J15Rik	RIKEN cDNA A130022J15 gene	101351	0.37	0.32	0.34	1.07	0.36	ns
D5Ertd579e	DNA segment, Chr 5, ERATO Doi 579, expressed	320661	1.85	1.99	2.17	0.85	-0.55	ns
Rbm35a	RNA binding motif protein 35A	207920	2.59	2.48	2.44	1.06	0.18	ns
A430005L14Rik	RIKEN cDNA A430005L14 gene	97159	0.69	0.83	1.27	0.54	-0.50	ns
Gpr146	G protein-coupled receptor 146	80290	0.30	0.32	0.27	1.12	-0.22	ns
Srrm1	serine/arginine repetitive matrix 1	51796	2.09	1.84	2.50	0.83	-0.45	ns
Ikbkg	inhibitor of kappaB kinase gamma	16151	0.52	0.50	0.79	0.65	-0.64	ns
Top2a	topoisomerase (DNA) II alpha	21973	6.98	6.89	9.04	0.77	-0.02	ns
Lrfn4	leucine rich repeat and fibronectin type III domain containing 4	225875	0.67	0.59	0.37	1.79	0.86	*
Scarb2	scavenger receptor class B, member 2	12492	0.44	1.36	0.94	0.47	-0.65	ns
D15Ertd621e	DNA segment, Chr 15, ERATO Doi 621, expressed	210998	2.82	2.19	2.51	1.12	0.30	ns
Uvrag	UV radiation resistance associated gene	78610	0.65	0.51	0.63	1.02	-0.21	ns
Ablim1	actin-binding LIM protein 1	226251	1.87	2.02	1.34	1.39	0.49	ns
Phgdh		236539	9.17	9.98	6.45	1.41	0.67	ns
Ankrd27	ankyrin repeat domain 27 (VPS9 domain)	245886	0.64	0.69	0.70	0.91	-0.06	ns
Pten	phosphatase and tensin homolog	19211	2.76	2.46	2.23	1.23	0.95	**
1110033M05Rik	RIKEN cDNA 1110033M05 gene	68675	0.23	0.39	0.43	0.53	-0.53	ns
Tra2a	transformer 2 alpha homolog (Drosophila)	101214	1.98	2.35	2.06	0.96	-0.48	ns
Afap1l1	actin filament associated protein 1-like 1	106877	1.02	0.99	0.67	1.50	0.76	ns
Tapt1	transmembrane anterior posterior transformation 1	231225	0.87	0.92	1.05	0.82	-0.82	*
Myo10	myosin X	17909	0.80	0.83	1.16	0.69	-0.72	ns
Mtap1s	microtubule-associated protein 1S	270058	0.48	0.32	0.38	1.28	0.67	ns
Odf2	outer dense fiber of sperm tails 2	18286	1.19	1.32	1.12	1.06	0.60	ns
Ankrd57	ankyrin repeat domain 57	268301	0.70	0.94	0.70	0.99	-0.23	ns
Pex6	peroxisomal biogenesis factor 6	224824	1.35	1.22	1.05	1.28	0.86	*
Cdc27	cell division cycle 27 homolog (S. cerevisiae)	217232	1.11	1.06	1.23	0.90	-0.71	ns
Mib1	mindbomb homolog 1 (Drosophila)	225164	0.79	0.87	1.19	0.67	-0.62	ns
Tmem164	transmembrane protein 164	209497	0.52	0.56	0.65	0.80	-0.01	ns
Rasgef1b	RasGEF domain family, member 1B	320292	0.48	0.39	0.49	0.98	-0.34	ns
Nup205	nucleoporin 205	70699	1.93	2.16	3.02	0.64	-0.62	ns
F630043A04Rik	RIKEN cDNA F630043A04 gene	219114	0.35	0.40	0.27	1.27	0.42	ns
Arhgap29	Rho GTPase activating protein 29	214137	5.86	5.43	3.99	1.46	0.17	ns
BC057552	cDNA sequence BC057552	212123	0.66	0.70	0.77	0.84	-0.13	ns
G430022H21Rik	RIKEN cDNA G430022H21 gene	210529	0.76	0.80	0.62	1.22	0.61	ns
Rnpepl1	arginyl aminopeptidase (aminopeptidase B)-like 1	108657	1.40	1.30	1.01	1.38	0.60	ns
Aamp	angio-associated migratory protein	227290	2.18	1.84	1.85	1.17	0.13	ns
Lrch3	leucine-rich repeats and calponin homology (CH) domain containing 3	70144	1.00	0.61	0.85	1.16	0.40	ns
Git1	G protein-coupled receptor kinase-interactor 1	216963	0.37	0.46	0.37	1.01	0.33	ns
Htatsf1	HIV TAT specific factor 1	72459	1.26	1.52	1.61	0.78	-0.35	ns
Slc38a1	solute carrier family 38, member 1	105727	1.71	1.64	1.25	1.36	0.71	ns
Gtf3c3	general transcription factor IIIC, polypeptide 3	98488	0.45	0.44	0.45	0.99	-0.39	ns
C730024G19Rik	RIKEN cDNA C730024G19 gene	232566	0.31	0.32	0.42	0.73	-0.47	ns
LOC100046680	hypothetical protein LOC100046680	#######	0.39	0.35	0.32	1.19	0.59	ns
Rxra	retinoid X receptor alpha	20181	0.73	0.72	0.42	1.73	0.66	ns
Zfp445	zinc finger protein 445	235682	2.52	2.34	1.99	1.26	0.80	ns
Ehmt1	euchromatic histone methyltransferase 1	77683	1.66	1.70	1.19	1.38	0.50	ns
LOC100048156	similar to ribosomal protein S28	#######	23.62	21.73	16.03	1.47	0.85	*
Il13ra1	interleukin 13 receptor, alpha 1	16164	0.41	0.54	1.10	0.37	-0.85	*
Dusp11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	72102	1.39	1.43	1.84	0.75	-0.82	*
Zdhhc9	zinc finger, DHHC domain containing 9	208884	0.24	0.17	0.40	0.58	-0.72	ns
Arl4c		320982	3.03	3.06	1.59	1.90	0.18	ns
LOC632433		632433	3.03	3.06	1.59	1.90	0.18	ns
Wdr35	WD repeat domain 35	74682	1.03	0.99	0.85	1.21	0.31	ns
Sephs1	selenophosphate synthetase 1	109079	1.19	1.11	0.97	1.22	0.65	ns
Spast	spastin	50850	1.31	1.21	0.99	1.32	0.93	**
Cobll1	Cobl-like 1	319876	1.94	1.75	1.15	1.67	0.34	ns
Tmem55b	transmembrane protein 55b	219024	1.30	1.34	1.43	0.91	-0.77	ns
Morn2	MORN repeat containing 2	378462	0.47	0.42	0.23	2.04	0.64	ns
Arih2	ariadne homolog 2 (Drosophila)	23807	2.01	1.98	2.69	0.74	0.06	ns
Nploc4	nuclear protein localization 4 homolog (S. cerevisiae)	217365	0.89	0.84	1.00	0.89	0.27	ns
Snx12	sorting nexin 12	55988	0.61	0.66	0.93	0.65	-0.54	ns
Efha1	EF hand domain family A1	68514	1.30	1.74	1.66	0.78	-0.18	ns
Ncoa7	nuclear receptor coactivator 7	211329	0.36	0.35	0.28	1.30	0.33	ns
Vps8	vacuolar protein sorting 8 homolog (S. cerevisiae)	209018	0.23	0.33	0.35	0.66	-0.90	*
Ccdc72	coiled-coil domain containing 72	66167	7.11	6.95	6.90	1.03	0.52	ns
Sertad2	SERTA domain containing 2	58172	1.34	1.55	1.45	0.92	-0.60	ns
Utp18	UTP18, small subunit (SSU) processome component, homolog (yeast)	217109	1.03	0.98	1.28	0.80	-0.87	*
Gmeb2	glucocorticoid modulatory element binding protein 2	229004	0.65	0.61	0.63	1.03	-0.05	ns
1110014N23Rik	RIKEN cDNA 1110014N23 gene	68505	0.83	0.78	0.53	1.55	0.76	ns
Zbtb11	zinc finger and BTB domain containing 11	271377	0.92	1.00	1.29	0.71	-0.90	*
Rundc1	RUN domain containing 1	217201	0.45	0.46	0.45	1.00	0.47	ns
Foxn2	forkhead box N2	14236	0.27	0.37	0.26	1.01	0.11	ns
Tmem18	transmembrane protein 18	211986	0.97	1.26	0.91	1.07	0.47	ns
Cln6	ceroid-lipofuscinosis, neuronal 6	76524	1.21	0.96	1.13	1.07	0.49	ns
Mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	78038	0.46	0.46	0.37	1.25	-0.08	ns
Prps2	phosphoribosyl pyrophosphate synthetase 2	110639	3.03	3.45	3.05	0.99	0.43	ns
Nr2c2	nuclear receptor subfamily 2, group C, member 2	22026	2.15	1.76	1.91	1.12	0.63	ns
AI987944		233168	0.54	0.42	0.45	1.19	0.26	ns
AW146154		101835	0.54	0.42	0.45	1.19	0.26	ns
Rnf122	ring finger protein 122	68867	0.35	0.40	0.37	0.93	0.31	ns
Rpl23	ribosomal protein L23	65019	35.90	32.48	26.67	1.34	0.97	**

Txlna	taxilin alpha	109658	0.64	0.64	0.70	0.90	-0.56	ns
Phldb2	pleckstrin homology-like domain, family B, member 2	208177	3.80	3.38	4.77	0.79	-0.30	ns
Btbd7	BTB (POZ) domain containing 7	238386	2.36	2.23	2.68	0.88	-0.61	ns
Sertad4	SERTA domain containing 4	214791	1.08	0.98	0.78	1.38	0.43	ns
1700052N19Rik	RIKEN cDNA 1700052N19 gene	73419	0.36	0.43	0.38	0.94	-0.15	ns
Bmf	Bcl2 modifying factor	171543	0.47	0.53	0.35	1.33	0.42	ns
Upk3b	uroplakin 3B	100647	2.11	1.40	0.60	3.50	0.63	ns
Pak2	p21 (CDKN1A)-activated kinase 2	224105	2.05	1.78	1.86	1.10	0.40	ns
Pfdn4	prefoldin 4	109054	1.89	1.71	1.80	1.05	0.00	ns
Amot	angiomotin	27494	1.07	1.08	1.22	0.87	0.20	ns
Pitpnb	phosphatidylinositol transfer protein, beta	56305	2.88	2.89	3.20	0.90	-0.41	ns
Smurf2	SMAD specific E3 ubiquitin protein ligase 2	66313	1.46	1.26	1.39	1.05	0.56	ns
Rbpj	recombination signal binding protein for immunoglobulin kappa J region	19664	1.09	1.29	1.97	0.55	-0.82	*
Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	18053	0.40	0.38	0.53	0.75	-0.67	ns
Ibtk	inhibitor of Bruton agammaglobulinemia tyrosine kinase	108837	0.35	0.38	0.41	0.83	-0.03	ns
2610101N10Rik	RIKEN cDNA 2610101N10 gene	67958	1.97	1.94	2.19	0.90	0.06	ns
Rab3gap2	RAB3 GTPase activating protein subunit 2	98732	0.62	0.60	0.52	1.17	-0.04	ns
Arfip1	ADP-ribosylation factor interacting protein 1	99889	3.49	3.46	2.97	1.17	0.31	ns
Alg10b	asparagine-linked glycosylation 10 homolog B (yeast, alpha-1,2-glucosyltransferase)	380959	1.65	1.61	1.49	1.11	0.43	ns
Agps	alkylglycerone phosphate synthase	228061	0.73	0.89	0.66	1.09	-0.13	ns
Uhrf2	ubiquitin-like, containing PHD and RING finger domains 2	109113	0.71	0.80	0.46	1.54	0.64	ns
Gm561	gene model 561, (NCBI)	228715	0.51	0.51	0.53	0.96	0.12	ns
Zfp41	zinc finger protein 41	22701	0.40	0.32	0.41	0.99	0.09	ns
Safb	scaffold attachment factor B	224903	1.19	1.00	0.92	1.28	0.61	ns
Tbcel	tubulin folding cofactor E-like	272589	0.55	0.62	0.36	1.55	0.74	ns
Ppm1f	protein phosphatase 1F (PP2C domain containing)	68606	0.30	0.33	0.42	0.71	-0.91	*
D930001I22Rik	RIKEN cDNA D930001I22 gene	228859	0.40	0.43	0.34	1.14	0.61	ns
B630005N14Rik	RIKEN cDNA B630005N14 gene	101148	1.17	1.41	1.79	0.65	-0.89	*
Hic2	hypermethylated in cancer 2	58180	0.33	0.30	0.41	0.81	-0.38	ns
Ncapd3	non-SMC condensin II complex, subunit D3	78658	1.45	1.40	1.75	0.83	0.11	ns
Ipo7	importin 7	233726	3.10	3.09	4.24	0.73	-0.70	ns
Rps6kb1	ribosomal protein S6 kinase, polypeptide 1	72508	0.60	0.58	0.66	0.91	-0.73	ns
Nob1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	67619	0.53	0.55	0.39	1.35	0.29	ns
Gsk3b	glycogen synthase kinase 3 beta	56637	4.19	3.64	3.79	1.10	-0.22	ns
Smad3	MAD homolog 3 (Drosophila)	17127	1.65	1.13	1.13	1.46	0.86	*
Synj1	synaptojanin 1	104015	0.94	0.75	0.87	1.07	0.19	ns
E430028B21Rik	RIKEN cDNA E430028B21 gene	211948	0.76	0.83	0.83	0.92	-0.73	ns
Tsc22d1	TSC22 domain family, member 1	21807	16.85	16.47	12.36	1.36	0.46	ns
Atf7ip	activating transcription factor 7 interacting protein	54343	0.59	0.58	0.61	0.97	-0.18	ns
Ttyh3	tweety homolog 3 (Drosophila)	78339	0.29	0.34	0.38	0.76	-0.62	ns
Diap1		13367	1.46	1.50	1.62	0.89	0.16	ns
4930402E16Rik	RIKEN cDNA 4930402E16 gene	319518	0.58	0.58	0.40	1.46	0.69	ns
D4Ertd22e	DNA segment, Chr 4, ERATO Doi 22, expressed	213491	0.73	0.64	0.68	1.07	0.59	ns
Arfgef2		99371	0.65	0.63	0.60	1.08	-0.08	ns
H2-Ke6	H2-K region expressed gene 6	14979	0.38	0.35	0.22	1.73	0.29	ns
Rab22a	RAB22A, member RAS oncogene family	19334	1.20	0.98	1.03	1.15	-0.03	ns
Cspp1	centrosome and spindle pole associated protein 1	211660	1.03	0.99	0.81	1.27	0.11	ns
Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	11987	9.18	8.80	6.02	1.52	0.53	ns
Hsdl1	hydroxysteroid dehydrogenase like 1	72552	0.75	0.77	0.51	1.47	0.65	ns
Msrb3	methionine sulfoxide reductase B3	320183	0.74	0.65	0.14	5.09	0.65	ns
1200011I18Rik	RIKEN cDNA 1200011I18 gene	67467	0.82	0.73	0.71	1.14	0.51	ns
Thap1	THAP domain containing, apoptosis associated protein 1	73754	0.50	0.60	0.54	0.91	0.20	ns
2310016M24Rik	RIKEN cDNA 2310016M24 gene	66379	2.10	2.06	2.21	0.94	-0.27	ns
Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	108682	0.43	0.51	0.36	1.18	0.41	ns
Gna12	guanine nucleotide binding protein, alpha 12	14673	0.44	0.39	0.43	1.03	0.42	ns
Cpd	carboxypeptidase D	12874	1.67	1.61	1.64	1.02	-0.30	ns
1500012F01Rik	RIKEN cDNA 1500012F01 gene	68949	5.25	5.76	4.51	1.16	-0.36	ns
Trim37	tripartite motif protein 37	68729	1.58	1.61	1.47	1.07	0.37	ns
Lmtk2	lemur tyrosine kinase 2	231876	1.18	1.15	1.20	0.98	-0.64	ns
Ckap4	cytoskeleton-associated protein 4	216197	0.42	1.06	1.07	0.39	-0.74	ns
Snx25	sorting nexin 25	102141	0.36	0.28	0.40	0.90	-0.02	ns
Gabbr1	gamma-aminobutyric acid (GABA-B) receptor, 1	54393	0.33	0.24	0.16	2.08	0.58	ns
Strn	striatin, calmodulin binding protein	268980	0.97	0.83	0.71	1.36	0.72	ns
Tlk1	tousled-like kinase 1	228012	1.79	1.80	1.40	1.28	0.18	ns
Kif21a	kinesin family member 21A	16564	0.04	0.18	0.47	0.08	-0.94	**
Ptprj	protein tyrosine phosphatase, receptor type, J	19271	1.17	1.05	0.78	1.49	0.18	ns
Cdc2l6	cell division cycle 2-like 6 (CDK8-like)	78334	2.03	1.89	1.65	1.22	0.63	ns
Ccnyl1	cyclin Y-like 1	227210	0.71	0.57	0.38	1.84	0.18	ns
Nr4a2	Nuclear receptor subfamily 4, group A, member 2	18227	0.22	0.27	0.26	0.83	-0.57	ns
Nol5a	nucleolar protein 5A	67134	2.64	3.04	2.71	0.97	-0.34	ns
LOC675851		675851	4.35	4.29	4.89	0.89	-0.44	ns
Ndufc2		68197	4.35	4.29	4.89	0.89	-0.44	ns
Tbl1x	Transducin (beta)-like 1 X-linked	21372	2.77	2.67	3.69	0.75	-0.71	ns
Pogz	pogo transposable element with ZNF domain	229584	1.23	1.36	1.09	1.13	-0.34	ns
Igsf3	immunoglobulin superfamily, member 3	78908	0.15	0.43	0.53	0.27	-0.77	ns
2410129H14Rik	RIKEN cDNA 2410129H14 gene	76789	2.50	2.31	3.02	0.82	-0.32	ns
Dcun1d1		114893	1.00	0.94	1.04	0.95	-0.60	ns
Lmo7	LIM domain only 7	380928	1.27	1.41	1.86	0.68	-0.89	*
Mia3	melanoma inhibitory activity 3	338366	1.27	1.48	0.97	1.31	0.67	ns
Dcp2	DCP2 decapping enzyme homolog (S. cerevisiae)	70640	0.90	1.07	1.11	0.80	-0.01	ns
Cep350	centrosomal protein 350	74081	1.10	1.01	1.10	1.00	-0.36	ns
Dcun1d4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	100737	0.32	0.32	0.44	0.71	-0.25	ns
Cblb	Casitas B-lineage lymphoma b	208650	1.13	0.66	0.97	1.17	-0.10	ns
Atp11c	Atpase, class VI, type 11C	320940	0.39	0.42	0.62	0.62	-0.42	ns
Shmt2	serine hydroxymethyltransferase 2 (mitochondrial)	108037	1.75	2.35	1.89	0.92	-0.43	ns

Gng12	guanine nucleotide binding protein (G protein), gamma 12	14701	2.10	1.63	1.91	1.09	0.12	ns
Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	212880	1.10	1.22	1.20	0.91	0.07	ns
Srpk1	serine/arginine-rich protein specific kinase 1	20815	1.54	1.52	0.98	1.57	0.80	ns
Gabpb2	GA repeat binding protein, beta 2	213054	1.72	1.79	1.47	1.16	0.31	ns
Yipf6	Yip1 domain family, member 6	77929	0.34	0.35	0.49	0.70	-0.87	*
2310028O11Rik	RIKEN cDNA 2310028O11 gene	433771	3.07	3.01	3.56	0.86	-0.35	ns
Mtdh	Metadherin	67154	2.06	2.29	2.19	0.94	0.10	ns
Spty2d1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	101685	0.31	0.45	0.51	0.61	-0.87	*
Opa3	optic atrophy 3 (human)	403187	0.52	0.66	0.53	0.98	0.33	ns
D730040F13Rik	RIKEN cDNA D730040F13 gene	242474	0.52	0.54	0.73	0.71	-0.70	ns
2610014I16Rik	RIKEN cDNA 2610014I16 gene	66300	0.28	0.26	0.37	0.77	-0.18	ns
Cfl1	cofilin 1, non-muscle	12631	18.49	17.56	14.66	1.26	0.90	*
Pitpnm3	PITPNM family member 3	327958	0.37	0.36	0.28	1.31	0.22	ns
Socs4	suppressor of cytokine signaling 4	67296	1.60	1.46	1.84	0.86	-0.64	ns
Nlgn2	neuroligin 2	216856	0.50	0.72	0.94	0.53	-0.70	ns
Pcdh19	protocadherin 19	279653	0.33	0.18	0.02	14.90	0.43	ns
Sh3rf1	SH3 domain containing ring finger 1	59009	0.87	0.87	1.41	0.62	-0.73	ns
AI462493	expressed sequence AI462493	107197	0.70	0.79	0.53	1.33	0.46	ns
Lsm14b	LSM14 homolog B (SCD6, S. cerevisiae)	241846	0.88	0.89	0.88	1.00	-0.19	ns
BC039210	cDNA sequence BC039210	234839	0.93	1.13	0.80	1.15	0.44	ns
Itga3	integrin alpha 3	16400	2.87	2.84	2.61	1.09	-0.02	ns
Appl1	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	72993	0.81	0.76	0.76	1.06	0.49	ns
Arl5b	ADP-ribosylation factor-like 5B	75869	0.65	0.73	0.60	1.08	0.37	ns
Gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	14694	19.91	18.13	15.72	1.26	0.79	ns
Rab11fip2	RAB11 family interacting protein 2 (class I)	74998	0.60	0.70	0.53	1.13	0.22	ns
Rps19bp1	ribosomal protein S19 binding protein 1	66538	0.89	1.08	1.06	0.83	-0.37	ns
Phf13	PHD finger protein 13	230936	0.45	0.43	0.50	0.90	0.15	ns
Mpp7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	75739	0.61	0.53	0.50	1.21	-0.09	ns
Mobkl1a	MOB1, Mps One Binder kinase activator-like 1A (yeast)	68473	1.20	1.23	1.27	0.94	-0.37	ns
Pip5k1b	Phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	18719	0.88	0.88	0.81	1.07	-0.38	ns
AA987161	expressed sequence AA987161	380856	0.29	0.34	0.40	0.72	-0.55	ns
Pak6	p21 (CDKN1A)-activated kinase 6	214230	0.64	0.58	0.38	1.70	0.85	*
Usp19	ubiquitin specific peptidase 19	71472	0.61	0.73	0.60	1.00	0.40	ns
Timm13	translocase of inner mitochondrial membrane 13 homolog (yeast)	30055	3.03	3.02	2.79	1.08	0.52	ns
Wdr24	WD repeat domain 24	268933	0.57	0.49	0.37	1.52	0.85	*
Lrig2	leucine-rich repeats and immunoglobulin-like domains 2	269473	0.58	0.60	0.45	1.29	0.29	ns
6330503K22Rik	RIKEN cDNA 6330503K22 gene	101565	0.72	0.73	0.91	0.79	-0.21	ns
Frat2	frequently rearranged in advanced T-cell lymphomas 2	212398	0.37	0.42	0.39	0.93	-0.24	ns
Ubp1	upstream binding protein 1	22221	1.47	1.62	1.45	1.01	0.56	ns
Aadacl1	arylacetamide deacetylase-like 1	320024	1.35	1.13	0.58	2.30	0.03	ns
Usp36	ubiquitin specific peptidase 36	72344	0.51	0.48	0.46	1.10	0.50	ns
Daam1	dishevelled associated activator of morphogenesis 1	208846	1.25	1.37	1.83	0.68	-0.94	**
Rpl13	ribosomal protein L13	270106	23.05	22.37	16.34	1.40	0.73	ns
Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	20588	2.22	2.30	1.92	1.15	0.79	ns
Ccdc127	coiled-coil domain containing 127	67433	0.36	0.46	0.47	0.76	-0.29	ns
Tsc1	tuberous sclerosis 1	64930	0.48	0.45	0.48	1.00	-0.37	ns
Zbtb6	zinc finger and BTB domain containing 6	241322	0.72	0.63	0.39	1.86	0.87	*
Btbd1	BTB (POZ) domain containing 1	83962	1.74	1.74	1.72	1.00	0.18	ns
Rfxap	regulatory factor X-associated protein	170767	0.43	0.39	0.46	0.92	-0.03	ns
BC037112	cDNA sequence BC037112	231128	0.51	0.48	0.44	1.13	0.49	ns
Dgcr8	DiGeorge syndrome critical region gene 8	94223	1.17	1.26	1.16	1.01	0.30	ns
Phc3	polyhomeotic-like 3 (Drosophila)	241915	1.58	1.39	1.22	1.29	0.52	ns
Lpp	LIM domain containing preferred translocation partner in lipoma	210126	4.85	4.56	4.12	1.17	0.61	ns
Trp53i13	transformation related protein 53 inducible protein 13	216964	0.33	0.29	0.29	1.15	0.67	ns
Epc2	enhancer of polycomb homolog 2 (Drosophila)	227867	1.61	1.56	1.12	1.44	0.35	ns
Ttc21b	tetratricopeptide repeat domain 21B	73668	0.56	0.50	0.30	1.88	0.75	ns
Rbak	RB-associated KRAB repressor	57782	0.49	0.52	0.49	0.99	0.26	ns
Plcxd2	phosphatidylinositol-specific phospholipase C, X domain containing 2	433022	0.42	0.50	0.52	0.80	-0.72	ns
Nol9	nucleolar protein 9	74035	0.24	0.27	0.36	0.66	-0.54	ns
Tns3	tensin 3	319939	3.28	2.43	2.70	1.21	0.34	ns
D330038O06Rik	RIKEN cDNA D330038O06 gene	330788	0.43	0.40	0.38	1.11	0.62	ns
Thap2	THAP domain containing, apoptosis associated protein 2	66816	0.53	0.60	0.34	1.54	0.18	ns
Fgd4	FYVE, RhoGEF and PH domain containing 4	224014	0.95	0.90	0.64	1.48	0.62	ns
Fkbp15	FK506 binding protein 15	338355	0.48	0.44	0.37	1.27	0.98	***
Phf15	PHD finger protein 15	76901	0.72	0.81	0.57	1.25	0.71	ns
Tmem62	transmembrane protein 62	96957	0.63	0.50	0.42	1.50	0.85	*
Tmcc1	transmembrane and coiled coil domains 1	330401	0.42	0.46	0.42	1.00	-0.42	ns
Wdr22	WD repeat domain 22	320808	0.27	0.40	0.44	0.63	-0.75	ns
Camsap1	calmodulin regulated spectrin-associated protein 1	227634	0.68	0.66	0.58	1.16	0.55	ns
Ptpn14	protein tyrosine phosphatase, non-receptor type 14	19250	5.28	4.87	2.70	1.94	0.36	ns
4921513D23Rik	RIKEN cDNA 4921513D23 gene	223989	0.80	0.82	0.82	0.97	0.03	ns
Nufip2	nuclear fragile X mental retardation protein interacting protein 2	68564	1.52	1.62	1.18	1.29	-0.25	ns
Alkbh6		233065	0.60	0.69	0.85	0.71	-0.70	ns
Clip3		76686	0.60	0.69	0.85	0.71	-0.70	ns
Rad23a	RAD23a homolog (S. cerevisiae)	19358	1.63	1.68	2.23	0.73	-0.29	ns
Oxsm	3-oxoacyl-ACP synthase, mitochondrial	71147	0.22	0.16	0.37	0.60	-0.60	ns
Atp8b1	ATPase, class I, type 8B, member 1	54670	0.69	0.80	0.90	0.76	-0.17	ns
Lrrc8c	leucine rich repeat containing 8 family, member C	100604	0.46	0.50	0.35	1.32	0.51	ns
Cnksr1		194231	0.39	0.60	0.59	0.66	-0.68	ns
Socs7	suppressor of cytokine signaling 7	192157	0.81	0.84	1.10	0.74	-0.78	ns
Manea	mannosidase, endo-alpha	242362	0.56	0.51	0.52	1.07	0.39	ns
Kcnj11	potassium inwardly rectifying channel, subfamily J, member 11	16514	0.71	0.84	1.38	0.51	-0.76	ns
AI450540	expressed sequence AI450540	226252	0.56	0.54	0.50	1.11	0.61	ns
Prr8	proline rich 8	381626	0.76	0.75	0.82	0.92	0.05	ns

Ktn1	kinectin 1	16709	2.01	2.11	2.52	0.79	-0.91	*
Chdh	Choline dehydrogenase	218865	2.46	1.95	1.69	1.45	0.74	ns
BC033915	cDNA sequence BC033915	70661	1.13	0.91	0.78	1.44	0.93	**
Lgals1	lectin, galactose binding, soluble 1	16852	13.53	13.96	10.97	1.23	0.66	ns
Ptpn3	Protein tyrosine phosphatase, non-receptor type 3	545622	1.09	1.16	1.29	0.85	-0.74	ns
Akr1c19	aldo-keto reductase family 1, member C19	432720	2.11	1.43	1.02	2.06	0.47	ns
Glt28d2	glycosyltransferase 28 domain containing 2	320302	0.68	0.62	0.37	1.84	0.73	ns
Timm50	translocase of inner mitochondrial membrane 50 homolog (yeast)	66525	0.66	0.89	1.02	0.64	-0.71	ns
Prdm15	PR domain containing 15	114604	0.33	0.37	0.40	0.83	-0.86	*
Lasp1	LIM and SH3 protein 1	16796	6.28	6.22	7.59	0.82	-0.66	ns
Gse1	genetic suppressor element 1	382034	0.81	0.81	0.73	1.11	0.50	ns
Ppfia1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein, alpha 1	233977	0.41	0.36	0.53	0.76	-0.78	ns
Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	66105	11.32	10.31	8.91	1.26	0.53	ns
Ids	iduronate 2-sulfatase	15931	1.79	1.43	1.93	0.92	-0.06	ns
Rpl13a	ribosomal protein L13a	22121	22.13	20.90	17.59	1.25	0.69	ns
Mfsd11	major facilitator superfamily domain containing 11	69900	0.57	0.67	0.69	0.83	-0.21	ns
6230416J20Rik	RIKEN cDNA 6230416J20 gene	230376	0.47	0.59	0.69	0.68	-0.65	ns
Abl2	v-abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene)	11352	0.80	0.61	0.58	1.38	0.57	ns
Pfas	phosphoribosylformylglycinamidine synthase (FGAR amidotransferase)	237823	1.00	1.04	1.08	0.92	-0.35	ns
Madd	MAP-kinase activating death domain	228355	0.44	0.24	0.30	1.45	0.40	ns
A530082C11Rik	RIKEN cDNA A530082C11 gene	320541	0.50	0.64	0.60	0.83	-0.18	ns
Taf1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor	270627	0.85	0.73	1.22	0.69	-0.55	ns
2810046L04Rik	RIKEN cDNA 2810046L04 gene	212127	0.53	0.41	0.49	1.07	-0.25	ns
Osbpl11	oxysterol binding protein-like 11	106326	1.09	1.22	1.37	0.79	-0.71	ns
Zranb3	zinc finger, RAN-binding domain containing 3	226409	0.65	0.61	0.48	1.36	0.96	**
Sf3a2	splicing factor 3a, subunit 2	20222	4.65	3.92	3.47	1.33	0.64	ns
Zc3h7b	zinc finger CCCH type containing 7B	20286	0.75	0.78	0.88	0.85	-0.55	ns
Sestd1	SEC14 and spectrin domains 1	228071	3.27	2.64	2.10	1.55	0.26	ns
Serinc3	serine incorporator 3	26943	5.34	5.85	5.66	0.94	-0.39	ns
Notch2	Notch gene homolog 2 (Drosophila)	18129	2.94	3.07	2.14	1.36	0.38	ns
Sox12	SRY-box containing gene 12	20667	0.31	0.49	0.35	0.88	-0.01	ns
Ddx49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	234374	0.94	1.10	1.21	0.77	-0.72	ns
Bcr	breakpoint cluster region homolog	110279	0.57	0.61	0.52	1.09	-0.25	ns
Calm1	calmodulin 1	12313	8.41	10.20	10.05	0.83	-0.68	ns
Rps18	ribosomal protein S18	20084	25.50	23.58	15.79	1.61	0.83	*
Smg7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	226517	0.97	0.89	1.02	0.95	-0.45	ns
Ccl28	Chemokine (C-C motif) ligand 28	56838	0.14	0.13	0.48	0.29	-0.77	ns
Rpl41	ribosomal protein L41	67945	30.86	26.85	21.75	1.41	0.86	*
Usp6nl	USP6 N-terminal like	98910	1.41	1.21	0.92	1.52	0.82	*
Rnf168	ring fnger protein 168	70238	1.63	1.56	2.22	0.73	-0.60	ns
Lyrm4	LYR motif containing 4	380840	0.54	0.37	0.40	1.36	0.69	ns
Map3k2	Mitogen activated protein kinase kinase kinase 2	26405	0.86	0.77	0.71	1.20	0.46	ns
Usp30	ubiquitin specific peptidase 30	100756	0.37	0.29	0.36	1.00	-0.42	ns
1110028C15Rik	RIKEN cDNA 1110028C15 gene	68691	0.44	0.49	0.57	0.76	-0.86	*
Fzd5	frizzled homolog 5 (Drosophila)	14367	0.48	0.39	0.30	1.62	-0.07	ns
Rufy3	RUN and FYVE domain containing 3	52822	0.32	0.35	0.47	0.68	-0.92	**
Sclt1	sodium channel and clathrin linker 1	67161	0.58	0.65	0.59	0.98	-0.25	ns
Tspan33	tetraspanin 33	232670	3.81	3.10	3.21	1.18	-0.06	ns
Hoxa9	homeo box A9	15405	1.78	1.55	2.36	0.75	-0.62	ns
Dnalc1	dynein, axonemal, light chain 1	105000	0.61	0.67	0.66	0.92	-0.68	ns
Zfp647	zinc finger protein 647	239546	0.22	0.24	0.46	0.46	-0.81	ns
Tsr1	TSR1, 20S rRNA accumulation, homolog (yeast)	104662	1.69	2.07	1.50	1.12	0.09	ns
Tardbp	TAR DNA binding protein	230908	2.29	2.34	2.64	0.86	-0.86	*
LOC631639		631639	0.54	0.83	0.89	0.60	-0.41	ns
Lonrf1		244421	0.54	0.83	0.89	0.60	-0.41	ns
Alkbh2	alkB, alkylation repair homolog 2 (E. coli)	231642	0.32	0.39	0.43	0.74	-0.50	ns
Wdr76	WD repeat domain 76	241627	0.74	0.56	0.61	1.20	0.52	ns
Tial1	Tia1 cytotoxic granule-associated RNA binding protein-like 1	21843	0.88	0.81	1.04	0.84	-0.26	ns
Sema4b	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	20352	0.93	0.84	0.55	1.69	0.69	ns
Zfp369	zinc finger protein 369	170936	0.51	0.57	0.51	1.01	-0.04	ns
Map3k9	mitogen-activated protein kinase kinase kinase 9	338372	0.33	0.41	0.42	0.77	-0.75	ns
EG434404		434404	22.02	20.41	18.02	1.22	0.82	*
LOC638497		638497	22.02	20.41	18.02	1.22	0.82	*
Nbeal2	neurobeachin-like 2	235627	0.39	0.42	0.34	1.15	0.65	ns
Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	19134	1.34	1.39	1.97	0.68	-0.70	ns
H3f3b	H3 histone, family 3B	15081	20.36	17.54	16.41	1.23	0.93	**
Gm71	gene model 71, (NCBI)	207965	0.78	0.87	1.34	0.58	-0.62	ns
Zrsr2	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2	22184	0.40	0.48	0.53	0.75	0.22	ns
Gnaq	guanine nucleotide binding protein, alpha q polypeptide	14682	1.85	2.01	1.30	1.42	0.48	ns
Slc29a3	solute carrier family 29 (nucleoside transporters), member 3	71279	0.37	0.44	0.33	1.14	-0.09	ns
1700025G04Rik	RIKEN cDNA 1700025G04 gene	69399	0.43	0.47	0.08	5.17	0.46	ns
Ap1s3	adaptor-related protein complex AP-1, sigma 3	252903	2.01	2.00	1.00	2.00	0.34	ns
Kif13a	kinesin family member 13A	16553	0.49	0.55	0.44	1.10	0.36	ns
A230067G21Rik	RIKEN cDNA A230067G21 gene	241694	0.36	0.49	0.40	0.88	-0.14	ns
Tmem134	transmembrane protein 134	66990	1.10	0.92	0.98	1.11	0.50	ns
D3Ertd254e	DNA segment, Chr 3, ERATO Doi 254, expressed	241944	0.70	0.73	0.63	1.10	0.08	ns
Zfp192	zinc finger protein 192	93681	1.03	0.90	0.77	1.34	0.88	*
Hspa8	heat shock protein 8	15481	25.66	22.75	18.86	1.35	0.94	**
Galk2	galactokinase 2	69976	0.60	0.54	0.47	1.28	0.26	ns
Samm50	sorting and assembly machinery component 50 homolog (S. cerevisiae)	68653	3.23	3.21	3.94	0.82	-0.55	ns
Ric8	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	101489	0.66	0.81	1.07	0.62	-0.82	*
Vasn	vasorin	246154	0.84	1.09	1.91	0.44	-0.84	*

Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	54401	15.63	14.57	14.08	1.10	0.43	ns
Kctd3	potassium channel tetramerisation domain containing 3	226823	1.96	2.71	2.75	0.71	-0.32	ns
4930427A07Rik	RIKEN cDNA 4930427A07 gene	104732	1.31	1.21	1.54	0.85	-0.10	ns
Rod1	ROD1 regulator of differentiation 1 (S. pombe)	230257	7.05	6.85	7.86	0.89	-0.56	ns
C1qbp	complement component 1, q subcomponent binding protein	12261	11.62	9.93	8.91	1.30	0.82	*
Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	16430	5.07	5.06	4.90	1.03	0.61	ns
Lnx1	ligand of numb-protein X 1	16924	0.58	0.51	0.59	0.96	-0.19	ns
Bace1	beta-site APP cleaving enzyme 1	23821	0.88	0.82	0.79	1.11	0.60	ns
Ugcgl1	UDP-glucose ceramide glucosyltransferase-like 1	320011	1.15	0.96	0.78	1.46	0.55	ns
Ssh1	slingshot homolog 1 (Drosophila)	231637	1.53	1.47	1.22	1.26	0.19	ns
Pigh	phosphatidylinositol glycan anchor biosynthesis, class H	110417	0.58	0.60	0.82	0.70	-0.60	ns
Ubtd2	ubiquitin domain containing 2	327900	0.88	0.95	0.87	1.00	0.54	ns
Tubgcp2	tubulin, gamma complex associated protein 2	74237	1.05	1.04	1.19	0.88	-0.85	*
Camk2b	Calcium/calmodulin-dependent protein kinase II, beta	12323	20.98	16.44	11.73	1.78	0.44	ns
Akap2	A kinase (PRKA) anchor protein 2	11641	0.45	0.49	0.59	0.76	-0.86	*
Tax1bp3		76281	4.73	4.72	6.02	0.78	-0.65	ns
Tm9sf2	transmembrane 9 superfamily member 2	68059	7.91	7.62	8.48	0.93	-0.25	ns
2700023E23Rik	RIKEN cDNA 2700023E23 gene	70036	0.63	0.53	0.36	1.77	0.70	ns
Becn1	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	56208	2.59	3.00	3.56	0.72	-0.66	ns
Dpp9	dipeptidylpeptidase 9	224897	1.25	1.10	0.71	1.76	0.96	**
Alg8	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)	381903	0.27	0.30	0.39	0.70	-0.44	ns
Hmgn1	high mobility group nucleosomal binding domain 1	15312	20.21	22.51	19.79	1.02	0.14	ns
Socs3	suppressor of cytokine signaling 3	12702	0.23	0.32	0.42	0.55	-0.87	*
Scpep1	serine carboxypeptidase 1	74617	4.25	4.61	5.05	0.84	-0.75	ns
Unc45a	Unc-45 homolog A (C. elegans)	101869	0.25	0.31	0.42	0.60	-0.89	*
Galnt4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4	14426	0.46	0.37	0.37	1.25	0.20	ns
AI931714	expressed sequence AI931714	102182	0.39	0.35	0.40	0.98	0.32	ns
Rab3gap1	RAB3 GTPase activating protein subunit 1	226407	0.80	0.84	0.56	1.42	0.62	ns
Nsmce1	Non-SMC element 1 homolog (S. cerevisiae)	67711	0.95	0.95	1.14	0.82	-0.53	ns
Lztr1	leucine-zipper-like transcriptional regulator, 1	66863	1.80	2.26	2.97	0.61	-0.88	*
Srp14	signal recognition particle 14	20813	3.66	3.17	3.48	1.05	-0.18	ns
Wdr6	WD repeat domain 6	83669	2.85	2.78	2.32	1.22	0.72	ns
Fbxl11	F-box and leucine-rich repeat protein 11	225876	0.94	1.00	0.61	1.53	0.70	ns
Mars	methionine-tRNA synthetase	216443	2.52	2.19	1.94	1.29	0.31	ns
Snx17	sorting nexin 17	266781	7.14	7.12	6.44	1.10	0.50	ns
Pptc7	PTC7 protein phosphatase homolog (S. cerevisiae)	320717	1.61	1.56	1.48	1.08	0.10	ns
Gclc	Glutamate-cysteine ligase, catalytic subunit	14629	1.02	1.20	1.00	1.01	0.42	ns
Crkrs	Cdc2-related kinase, arginine/serine-rich	69131	0.57	0.58	0.59	0.96	0.01	ns
Tmed2	transmembrane emp24 domain trafficking protein 2	56334	11.00	10.78	10.89	1.01	-0.08	ns
Hadh	hydroxyacyl-Coenzyme A dehydrogenase	15107	6.53	6.31	4.09	1.59	0.21	ns
Dbi	diazepam binding inhibitor	13167	4.46	4.79	4.45	1.00	-0.19	ns
Arid1b	AT rich interactive domain 1B (Swi1 like)	239985	1.09	1.21	0.83	1.31	0.59	ns
Cct6a	chaperonin subunit 6a (zeta)	12466	9.40	9.68	9.31	1.00	-0.43	ns
Kif23	kinesin family member 23	71819	2.17	2.26	2.36	0.92	0.41	ns
Uqcrb	ubiquinol-cytochrome c reductase binding protein	67530	15.35	16.82	16.90	0.90	-0.67	ns
Bcl2l11	BCL2-like 11 (apoptosis facilitator)	12125	2.07	3.57	2.69	0.77	-0.37	ns
Top3b	topoisomerase (DNA) III beta	21976	0.92	1.07	1.51	0.60	-0.84	*
Brd9	bromodomain containing 9	105246	0.49	0.77	0.80	0.62	-0.78	ns
Cwf19l2	CWF19-like 2, cell cycle control (S. pombe)	244672	0.84	0.65	0.30	2.76	0.58	ns
Rbm41	RNA binding motif protein 41	237073	0.30	0.38	0.38	0.81	0.20	ns
Preb	prolactin regulatory element binding	50907	1.22	1.23	1.69	0.72	-0.77	ns
Fbxl4	F-box and leucine-rich repeat protein 4	269514	0.27	0.27	0.37	0.72	-0.62	ns
Snx14	sorting nexin 14	244962	0.49	0.50	0.53	0.91	0.24	ns
Cramp1l	Crm, cramped-like (Drosophila)	57354	1.77	1.54	1.08	1.63	0.91	*
Pum1	pumilio 1 (Drosophila)	80912	0.99	1.22	0.82	1.20	0.33	ns
Pold1	polymerase (DNA directed), delta 1, catalytic subunit	18971	1.13	1.10	1.52	0.74	-0.78	ns
D6Wsu116e	DNA segment, Chr 6, Wayne State University 116, expressed	28006	2.23	2.23	2.51	0.88	-0.89	*
Rbm27	RNA binding motif protein 27	225432	0.66	0.72	0.66	0.99	0.48	ns
Gli3	GLI-Kruppel family member GLI3	14634	0.95	0.90	0.56	1.67	0.18	ns
Cycs		13063	6.90	7.86	9.51	0.72	-0.81	ns
LOC670717		670717	6.90	7.86	9.51	0.72	-0.81	ns
LOC672195		672195	6.90	7.86	9.51	0.72	-0.81	ns
Cdc25c	cell division cycle 25 homolog C (S. pombe)	12532	0.37	0.53	0.54	0.69	0.07	ns
Aacs	acetoacetyl-CoA synthetase	78894	0.63	0.54	0.58	1.09	-0.14	ns
LOC631302		631302	1.15	1.39	1.57	0.73	0.21	ns
Pqbp1		54633	1.15	1.39	1.57	0.73	0.21	ns
Pdhx	pyruvate dehydrogenase complex, component X	27402	0.41	0.33	0.38	1.08	-0.28	ns
Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	67733	0.28	0.28	0.50	0.57	-0.56	ns
Elmo2	engulfment and cell motility 2, ced-12 homolog (C. elegans)	140579	0.66	0.56	0.72	0.92	-0.59	ns
Mrps15	mitochondrial ribosomal protein S15	66407	0.88	0.92	1.14	0.77	-0.53	ns
Rrp1b	ribosomal RNA processing 1 homolog B (S. cerevisiae)	72462	0.70	0.76	0.45	1.54	0.64	ns
Mettl2	methyltransferase like 2	52686	0.71	0.75	0.69	1.03	0.34	ns
Pxn	paxillin	19303	4.98	4.07	4.85	1.02	-0.16	ns
A730098P11Rik		624582	12.41	11.70	11.29	1.09	0.76	ns
EG627352		627352	12.41	11.70	11.29	1.09	0.76	ns
Morf4l1		21761	12.41	11.70	11.29	1.09	0.76	ns
Ssh2	slingshot homolog 2 (Drosophila)	237860	0.75	0.67	0.54	1.37	0.44	ns
Setd5	SET domain containing 5	72895	1.44	1.56	2.02	0.71	-0.90	*
Ndrg1	N-myc downstream regulated gene 1	17988	8.49	6.44	12.12	0.70	-0.31	ns
Copb2	coatomer protein complex, subunit beta 2 (beta prime)	50797	2.11	2.24	2.22	0.95	0.43	ns
Zfp706	zinc finger protein 706	68036	3.47	3.34	3.89	0.89	-0.39	ns
Fkbp1a	FK506 binding protein 1a	14225	4.65	5.02	5.85	0.79	-0.19	ns
Ranbp9	RAN binding protein 9	56705	1.13	1.02	1.51	0.74	-0.59	ns

5430407P10Rik	RIKEN cDNA 5430407P10 gene	227545	0.81	0.70	0.59	1.35	0.93	**
Ddr1	discoidin domain receptor family, member 1	12305	7.54	7.28	6.57	1.14	0.94	**
Rbbp7	retinoblastoma binding protein 7	245688	9.06	9.27	11.49	0.78	-0.05	ns
Hoxb3	homeo box B3	15410	2.64	2.31	1.78	1.48	0.39	ns
Klhl17		231003	0.41	0.38	0.33	1.23	0.73	ns
Plekhn1		231002	0.41	0.38	0.33	1.23	0.73	ns
Emx2	empty spiracles homolog 2 (Drosophila)	13797	1.14	1.17	0.84	1.35	0.71	ns
Clspn	claspin homolog (Xenopus laevis)	269582	1.00	1.16	1.40	0.71	-0.25	ns
8430426H19Rik	RIKEN cDNA 8430426H19 gene	71508	0.59	0.67	0.53	1.11	0.62	ns
Tmem171	transmembrane protein 171	380863	0.27	0.51	1.11	0.24	-0.54	ns
Ccnh		66671	1.65	2.11	2.22	0.74	-0.75	ns
Trim28	tripartite motif protein 28	21849	6.10	5.73	5.89	1.03	-0.32	ns
2610002J02Rik	RIKEN cDNA 2610002J02 gene	67513	0.52	0.51	0.57	0.91	0.16	ns
Gsn	gelsolin	227753	6.95	5.55	3.66	1.89	0.72	ns
Cdk2ap1	CDK2 (cyclin-dependent kinase 2)-associated protein 1	13445	6.14	6.24	6.38	0.96	-0.02	ns
Zfp748	zinc finger protein 748	212276	0.32	0.26	0.47	0.67	-0.40	ns
Klf9	Kruppel-like factor 9	16601	1.75	1.67	1.10	1.58	0.90	*
Ppwd1	peptidylprolyl isomerase domain and WD repeat containing 1	238831	0.24	0.31	0.36	0.66	-0.66	ns
Rps20	ribosomal protein S20	67427	19.27	19.73	17.98	1.07	-0.07	ns
Limd2		67803	1.74	1.49	1.56	1.11	-0.26	ns
LOC632329		632329	1.74	1.49	1.56	1.11	-0.26	ns
Fbxl20	F-box and leucine-rich repeat protein 20	72194	0.92	0.80	1.02	0.90	-0.57	ns
Rsl1d1	ribosomal L1 domain containing 1	66409	1.86	1.99	2.10	0.88	-0.86	*
Atp11a	ATPase, class VI, type 11A	50770	3.26	4.14	4.05	0.80	-0.52	ns
Ppp2ca	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	19052	1.97	2.00	2.06	0.95	-0.09	ns
2310002J21Rik	RIKEN cDNA 2310002J21 gene	66360	3.57	3.17	1.63	2.19	0.64	ns
Dido1	death inducer-obliterator 1	23856	0.86	0.96	0.89	0.95	-0.56	ns
Pltp	phospholipid transfer protein	18830	0.32	0.35	0.24	1.30	0.05	ns
Rcbtb1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	71330	0.53	0.53	0.55	0.96	0.16	ns
Prkar2b	protein kinase, cAMP dependent regulatory, type II beta	19088	1.59	1.50	2.57	0.62	-0.71	ns
Ccnt1	cyclin T1	12455	0.86	0.89	1.13	0.76	-0.61	ns
Pik3r3	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	18710	0.42	0.46	0.80	0.53	-0.88	*
Npat	nuclear protein in the AT region	244879	1.19	1.09	0.88	1.35	0.88	*
Aph1b	anterior pharynx defective 1b homolog (C. elegans)	208117	0.52	0.33	0.25	2.05	0.83	*
Zfp652	zinc finger protein 652	268469	0.39	0.26	0.43	0.90	-0.32	ns
Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	54325	1.27	1.37	1.81	0.70	-0.87	*
Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	28000	9.12	9.91	7.87	1.15	0.38	ns
Sdccag8	serologically defined colon cancer antigen 8	76816	0.39	0.50	0.34	1.17	0.23	ns
Qrsl1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	76563	0.72	0.78	0.67	1.06	-0.21	ns
4933429F08Rik	RIKEN cDNA 4933429F08 gene	328967	0.49	0.34	0.14	3.44	0.53	ns
Atp5d	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	66043	7.46	7.18	5.98	1.24	0.41	ns
Cox5b	cytochrome c oxidase, subunit Vb	12859	8.49	8.07	6.58	1.28	0.61	ns
Heatr3	HEAT repeat containing 3	234549	0.53	0.44	0.49	1.06	0.23	ns
Nxt2	nuclear transport factor 2-like export factor 2	237082	0.42	0.38	0.86	0.48	-0.56	ns
Rnf7	ring finger protein 7	19823	1.51	1.62	1.29	1.16	0.72	ns
4932417I16Rik	RIKEN cDNA 4932417I16 gene	234740	0.46	0.46	0.35	1.31	0.08	ns
1500005K14Rik	RIKEN cDNA 1500005K14 gene	76566	1.51	1.70	0.69	2.17	0.34	ns
Vcpip1	valosin containing protein (p97)/p47 complex interacting protein 1	70675	0.66	0.70	0.50	1.30	0.24	ns
Camk2n1	calcium/calmodulin-dependent protein kinase II inhibitor 1	66259	0.38	0.32	0.11	3.54	0.61	ns
Jmjd3	jumonji domain containing 3	216850	1.37	1.46	1.53	0.89	-0.61	ns
Acn9	ACN9 homolog (S. cerevisiae)	71238	0.33	0.43	0.47	0.68	-0.45	ns
Bptf	bromodomain PHD finger transcription factor	207165	3.23	3.37	3.21	1.00	0.36	ns
Bsg	basigin	12215	11.91	10.67	13.09	0.91	-0.62	ns
Mthfd1l	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	270685	1.24	1.24	1.21	1.01	0.41	ns
LOC546058	Hypothetical protein LOC546058	546058	0.32	0.40	0.29	1.12	0.57	ns
E130016E03Rik	RIKEN cDNA E130016E03 gene	623474	0.49	0.38	0.53	0.92	0.17	ns
Qars	glutaminyl-tRNA synthetase	97541	1.99	2.26	2.16	0.92	0.18	ns
Aco1	aconitase 1	11428	1.41	1.89	1.73	0.81	-0.69	ns
Polr3k	Polymerase (RNA) III (DNA directed) polypeptide K	67005	1.32	1.44	1.20	1.10	-0.29	ns
Acpl2	acid phosphatase-like 2	235534	1.36	2.10	2.95	0.46	-0.91	*
Brp16	brain protein 16	59053	1.52	1.55	1.22	1.24	0.79	ns
Morf4l2		56397	7.81	8.39	9.52	0.82	0.16	ns
Foxn1	forkhead box N1	15218	0.37	0.62	0.72	0.51	-0.03	ns
EG382639	predicted gene, EG382639	382639	1.14	1.15	1.23	0.92	-0.64	ns
Phf20l1	PHD finger protein 20-like 1	239510	0.65	0.67	0.71	0.92	-0.12	ns
C130022K22Rik	RIKEN cDNA C130022K22 gene	232236	0.42	0.47	0.46	0.92	0.15	ns
2810455K09Rik	RIKEN cDNA 2810455K09 gene	72805	0.35	0.39	0.40	0.88	0.11	ns
Slc16a4	Solute carrier family 16 (monocarboxylic acid transporters), member 4	229699	0.36	0.44	0.27	1.34	0.32	ns
Tert	telomerase reverse transcriptase	21752	0.17	0.36	0.57	0.30	-0.90	*
Alms1	Alstrom syndrome 1 homolog (human)	236266	0.46	0.34	0.47	0.99	0.25	ns
Ikzf2	IKAROS family zinc finger 2	22779	0.29	0.26	0.21	1.38	-0.01	ns
D14Abb1e	DNA segment, Chr 14, Abbott 1 expressed	218850	0.72	0.67	0.82	0.87	-0.79	ns
Frem2	Fras1 related extracellular matrix protein 2	242022	2.38	2.45	0.79	3.00	-0.11	ns
B3galtl	beta 1,3-galactosyltransferase-like	381694	0.57	0.65	0.80	0.71	-0.36	ns
4732474O15Rik	RIKEN cDNA 4732474O15 gene	238455	1.40	1.53	1.33	1.05	-0.11	ns
Ascc3	activating signal cointegrator 1 complex subunit 3	77987	0.47	0.44	0.44	1.06	-0.36	ns
Plch1	phospholipase C, eta 1	269437	0.28	0.45	0.48	0.58	-0.87	*
Rai16	retinoic acid induced 16	239170	0.52	0.68	0.68	0.77	-0.46	ns
Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7	15490	0.45	0.42	0.39	1.14	0.72	ns
Pld2	phospholipase D2	18806	0.60	0.70	0.70	0.85	-0.28	ns
Dot1l	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	208266	0.45	0.46	0.39	1.14	0.24	ns
Zfp187	zinc finger protein 187	432731	1.01	0.95	0.89	1.13	0.74	ns
Amy2	Amylase 2, pancreatic	11723	0.78	0.71	0.29	2.65	0.83	*
Eya1	eyes absent 1 homolog (Drosophila)	14048	0.82	0.60	0.46	1.77	0.54	ns

Ptpla	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	30963	0.68	0.55	0.14	4.88	0.83	*
Shroom4	shroom family member 4	208431	1.20	0.93	1.02	1.17	0.47	ns
Zfp295	zinc finger protein 295	114565	0.57	0.47	0.68	0.84	-0.07	ns
Ifi202b	interferon activated gene 202B	26388	0.19	0.47	1.06	0.18	-0.64	ns
Vps13a	vacuolar protein sorting 13A (yeast)	271564	0.43	0.41	0.30	1.42	0.71	ns
2510002D24Rik	RIKEN cDNA 2510002D24 gene	72307	0.84	0.82	0.71	1.18	0.40	ns
Tirap	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein	117149	0.45	0.33	0.37	1.20	0.58	ns
Kcnq1	Potassium voltage-gated channel, subfamily Q, member 1	16535	0.57	0.59	0.97	0.58	-0.78	ns
1810043H04Rik	RIKEN cDNA 1810043H04 gene	208501	1.34	1.34	1.39	0.96	0.14	ns
Sgpp2	sphingosine-1-phosphate phosphotase 2	433323	1.46	1.63	0.70	2.09	-0.35	ns
Rwdd4a	RWD domain containing 4A	192174	1.99	2.20	1.78	1.11	0.69	ns
Pde7a	phosphodiesterase 7A	18583	2.55	2.18	2.03	1.25	0.07	ns
Cit	citron	12704	0.42	0.37	0.40	1.03	0.48	ns
Sbno2	strawberry notch homolog 2 (Drosophila)	216161	0.36	0.34	0.24	1.48	0.15	ns
Cnnm3	Cyclin M3	94218	0.34	0.36	0.75	0.45	-0.83	*
Bmp2k	BMP2 inducible kinase	140780	0.64	0.65	0.87	0.73	-0.57	ns
Rasef	RAS and EF hand domain containing	242505	0.40	0.36	0.33	1.20	-0.37	ns
4930519N13Rik	RIKEN cDNA 4930519N13 gene	78177	0.37	0.41	0.37	1.01	0.04	ns
Tatdn1	TatD DNase domain containing 1	69694	0.31	0.29	0.37	0.84	-0.30	ns
Csrp2bp	cysteine and glycine-rich protein 2 binding protein	228714	0.64	0.76	0.74	0.87	-0.27	ns
Gyg	glycogenin	27357	0.61	0.92	1.07	0.57	-0.64	ns
LOC669005		669005	0.82	0.95	0.94	0.88	-0.77	ns
Ppp1r13l		333654	0.82	0.95	0.94	0.88	-0.77	ns
Ppp1r16a	protein phosphatase 1, regulatory (inhibitor) subunit 16A	73062	0.86	0.84	0.88	0.98	-0.19	ns
Sf1	Splicing factor 1	22668	19.25	17.07	13.96	1.37	0.94	**
Snip1	Smad nuclear interacting protein 1	76793	0.80	0.62	0.95	0.83	-0.38	ns
Cno	cappuccino	117197	1.40	1.26	1.81	0.77	-0.46	ns
Lyrm5	LYR motif containing 5	67636	0.65	0.57	0.57	1.13	0.05	ns
Map3k4	mitogen activated protein kinase kinase kinase 4	26407	1.54	1.40	0.91	1.68	0.52	ns
Dus3l	dihydrouridine synthase 3-like (S. cerevisiae)	224907	0.75	0.71	0.44	1.68	0.68	ns
Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	192236	0.76	0.69	0.34	2.26	0.90	*
Ap1m1	adaptor-related protein complex AP-1, mu subunit 1	11767	0.65	0.71	0.66	0.98	0.29	ns
Smad1	MAD homolog 1 (Drosophila)	17125	0.99	1.12	0.76	1.30	0.57	ns
Chrac1	chromatin accessibility complex 1	93696	0.71	0.74	1.64	0.43	-0.51	ns
Fbxl10	F-box and leucine-rich repeat protein 10	30841	1.12	1.41	1.55	0.72	-0.91	*
Nipa2	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	93790	2.71	2.52	2.58	1.04	0.66	ns
Mtmr4	myotubularin related protein 4	170749	1.12	0.96	1.17	0.95	-0.31	ns
Rnf185	Ring finger protein 185	193670	0.96	0.87	0.84	1.14	0.55	ns
Sbsn	suprabasin	282619	0.44	0.52	1.17	0.38	-0.61	ns
ORF34	Open reading frame 34	207375	0.26	0.28	0.20	1.24	0.64	ns
Ccnjl	cyclin J-like	380694	0.70	0.51	0.14	5.02	0.40	ns
Rab3a	RAB3A, member RAS oncogene family	19339	0.71	0.69	0.69	1.03	-0.15	ns
Rps17	ribosomal protein S17	20068	24.35	21.10	18.50	1.31	0.93	**
Cln8	ceroid-lipofuscinosis, neuronal 8	26889	0.25	0.40	0.34	0.73	-0.25	ns
Zfp407	zinc finger protein 407	240476	0.49	0.47	0.54	0.90	0.24	ns
Stx6	syntaxin 6	58244	1.49	1.43	1.21	1.22	0.34	ns
EG667682		667682	25.43	24.53	20.38	1.24	0.67	ns
Ero1l		50527	25.43	24.53	20.38	1.24	0.67	ns
Rpl31		114641	25.43	24.53	20.38	1.24	0.67	ns
Zfyve27	zinc finger, FYVE domain containing 27	319740	0.71	0.66	0.56	1.26	0.78	ns
Samd4b	sterile alpha motif domain containing 4B	233033	0.46	0.52	0.39	1.19	0.72	ns
Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	108012	0.20	0.30	0.36	0.54	0.00	ns
2610510H03Rik	RIKEN cDNA 2610510H03 gene	68215	1.89	1.59	1.68	1.12	0.58	ns
Smyd4	SET and MYND domain containing 4	319822	0.48	0.48	0.35	1.36	0.20	ns
1700109F18Rik	RIKEN cDNA 1700109F18 gene	73429	1.38	1.29	0.59	2.33	0.52	ns
Ppp1ca	protein phosphatase 1, catalytic subunit, alpha isoform	19045	12.54	11.20	9.97	1.25	0.95	**
Aldh7a1	aldehyde dehydrogenase family 7, member A1	110695	0.54	0.56	0.33	1.65	0.47	ns
Slbp	stem-loop binding protein	20492	6.15	6.65	7.18	0.85	-0.30	ns
Ext2	exostoses (multiple) 2	14043	0.93	0.64	0.67	1.37	0.15	ns
Cops5	COP9 (constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana)	26754	2.75	2.61	2.08	1.31	0.37	ns
5730403B10Rik	RIKEN cDNA 5730403B10 gene	66626	0.64	0.69	1.33	0.48	-0.94	**
Dexi	dexamethasone-induced transcript	58239	0.33	0.35	0.38	0.87	-0.52	ns
Rps23	ribosomal protein S23	66475	17.89	20.93	18.47	0.96	-0.11	ns
Lonp2	lon peptidase 2, peroxisomal	66887	0.44	0.52	0.47	0.92	0.25	ns
Snx4	sorting nexin 4	69150	1.58	1.38	1.71	0.92	-0.56	ns
Tm9sf3	transmembrane 9 superfamily member 3	107358	5.28	5.22	4.78	1.10	0.32	ns
Ptpn6	protein tyrosine phosphatase, non-receptor type 6	15170	0.45	0.50	0.73	0.61	-0.88	*
Ap1m2	adaptor protein complex AP-1, mu 2 subunit	11768	2.15	2.17	2.10	1.02	0.58	ns
Osbpl1a	oxysterol binding protein-like 1A	64291	0.38	0.43	0.39	0.99	-0.25	ns
Phyh	phytanoyl-CoA hydroxylase	16922	0.51	0.44	0.22	2.26	0.95	**
Mrps11	mitochondrial ribosomal protein S11	67994	0.43	0.54	0.48	0.90	0.05	ns
Cbr1	carbonyl reductase 1	12408	0.70	0.67	0.73	0.96	-0.59	ns
Psmb3		26446	4.91	4.44	4.21	1.16	0.36	ns
EG668829		668829	24.01	22.91	21.67	1.10	0.21	ns
Rpl24		68193	24.01	22.91	21.67	1.10	0.21	ns
Itpr1	inositol 1,4,5-triphosphate receptor 1	16438	0.49	0.38	0.20	2.47	0.49	ns
Tec	cytoplasmic tyrosine kinase, Dscr28C related (Drosophila)	21682	0.40	0.46	0.41	0.96	0.00	ns
Dcakd	dephospho-CoA kinase domain containing	68087	0.92	0.87	0.89	1.02	0.18	ns
Pkd1	polycystic kidney disease 1 homolog	18763	0.33	0.42	0.22	1.50	0.61	ns
Kdelr1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	68137	1.77	1.92	2.57	0.69	-0.88	*
Acads	acyl-Coenzyme A dehydrogenase, short chain	11409	0.67	0.58	0.73	0.91	-0.45	ns
Csf1	colony stimulating factor 1 (macrophage)	12977	0.35	0.54	0.45	0.76	-0.66	ns
Sh3bp1	SH3-domain binding protein 1	20401	0.37	0.31	0.36	1.01	-0.03	ns
Snx2	sorting nexin 2	67804	1.71	1.52	2.29	0.74	-0.58	ns

Timp1	tissue inhibitor of metalloproteinase 1	21857	0.31	0.31	0.59	0.53	-0.47	ns
Wdr81	WD repeat domain 81	192652	0.53	0.48	0.32	1.66	0.45	ns
Msln	mesothelin	56047	1.78	2.02	1.94	0.91	0.24	ns
Sptlc2	serine palmitoyltransferase, long chain base subunit 2	20773	1.55	1.56	1.73	0.89	-0.94	**
Mecp2	methyl CpG binding protein 2	17257	0.40	0.43	0.59	0.67	-0.31	ns
Lnx2	ligand of numb-protein X 2	140887	0.46	0.43	0.44	1.03	-0.41	ns
Cmtm7	CKLF-like MARVEL transmembrane domain containing 7	102545	0.49	0.46	0.20	2.44	0.90	*
Kpna1	karyopherin (importin) alpha 1	16646	0.78	0.97	0.93	0.84	-0.45	ns
1700037H04Rik	RIKEN cDNA 1700037H04 gene	67326	1.18	1.31	1.46	0.80	0.07	ns
Gpr175	G protein-coupled receptor 175	24100	0.52	0.41	0.57	0.91	-0.09	ns
Ppp4c	protein phosphatase 4, catalytic subunit	56420	2.33	2.29	2.83	0.82	-0.27	ns
Ict1	immature colon carcinoma transcript 1	68572	1.77	1.81	1.89	0.93	0.34	ns
Tbk1	TANK-binding kinase 1	56480	1.72	1.60	1.69	1.01	0.14	ns
Tars	threonyl-tRNA synthetase	110960	1.94	1.95	1.73	1.11	0.78	ns
Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	18706	1.26	1.09	1.23	1.02	-0.04	ns
LOC675709	similar to Beta-1,4-galactosyltransferase 6 (Beta-1,4-GalTase 6) (Beta4Gal-T6) (b4Gal-T6) (UDP-galactose:beta-N-acetylglucosamine beta-1,4-galactosyltransferase 6) (UDP-Gal:beta-GlcNAc beta-1,4-galactosyltransferase 6)	675709	0.68	0.86	0.64	1.06	0.45	ns
Anxa3	annexin A3	11745	5.69	6.54	7.02	0.81	-0.84	*
Dbnl	drebrin-like	13169	0.99	1.11	1.23	0.80	-0.37	ns
Sh3kbp1	SH3-domain kinase binding protein 1	58194	0.25	0.35	0.70	0.36	-0.39	ns
Crlf3	cytokine receptor-like factor 3	54394	0.56	0.72	0.76	0.73	-0.91	*
Psma4	proteasome (prosome, macropain) subunit, alpha type 4	26441	3.52	2.93	2.97	1.18	0.74	ns
Plekhb2	pleckstrin homology domain containing, family B (evectins) member 2	226971	1.85	1.77	1.54	1.20	0.09	ns
Arsa	arylsulfatase A	11883	0.98	1.24	1.24	0.78	-0.80	ns
Mad2l2	MAD2 mitotic arrest deficient-like 2 (yeast)	71890	0.43	0.51	0.68	0.63	-0.94	**
Prr14	proline rich 14	233895	0.60	0.70	0.72	0.82	-0.68	ns
Osbp	oxysterol binding protein	76303	2.11	1.80	1.33	1.58	0.91	*
S100a11	S100 calcium binding protein A11 (calgizzarin)	20195	20.33	17.96	15.25	1.33	0.77	ns
Pik3r4	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 4, p150	75669	0.42	0.49	0.56	0.74	-0.71	ns
Nudt22	nudix (nucleoside diphosphate linked moiety X)-type motif 22	68323	0.91	0.69	0.48	1.90	0.98	***
5033414D02Rik	RIKEN cDNA 5033414D02 gene	67759	0.97	1.33	0.99	0.97	0.25	ns
2410001C21Rik	RIKEN cDNA 2410001C21 gene	66404	0.89	0.90	1.10	0.81	-0.88	*
Eml3	echinoderm microtubule associated protein like 3	225898	0.99	1.11	0.75	1.32	0.55	ns
Hbp1	high mobility group box transcription factor 1	73389	2.56	2.33	2.45	1.04	-0.21	ns
Hoxb4	homeo box B4	15412	0.59	0.38	0.34	1.71	0.44	ns
Cdk8	cyclin-dependent kinase 8	264064	1.39	1.34	1.73	0.80	-0.87	*
Inppl1	inositol polyphosphate phosphatase-like 1	16332	0.60	0.55	0.62	0.96	-0.18	ns
Nudcd3	NudC domain containing 3	209586	1.31	1.10	1.55	0.84	-0.31	ns
Phf8	PHD finger protein 8	320595	0.50	0.58	0.66	0.75	0.10	ns
Edem3	ER degradation enhancer, mannosidase alpha-like 3	66967	1.17	1.24	1.08	1.08	-0.12	ns
Brpf1	bromodomain and PHD finger containing, 1	78783	0.95	0.89	1.00	0.94	-0.62	ns
Psip1	PC4 and SFRS1 interacting protein 1	101739	1.42	1.36	1.61	0.88	-0.71	ns
AI427122	expressed sequence AI427122	102502	0.62	0.57	0.77	0.80	-0.07	ns
Cpt1a	carnitine palmitoyltransferase 1a, liver	12894	2.49	1.89	2.24	1.10	0.15	ns
Tmem160	transmembrane protein 160	69094	0.59	0.66	0.70	0.84	-0.38	ns
Ankrd13a	ankyrin repeat domain 13a	68420	1.82	1.87	2.17	0.84	-0.83	*
Cdc5l	cell division cycle 5-like (S. pombe)	71702	3.37	3.19	2.23	1.50	0.92	**
Gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2	14537	1.71	1.97	1.08	1.58	0.39	ns
1500002O20Rik	RIKEN cDNA 1500002O20 gene	71997	0.39	0.33	0.38	1.00	-0.42	ns
Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	15531	2.47	3.01	2.62	0.94	0.30	ns
Wrb	tryptophan rich basic protein	71446	0.70	0.69	0.63	1.11	-0.01	ns
Mospd3	motile sperm domain containing 3	68929	0.36	0.45	0.32	1.10	-0.02	ns
Tagap	T-cell activation Rho GTPase-activating protein	72536	0.90	0.74	0.41	2.18	0.79	ns
Paqr5	progestin and adipoQ receptor family member V	74090	1.37	0.97	1.24	1.10	0.46	ns
Med18	mediator of RNA polymerase II transcription, subunit 18 homolog (yeast)	67219	0.41	0.35	0.44	0.93	0.05	ns
Coq10b	coenzyme Q10 homolog B (S. cerevisiae)	67876	0.71	0.82	0.82	0.86	-0.59	ns
Mettl5	methyltransferase like 5	75422	1.04	1.03	0.86	1.20	0.29	ns
Mdm4	transformed mouse 3T3 cell double minute 4	17248	0.71	0.64	0.60	1.18	-0.07	ns
Rpl37a	ribosomal protein L37a	19981	24.25	22.41	15.45	1.56	0.80	ns
Thrap3	thyroid hormone receptor associated protein 3	230753	2.20	2.18	2.75	0.80	-0.60	ns
Eral1	Era (G-protein)-like 1 (E. coli)	57837	1.18	1.20	0.97	1.21	0.39	ns
Mtmr11	myotubularin related protein 11	194126	0.28	0.43	0.37	0.74	-0.37	ns
Ascc3l1	activating signal cointegrator 1 complex subunit 3-like 1	320632	2.84	2.59	2.28	1.24	0.72	ns
6330500D04Rik	RIKEN cDNA 6330500D04 gene	193385	0.40	0.35	0.53	0.75	-0.32	ns
Supv3l1	suppressor of var1, 3-like 1 (S. cerevisiae)	338359	0.57	0.62	0.70	0.81	-0.56	ns
Ccdc32	coiled-coil domain containing 32	269336	0.48	0.38	0.42	1.15	0.05	ns
Sepw1	selenoprotein W, muscle 1	20364	5.63	5.04	4.59	1.22	0.83	*
Slc41a1	solute carrier family 41, member 1	98396	0.46	0.52	0.45	1.02	0.36	ns
Cldn3	claudin 3	12739	7.35	6.83	5.63	1.30	0.76	ns
Dicer1	Dicer1, Dcr-1 homolog (Drosophila)	192119	1.03	0.87	0.89	1.14	0.59	ns
AI848100	expressed sequence AI848100	226551	3.51	2.93	2.48	1.41	0.57	ns
Eif2a	eukaryotic translation initiation factor 2a	229317	1.24	1.37	1.31	0.94	-0.31	ns
Exoc6	exocyst complex component 6	107371	0.66	0.63	0.46	1.42	0.67	ns
EG668182		668182	21.71	21.72	17.61	1.23	0.57	ns
LOC675192		675192	21.71	21.72	17.61	1.23	0.57	ns
Hisppd2a	histidine acid phosphatase domain containing 2A	327655	0.74	0.52	0.62	1.20	0.17	ns
Megf8	multiple EGF-like-domains 8	269878	0.60	0.71	0.57	1.05	0.15	ns
Susd4	sushi domain containing 4	96935	1.10	1.17	0.90	1.21	0.62	ns
Gmppa	GDP-mannose pyrophosphorylase A	69080	0.79	0.88	0.76	1.03	0.12	ns
Asxl2	Additional sex combs like 2 (Drosophila)	75302	0.82	0.87	1.22	0.67	-0.74	ns
LOC245350	similar to ubiquitin-conjugating enzyme E2Q (putative) 2	245350	0.27	0.27	0.27	0.98	0.03	ns
Samd9l	sterile alpha motif domain containing 9-like	209086	3.44	3.67	4.58	0.75	-0.53	ns
Mier3	mesoderm induction early response 1, family member 3	218613	0.67	0.89	0.82	0.82	-0.05	ns
Nt5dc1	5'-nucleotidase domain containing 1	319638	0.58	0.55	0.38	1.52	0.16	ns

Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	108155	1.84	1.77	2.55	0.72	-0.69 ns
Ralgds	ral guanine nucleotide dissociation stimulator	19730	0.42	0.32	0.37	1.13	0.53 ns
Pfdn5	prefoldin 5	56612	5.90	5.93	6.14	0.96	0.14 ns
Yars	tyrosyl-tRNA synthetase	107271	0.62	0.62	0.64	0.96	-0.70 ns
2310022K01Rik		71909	0.33	0.32	0.44	0.75	-0.72 ns
Traf4	Tnf receptor associated factor 4	22032	0.67	0.77	0.50	1.34	0.15 ns
Ell	elongation factor RNA polymerase II	13716	0.51	0.43	0.42	1.19	0.79 ns
Bckdk	branched chain ketoacid dehydrogenase kinase	12041	0.73	0.70	0.85	0.85	-0.55 ns
Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	66917	2.32	1.76	0.77	2.99	0.96 **
Nr2f6	nuclear receptor subfamily 2, group F, member 6	13864	2.04	2.21	1.87	1.08	0.61 ns
Esrra	estrogen related receptor, alpha	26379	0.51	0.46	0.46	1.10	0.07 ns
Sft2d1		106489	0.96	0.84	0.66	1.46	0.70 ns
Wnt10a	wingless related MMTV integration site 10a	22409	0.69	0.90	0.48	1.42	0.47 ns
Rer1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	67830	0.75	0.65	0.81	0.92	-0.39 ns
Ilf3	interleukin enhancer binding factor 3	16201	1.92	1.73	1.50	1.27	0.88 *
Gpx1	glutathione peroxidase 1	14775	5.19	4.45	4.50	1.15	0.38 ns
Paqr7	progestin and adipoQ receptor family member VII	71904	0.31	0.38	0.38	0.81	-0.77 ns
Igsf8	immunoglobulin superfamily, member 8	140559	1.15	1.03	1.15	1.00	0.46 ns
Josd1	Josephin domain containing 1	74158	1.77	1.63	1.98	0.89	0.10 ns
Spats2	spermatogenesis associated, serine-rich 2	72572	1.53	1.43	1.47	1.04	0.39 ns
Tm7sf2	transmembrane 7 superfamily member 2	73166	0.45	0.33	0.29	1.54	0.81 ns
BC003940	cDNA sequence BC003940	192173	0.81	0.88	0.96	0.84	0.06 ns
Zfp598	zinc finger protein 598	213753	1.11	1.08	1.01	1.10	0.65 ns
Ehmt2	euchromatic histone lysine N-methyltransferase 2	110147	3.81	3.58	2.89	1.31	0.90 *
Svil	supervillin	225115	0.59	0.76	0.69	0.85	-0.05 ns
2010111I01Rik	RIKEN cDNA 2010111I01 gene	72061	0.91	0.75	0.58	1.56	0.63 ns
2610209M04Rik	RIKEN cDNA 2610209M04 gene	66618	3.33	3.53	4.41	0.75	-0.40 ns
Sec11c	SEC11 homolog C (S. cerevisiae)	66286	0.34	0.55	0.68	0.50	-0.61 ns
Mrpl52	mitochondrial ribosomal protein L52	68836	1.95	2.21	1.97	0.99	0.09 ns
Triap1	TP53 regulated inhibitor of apoptosis 1	69076	0.52	0.44	0.58	0.90	0.16 ns
Ascc1	activating signal cointegrator 1 complex subunit 1	69090	0.82	0.83	0.70	1.17	0.33 ns
Rfng	radical fringe gene homolog (Drosophila)	19719	0.48	0.46	0.49	0.97	0.45 ns
Cdc42	cell division cycle 42 homolog (S. cerevisiae)	12540	4.92	4.54	5.20	0.94	-0.48 ns
4930461P20Rik	RIKEN cDNA 4930461P20 gene	78244	0.87	0.83	1.25	0.69	-0.44 ns
BC048355	cDNA sequence BC048355	381101	0.59	0.66	0.35	1.65	0.82 *
Cbfb	core binding factor beta	12400	5.44	4.16	5.34	1.01	0.32 ns
Mtch1	mitochondrial carrier homolog 1 (C. elegans)	56462	2.74	2.41	1.38	1.97	0.96 **
Trpc4ap	transient receptor potential cation channel, subfamily C, member 4 associated protein	56407	1.41	1.08	1.36	1.03	0.29 ns
Adss	adenylosuccinate synthetase, non muscle	11566	3.67	3.72	2.70	1.36	0.49 ns
Ing4	inhibitor of growth family, member 4	28019	0.74	0.67	0.78	0.95	-0.23 ns
Eif2b1	eukaryotic translation initiation factor 2B, subunit 1 (alpha)	209354	0.68	0.75	0.87	0.79	-0.72 ns
Ppl	periplakin	19041	1.78	1.84	2.13	0.83	-0.88 *
A230054D04Rik	RIKEN cDNA A230054D04 gene	665775	0.47	0.44	0.47	1.00	0.48 ns
Zmiz2	zinc finger, MIZ-type containing 2	52915	0.56	0.61	0.61	0.91	-0.35 ns
D17Wsu92e	DNA segment, Chr 17, Wayne State University 92, expressed	224647	0.76	0.74	0.58	1.31	0.88 *
Alg3	asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)	208624	0.50	0.49	0.49	1.03	0.51 ns