Top 5% Differentially Expressed Genes, Tg26 Lymphoma vs. Tg26 Asymptomatic Lymph Node and Spleen

SYMBOL	logFC	AveExpr	t	P.Value	adj.P.Val	B	ENTREZ ID	GENE NAME
0610010F05Rik	0.9297	7.256	9.068	4.73E-09	1.74E-07	10.74	71675	RIKEN cDNA 0610010F05 gene
1700021K19Rik	-0.9421	8.26	-12.33	1.30E-11	1.24E-09	16.68	100502698	RIKEN cDNA 1700021K19 gene
1700048O20Rik	2.36	8.331	15.94	6.49E-14	1.76E-11	21.97	69430	RIKEN cDNA 1700048O20 gene
2010016I18Rik	-1.561	7.863	-10.22	5.11E-10	2.63E-08	12.99	69206	RIKEN cDNA 2010016I18 gene
2010111I01Rik	0.7153	7.255	9.437	2.28E-09	9.32E-08	11.47	72061	RIKEN cDNA 2010111I01 gene
2610318N02Rik	2.704	7.631	15.69	9.09E-14	2.24E-11	21.64	70458	RIKEN cDNA 2610318N02 gene
2610528A11Rik	-0.8579	7.827	-8.625	1.16E-08	3.63E-07	9.826	70045	RIKEN cDNA 2610528A11 gene
2700094K13Rik	0.783	7.596	8.664	1.07E-08	3.38E-07	9.906	72657	RIKEN cDNA 2700094K13 gene
2810025M15Rik	0.8209	7.7	13.06	4.08E-12	4.74E-10	17.85	69953	RIKEN cDNA 2810025M15 gene
2810417H13Rik	2.459	9.522	18.32	3.33E-15	2.07E-12	24.89	68026	RIKEN cDNA 2810417H13 gene
2900026A02Rik	1.185	7.619	9.905	9.26E-10	4.40E-08	12.39	243219	RIKEN cDNA 2900026A02 gene
3010003L21Rik	0.8263	6.848	8.606	1.21E-08	3.74E-07	9.787	109163	RIKEN cDNA 3010003L21 gene
3110007F17Rik	1.751	5.995	19.88	5.69E-16	6.74E-13	26.6	73061	RIKEN cDNA 3110007F17 gene
4921507P07Rik	-0.8962	5.894	-8.637	1.14E-08	3.55E-07	9.85	70821	RIKEN cDNA 4921507P07 gene
4930427A07Rik	1.289	7.584	15.26	1.63E-13	3.50E-11	21.06	104732	RIKEN cDNA 4930427A07 gene
4930506M07Rik	-1.298	6.74	-8.63	1.15E-08	3.60E-07	9.836	71653	RIKEN cDNA 4930506M07 gene
4930524J08Rik	0.5529	6.91	9.544	1.85E-09	7.80E-08	11.69	---	RIKEN cDNA 4930524J08 gene
4930579G24Rik	1.015	7.746	12.28	1.41E-11	1.32E-09	16.6	75939	RIKEN cDNA 4930579G24 gene
4931429I11Rik	2.166	9.04	18.61	2.36E-15	1.68E-12	25.22	70989	RIKEN cDNA 4931429I11 gene
4933426M11Rik	-0.8203	9.443	-10.76	1.90E-10	1.17E-08	13.99	217684	RIKEN cDNA 4933426M11 gene
4933439C10Rik	1.525	8.019	8.331	2.14E-08	6.12E-07	9.207	74476	RIKEN cDNA 4933439C10 gene
A130050O07Rik	1.544	6.021	8.82	7.80E-09	2.59E-07	10.23	320138	RIKEN cDNA A130050O07 gene
A630038E17Rik	-1.061	6.492	-12.14	1.77E-11	1.60E-09	16.38	219065	RIKEN cDNA A630038E17 gene
AA415398	-0.7155	6.365	-9.54	1.86E-09	7.84E-08	11.68	433752	expressed sequence AA415398
AA467197	1.075	5.959	8.315	2.22E-08	6.30E-07	9.173	433470	expressed sequence AA467197

Abca1	-2.129	8.307	-9.261	3.22E-09	1.25E-07	11.12	11303	ATP-binding cassette sub-family A (ABC1) member 1
Abcf2	0.5166	9.182	8.97	5.76E-09	2.04E-07	10.54	27407	ATP-binding cassette sub-family F (GCN20) member 2
Abcg3	-1.607	8.047	-8.341	2.10E-08	6.05E-07	9.227	27405	ATP-binding cassette sub-family G (WHITE) member 3
Abhd15	1.314	7.273	8.238	2.61E-08	7.25E-07	9.008	67477	abhydrolase domain containing 15
Abl1	0.5135	9.419	9.032	5.09E-09	1.85E-07	10.66	11350	c-abl oncogene 1 non-receptor tyrosine kinase
Abtb2	-1.326	7.69	-11.38	6.40E-11	4.64E-09	15.08	99382	ankyrin repeat and BTB (POZ) domain containing 2
Acp6	0.9899	8.839	8.842	7.46E-09	2.50E-07	10.28	66659	acid phosphatase 6 lysophosphatidic
Actl6a	0.7127	9.976	12.05	2.06E-11	1.81E-09	16.22	56456	actin-like 6A
Actn1	-2.698	9.292	-17.74	6.66E-15	3.38E-12	24.21	109711	actinin alpha 1
Acvrl1	-1.022	7.475	-12.55	9.16E-12	9.31E-10	17.04	11482	activin A receptor type II-like 1
Ada	0.7729	8.017	8.521	1.44E-08	4.35E-07	9.608	11486	adenosine deaminase
Adam22	-0.6282	5.578	-8.024	4.11E-08	1.08E-06	8.547	11496	a disintegrin and metallopeptidase domain 22
Adam23	-1.874	7.778	-12.5	9.83E-12	9.88E-10	16.97	23792	a disintegrin and metallopeptidase domain 23
Adamts14	-0.6046	6.83	-8.09	3.57E-08	9.56E-07	8.69	237360	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif 14
Adcy3	-0.7716	7.515	-8.528	1.42E-08	4.29E-07	9.624	104111	adenylate cyclase 3
Adcy6	-1.22	7.055	-11.66	3.94E-11	3.11E-09	15.57	11512	adenylate cyclase 6
Add1	-0.7164	9.739	-9.929	8.84E-10	4.23E-08	12.43	11518	adducin 1 (alpha)

Add3	-0.9563	10.25	-9.081	4.61E-09	1.70E-07	10.76	27360	adducin 3 (gamma)
Adh1	-2.544	7.797	-14.72	3.47E-13	6.59E-11	20.31	11522	alcohol dehydrogenase 1 (class I)
Adrbk2	-1.581	7.48	-9.829	1.07E-09	4.93E-08	12.24	320129	adrenergic receptor kinase beta 2
Adss	0.469	9.486	8.468	1.61E-08	4.79E-07	9.497	11566	adenylosuccinate synthetase non muscle
Aes	-1.079	10.77	-9.068	4.73E-09	1.74E-07	10.74	14797	amino-terminal enhancer of split
Aff1	0.5168	8.168	8.316	2.21E-08	6.29E-07	9.175	17355	AF4/FMR2 family member 1
Agpat9	1.48	7.225	12.1	1.91E-11	1.71E-09	16.3	231510	1-acylglycerol-3-phosphate O-acyltransferase 9
Ahcy	1.09	8.991	9.152	4.00E-09	1.50E-07	10.91	269378	S-adenosylhomocysteine hydrolase
AI314180	0.8272	9.291	11.03	1.19E-10	7.83E-09	14.46	230249	expressed sequence AI314180
Akap12	1.669	8.133	11.62	4.26E-11	3.31E-09	15.49	83397	A kinase (PRKA) anchor protein (gravin) 12
Aldh1b1	1.588	7.713	8.597	1.23E-08	3.80E-07	9.766	72535	aldehyde dehydrogenase 1 family member B1
Aldh4a1	-1.314	6.961	-8.961	5.86E-09	2.07E-07	10.52	212647	aldehyde dehydrogenase 4 family member A1
Alg6	0.9056	7.001	10.83	1.69E-10	1.06E-08	14.11	320438	asparagine-linked glycosylation 6 (alpha-1 3 -glucosyltransferase)
Alkbh8	0.5824	8.53	8.659	1.08E-08	3.41E-07	9.897	67667	alkB alkylation repair homolog 8 (E. coli)
Alms1	1.105	7.199	9.939	8.68E-10	4.18E-08	12.45	236266	Alstrom syndrome 1
Alyref	0.7895	9.829	9.306	2.95E-09	1.16E-07	11.22	21681	Aly/REF export factor

Amd2	1.273	8.862	11.72	3.61E-11	2.90E-09	15.66	100041585	S-adenosylmethionine decarboxylase 2
Ammecr1	1.283	8.448	13.22	3.18E-12	3.85E-10	18.1	56068	Alport syndrome mental retardation midface hypoplasia and elliptocytosis chromosomal region gene 1
Angel1	-0.8102	7.335	-8.928	6.27E-09	2.18E-07	10.45	68737	angel homolog 1 (Drosophila)
Ank	-1.549	8.376	-9.878	9.75E-10	4.58E-08	12.33	11732	progressive ankylosis
Ankrd13d	0.9477	7.605	8.802	8.09E-09	2.66E-07	10.19	68423	ankyrin repeat domain 13 family member D
Ankrd28	1.467	9.371	12.43	1.11E-11	1.09E-09	16.84	105522	ankyrin repeat domain 28
Ankrd52	0.8388	9.106	8.226	2.67E-08	7.42E-07	8.983	237615	ankyrin repeat domain 52
Ankrd6	1.087	6.777	11.88	2.72E-11	2.29E-09	15.94	140577	ankyrin repeat domain 6
Anln	2.389	7.33	15.75	8.36E-14	2.11E-11	21.72	68743	anillin actin binding protein
Anp32e	1.039	9.318	8.557	1.34E-08	4.07E-07	9.684	66471	acidic (leucine-rich) nuclear phosphoprotein 32 family member E
Anxa5	-1.514	9.273	-9.777	1.18E-09	5.36E-08	12.14	11747	annexin A5
Ap1ar	0.8949	9.965	10.49	3.12E-10	1.73E-08	13.48	211556	adaptor-related protein complex 1 associated regulatory protein
Apaf1	0.83	8.489	11.18	9.02E-11	6.23E-09	14.74	11783	apoptotic peptidase activating factor 1
Apex1	0.9911	8.969	10.84	1.66E-10	1.05E-08	14.12	11792	apurinic/apyrimidinic endonuclease 1
Apitd1	1.239	7.739	9.635	1.55E-09	6.71E-08	11.86	69928	apoptosis-inducing TAF9-like domain 1

Appl2	-1.011	8.208	-8.375	1.96E-08	5.69E-07	9.299	216190	adaptor protein phosphotyrosine interaction PH domain and leucine zipper containing 2
Ar	-1.999	6.356	-17.35	1.07E-14	4.62E-12	23.75	11835	androgen receptor
Arhgap11a	1.881	8.459	16.59	2.79E-14	9.46E-12	22.8	228482	Rho GTPase activating protein 11A
Arhgap19	1.444	7.943	13.63	1.71E-12	2.29E-10	18.72	71085	Rho GTPase activating protein 19
Arhgap28	-0.7321	5.861	-8.992	5.51E-09	1.97E-07	10.58	268970	Rho GTPase activating protein 28
Arhgap5	-2.14	6.685	-10.17	5.62E-10	2.86E-08	12.89	11855	Rho GTPase activating protein 5
Arhgef39	0.8367	7.45	9.91	9.18E-10	4.37E-08	12.4	230098	Rho guanine nucleotide exchange factor (GEF) 39
Arid5b	-0.7532	9.504	-8.147	3.16E-08	8.54E-07	8.814	71371	AT rich interactive domain 5B (MRF1-like)
Arl4c	-1.397	7.587	-10.49	3.10E-10	1.73E-08	13.49	320982	ADP-ribosylation factor-like 4C
Arl5c	1.013	9.154	8.783	8.41E-09	2.75E-07	10.15	217151	ADP-ribosylation factor-like 5C
Arl6ip1	0.6137	10.82	9.895	9.43E-10	4.46E-08	12.37	54208	ADP-ribosylation factor-like 6 interacting protein 1
Arntl2	1.715	6.495	20.36	3.36E-16	4.58E-13	27.11	272322	aryl hydrocarbon receptor nuclear translocator-like 2
Arrdc4	-1.28	6.928	-10.06	6.89E-10	3.41E-08	12.68	66412	arrestin domain containing 4
Art2a-ps	-0.9625	5.779	-9.551	1.83E-09	7.72E-08	11.7	11871	ADP-ribosyltransferase 2a pseudogene
Art2b	-2.367	6.447	-12.4	1.16E-11	1.13E-09	16.8	11872	ADP-ribosyltransferase 2b
Asf1a	0.8386	8.465	10.46	3.30E-10	1.83E-08	13.43	66403	anti-silencing function 1A histone chaperone

Asf1b	1.774	9.481	12.19	1.63E-11	1.51E-09	16.46	66929	anti-silencing function 1B histone chaperone
Aspm	2.163	7.125	15.76	8.29E-14	2.10E-11	21.73	12316	asp (abnormal spindle)-like microcephaly associated (Drosophila)
Atad2	1.033	8.41	9.148	4.03E-09	1.51E-07	10.9	70472	ATPase family AAA domain containing 2
Atad5	1.606	6.844	13.46	2.22E-12	2.85E-10	18.46	237877	ATPase family AAA domain containing 5
Atl2	0.8457	8.404	9.348	2.72E-09	1.08E-07	11.3	56298	atlastin GTPase 2
Atp11a	-1.28	7.628	-14.77	3.22E-13	6.19E-11	20.38	50770	ATPase class VI type 11A
Atp13a2	0.6461	8.937	8.693	1.01E-08	3.22E-07	9.967	74772	ATPase type 13A2
Atp13a3	0.9206	9.997	8.208	2.78E-08	7.65E-07	8.945	224088	ATPase type 13A3
Atp2b1	-0.7638	9.542	-8.965	5.82E-09	2.06E-07	10.53	67972	ATPase Ca++ transporting plasma membrane 1
Atp9a	-1.503	7.046	-8.031	4.05E-08	1.07E-06	8.563	11981	ATPase class II type 9A
Aurka	1.534	8.049	17.42	9.79E-15	4.48E-12	23.83	20878	aurora kinase A
Aurkb	2.044	9.184	18.84	1.82E-15	1.35E-12	25.47	20877	aurora kinase B
Axin2	-1.362	7.198	-14.52	4.60E-13	8.06E-11	20.03	12006	axin2
B230118H07Rik	1.748	4.283	10.43	3.46E-10	1.90E-08	13.38	68170	RIKEN cDNA B230118H07 gene
B3glct	0.9477	8.298	11.35	6.78E-11	4.88E-09	15.02	381694	beta-3-glucosyltransferase
Bard1	1.393	7.064	10.63	2.41E-10	1.41E-08	13.75	12021	BRCA1 associated RING domain 1
Basp1	-1.267	9.01	-13.31	2.75E-12	3.41E-10	18.24	70350	brain abundant membrane attached signal protein 1
BC021614	-1.615	7.239	-8.833	7.60E-09	2.53E-07	10.26	225884	cDNA sequence BC021614
BC030867	0.9419	6.223	11.17	9.28E-11	6.36E-09	14.71	217216	cDNA sequence BC030867
BC043934	1.371	7.115	8.179	2.95E-08	8.06E-07	8.882	270185	cDNA sequence BC043934
BC055324	1.165	7.191	11.16	9.43E-11	6.42E-09	14.69	381306	cDNA sequence BC055324

Bcat1	2.42	7.68	9.749	1.25E-09	5.61E-08	12.09	12035	branched chain aminotransferase 1 cytosolic
Bcl11b	-2.383	8.937	-14.27	6.61E-13	1.08E-10	19.67	58208	B cell leukemia/lymphoma 11B
Bcl2	-1.328	9.18	-10.54	2.84E-10	1.61E-08	13.58	12043	B cell leukemia/lymphoma 2
Bcl7a	1.21	9.559	12.46	1.06E-11	1.05E-09	16.89	77045	B cell CLL/lymphoma 7A
Bcr	1.182	8.396	10.56	2.73E-10	1.55E-08	13.62	110279	breakpoint cluster region
Bend5	-1.35	7.517	-13.9	1.14E-12	1.66E-10	19.12	67621	BEN domain containing 5
Bfsp2	2	7.45	16.36	3.72E-14	1.18E-11	22.52	107993	beaded filament structural protein 2 phakinin
Birc5	1.709	7.218	11.16	9.40E-11	6.42E-09	14.7	11799	baculoviral IAP repeat-containing 5
Blm	1.489	7.736	16.64	2.60E-14	8.97E-12	22.87	12144	Bloom syndrome RecQ helicase-like
Blmh	0.9657	8.754	13.66	1.64E-12	2.21E-10	18.76	104184	bleomycin hydrolase
Bmf	1.17	8.556	10.92	1.43E-10	9.27E-09	14.27	171543	BCL2 modifying factor
Bmp7	-0.8257	7.173	-11.03	1.18E-10	7.76E-09	14.47	12162	bone morphogenetic protein 7
Bmpr2	-1.736	7.641	-8.232	2.64E-08	7.34E-07	8.995	12168	bone morphogenetic protein receptor type II (serine/threonine kinase)
Boll	-1.132	5.505	-10.7	2.13E-10	1.28E-08	13.87	75388	bol boule-like (Drosophila)
Bora	1.615	7.592	11.08	1.08E-10	7.18E-09	14.56	77744	bora aurora kinase A activator
Brca1	1.27	6.945	11.56	4.71E-11	3.62E-09	15.39	12189	breast cancer 1
Brca2	1.175	7.087	10.14	5.99E-10	3.03E-08	12.83	12190	breast cancer 2
Brd7	0.5342	9.315	10.16	5.76E-10	2.92E-08	12.87	26992	bromodomain containing 7
Brip1	1.834	6.811	15.98	6.15E-14	1.71E-11	22.02	237911	BRCA1 interacting protein C-terminal helicase 1
Brwd1	-2.28	7.733	-16.41	3.52E-14	1.14E-11	22.58	93871	bromodomain and WD repeat domain containing 1

Btbd11	-0.7295	6.66	-8.295	2.31E-08	6.52E-07	9.131	74007	BTB (POZ) domain containing 11
Btk	0.835	9.687	9.004	5.37E-09	1.94E-07	10.61	12229	Bruton agammaglobulinemia tyrosine kinase
Btla	-2.174	8.515	-9.658	1.49E-09	6.48E-08	11.91	208154	B and T lymphocyte associated
Bub1	2.695	7.713	16.22	4.49E-14	1.35E-11	22.33	12235	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)
Bub1b	2.561	8.085	19.44	9.23E-16	8.82E-13	26.13	12236	budding uninhibited by benzimidazoles 1 homolog beta (S. cerevisiae)
Bub3	0.7336	9.623	11.96	2.40E-11	2.06E-09	16.07	12237	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)
C330027C09Rik	2.592	7.214	19.3	1.08E-15	8.90E-13	25.98	224171	RIKEN cDNA C330027C09 gene
C78339	-0.5032	9.176	-8.67	1.06E-08	3.35E-07	9.919	97863	expressed sequence C78339
Cabp4	1.648	8.031	15.96	6.29E-14	1.72E-11	22	73660	calcium binding protein 4
Cacna1d	-0.7248	6.169	-8.284	2.37E-08	6.66E-07	9.107	12289	calcium channel voltage-dependent L type alpha 1D subunit
Cacnb3	-1.795	7.736	-13.48	2.12E-12	2.74E-10	18.5	12297	calcium channel voltage-dependent beta 3 subunit
Cadm1	-1.096	7.166	-11.52	5.02E-11	3.80E-09	15.33	54725	cell adhesion molecule 1
Camk4	-1.811	6.953	-12.25	1.48E-11	1.39E-09	16.55	12326	calcium/calmodulin-dependent protein kinase IV
Capsl	1.979	6.044	17.66	7.35E-15	3.63E-12	24.11	75568	calcyphosine-like
Card11	-1.289	9.385	-8.339	2.11E-08	6.07E-07	9.224	108723	caspase recruitment domain family member 11

Casc5	2.224	8.207	14.28	6.49E-13	1.06E-10	19.69	76464	cancer susceptibility candidate 5
Cast	-0.6945	9.334	-8.359	2.02E-08	5.87E-07	9.265	12380	calpastatin
Cbx1	0.7329	8.861	9.288	3.05E-09	1.19E-07	11.18	12412	chromobox 1
Cbx3	0.6814	10.18	9.516	1.95E-09	8.14E-08	11.63	12417	chromobox 3
Cbx5	1.067	9.066	10.69	2.19E-10	1.31E-08	13.84	12419	chromobox 5
Cbx7	-1.327	8.281	-9.2	3.64E-09	1.39E-07	11	52609	chromobox 7
Ccdc122	-1.046	5.381	-8.75	9.00E-09	2.91E-07	10.08	108811	coiled-coil domain containing 122
Ccdc135	4.556	7.593	25.79	1.83E-18	1.30E-14	32.02	330830	coiled-coil domain containing 135
Ccdc138	0.8633	6.232	8.485	1.55E-08	4.66E-07	9.533	76138	coiled-coil domain containing 138
Ccdc14	0.7662	6.74	7.988	4.44E-08	1.16E-06	8.47	239839	coiled-coil domain containing 14
Ccdc18	1.484	5.721	11.2	8.69E-11	6.05E-09	14.77	73254	coiled-coil domain containing 18
Ccdc34	1.11	7.113	11.47	5.46E-11	4.09E-09	15.24	68201	coiled-coil domain containing 34
Ccl22	-1.426	7.093	-9.683	1.41E-09	6.21E-08	11.96	20299	chemokine (C-C motif) ligand 22
Ccl5	-2.474	10.2	-9.872	9.85E-10	4.61E-08	12.32	20304	chemokine (C-C motif) ligand 5
Ccna2	2.126	9.449	15.61	1.00E-13	2.41E-11	21.54	12428	cyclin A2
Ccnb1	2.519	7.133	19.43	9.32E-16	8.82E-13	26.12	268697	cyclin B1
Ccnb2	2.12	9.35	14.98	2.40E-13	4.90E-11	20.68	12442	cyclin B2
Ccnd3	1.068	10.09	9.052	4.88E-09	1.79E-07	10.7	12445	cyclin D3
Ccne2	1.748	6.816	13.03	4.27E-12	4.91E-10	17.8	12448	cyclin E2
Ccnf	1.895	7.678	17.32	1.11E-14	4.75E-12	23.71	12449	cyclin F
Ccp110	0.9377	7.146	10.79	1.80E-10	1.12E-08	14.04	101565	centriolar coiled coil protein 110

Cct3	0.6627	9.909	8.41	1.82E-08	5.32E-07	9.374	12462	chaperonin containing Tcp1 subunit 3 (gamma)
Cd200	-1.776	7.556	-8.932	6.22E-09	2.17E-07	10.46	17470	CD200 antigen
Cd200r4	-0.8537	4.207	-8.336	2.12E-08	6.09E-07	9.216	239849	CD200 receptor 4
Cd209d	-2.268	7.296	-14.12	8.27E-13	1.25E-10	19.44	170779	CD209d antigen
Cd226	-2.579	7.266	-13.74	1.44E-12	2.02E-10	18.89	225825	CD226 antigen
Cd244	1.851	7.79	10.34	4.08E-10	2.18E-08	13.22	18106	CD244 natural killer cell receptor 2B4
Cd247	-1.687	7.591	-11.4	6.20E-11	4.50E-09	15.11	12503	CD247 antigen
Cd27	-3.069	8.904	-12.62	8.22E-12	8.48E-10	17.15	21940	CD27 antigen
Cd274	-1.554	9.195	-9.237	3.38E-09	1.30E-07	11.08	60533	CD274 antigen
Cd28	-2.775	8.566	-13.72	1.50E-12	2.07E-10	18.85	12487	CD28 antigen
Cd3d	-2.883	7.858	-13.18	3.37E-12	4.02E-10	18.04	12500	CD3 antigen delta polypeptide
Cd3e	-2.896	10.13	-12.56	9.03E-12	9.20E-10	17.05	12501	CD3 antigen epsilon polypeptide
Cd3g	-3.851	9.449	-12.76	6.56E-12	6.99E-10	17.37	12502	CD3 antigen gamma polypeptide
Cd4	-3.307	9.456	-13.24	3.09E-12	3.77E-10	18.13	12504	CD4 antigen
Cd40	-1.569	9.228	-11.25	8.03E-11	5.64E-09	14.85	21939	CD40 antigen
Cd40lg	-2.185	6.448	-10.81	1.75E-10	1.10E-08	14.07	21947	CD40 ligand
Cd5	-2.274	9.213	-8.744	9.10E-09	2.93E-07	10.07	12507	CD5 antigen
Cd55	-1.494	9.296	-8.081	3.64E-08	9.72E-07	8.671	13136	CD55 antigen
Cd6	-2.344	8.247	-12.41	1.14E-11	1.11E-09	16.82	12511	CD6 antigen
Cd7	-2.652	9.423	-13.02	4.36E-12	4.99E-10	17.78	12516	CD7 antigen
Cd74	-1.442	12.26	-8.926	6.29E-09	2.18E-07	10.45	16149	CD74 antigen (invariant polypeptide of major histocompatibility complex class II antigen-associated)
Cd83	-2.334	8.997	-11.08	1.08E-10	7.18E-09	14.56	12522	CD83 antigen

Cd8a	-2.749	8.795	-15.43	1.28E-13	2.92E-11	21.3	12525	CD8 antigen alpha chain
Cd8b1	-2.917	8.484	-13.46	2.20E-12	2.83E-10	18.47	12526	CD8 antigen beta chain 1
Cd93	3.12	9.141	19.31	1.07E-15	8.90E-13	25.99	17064	CD93 antigen
Cd96	-3.117	8.222	-14.24	6.89E-13	1.11E-10	19.63	84544	CD96 antigen
Cdc14b	-1.275	7.364	-8.988	5.55E-09	1.98E-07	10.57	218294	CDC14 cell division cycle 14B
Cdc20	1.744	8.17	21.23	1.35E-16	2.17E-13	27.99	107995	cell division cycle 20
Cdc25a	1.106	8.355	15.54	1.11E-13	2.59E-11	21.44	12530	cell division cycle 25A
Cdc25c	2.181	6.615	14.63	3.93E-13	7.21E-11	20.18	12532	cell division cycle 25C
Cdc45	1.401	7.591	14.02	9.52E-13	1.42E-10	19.3	12544	cell division cycle 45
Cdc6	1.315	7.308	14.48	4.84E-13	8.35E-11	19.98	23834	cell division cycle 6
Cdca2	2.242	7.433	13.72	1.48E-12	2.06E-10	18.86	108912	cell division cycle associated 2
Cdca3	1.656	7.794	12.81	6.06E-12	6.55E-10	17.45	14793	cell division cycle associated 3
Cdca5	1.833	7.619	16.57	2.86E-14	9.58E-12	22.78	67849	cell division cycle associated 5
Cdca7	2.027	8.546	16.79	2.16E-14	7.75E-12	23.06	66953	cell division cycle associated 7
Cdca7l	1.121	8.486	13.67	1.60E-12	2.17E-10	18.78	217946	cell division cycle associated 7 like
Cdca8	2.067	7.58	15.62	9.93E-14	2.40E-11	21.55	52276	cell division cycle associated 8
Cdhr2	3.151	6.872	11.11	1.03E-10	6.94E-09	14.6	268663	cadherin-related family member 2
Cdhr4	0.9151	6.548	8.588	1.25E-08	3.85E-07	9.749	69398	cadherin-related family member 4
Cdk1	2.097	7.816	12.28	1.41E-11	1.32E-09	16.61	12534	cyclin-dependent kinase 1
Cdk14	-1.083	6.498	-8.972	5.73E-09	2.03E-07	10.54	18647	cyclin-dependent kinase 14
Cdk2	1.104	9.254	13.79	1.34E-12	1.90E-10	18.96	12566	cyclin-dependent kinase 2
Cdk4	0.7077	10.68	9.873	9.83E-10	4.61E-08	12.33	12567	cyclin-dependent kinase 4
Cdk6	1.322	9.289	8.948	6.02E-09	2.11E-07	10.49	12571	cyclin-dependent kinase 6
Cdk9	0.4908	9.984	8.808	8.00E-09	2.64E-07	10.2	107951	cyclin-dependent kinase 9 (CDC2-related kinase)

Cdkn3	1.572	6.892	10.71	2.10E-10	1.27E-08	13.89	72391	cyclin-dependent kinase inhibitor 3
Cdyl2	-1.676	7.997	-17.65	7.45E-15	3.63E-12	24.1	75796	chromodomain protein Y chromosome-like 2
Cecr2	2.599	8.666	22.99	2.34E-17	5.93E-14	29.65	330409	cat eye syndrome chromosome region candidate 2
Cenpa	1.58	9.519	17.83	5.98E-15	3.18E-12	24.31	12615	centromere protein A
Cenpe	2.499	7.473	15.59	1.04E-13	2.47E-11	21.5	229841	centromere protein E
Cenpf	2.112	7.321	14.85	2.88E-13	5.66E-11	20.49	108000	centromere protein F
Cenph	2.047	6.602	20.32	3.51E-16	4.58E-13	27.07	26886	centromere protein H
Cenpi	1.77	6.202	17.01	1.64E-14	6.48E-12	23.33	102920	centromere protein I
Cenpk	1.643	6.186	13.69	1.54E-12	2.11E-10	18.82	60411	centromere protein K
Cenpl	0.9951	6.691	11.23	8.25E-11	5.76E-09	14.83	70454	centromere protein L
Cenpm	1.466	7.971	15.54	1.11E-13	2.59E-11	21.44	66570	centromere protein M
Cenpn	2.097	8.276	17.95	5.17E-15	2.83E-12	24.46	72155	centromere protein N
Cenpp	1.541	5.868	11.21	8.65E-11	6.03E-09	14.78	66336	centromere protein P
Cenpw	0.8512	6.231	9.052	4.89E-09	1.79E-07	10.7	66311	centromere protein W
Cep128	1.012	7.969	8.279	2.39E-08	6.70E-07	9.096	75216	centrosomal protein 128
Cep55	2.058	7.697	17.23	1.24E-14	5.19E-12	23.6	74107	centrosomal protein 55
Cep68	0.7798	9.115	8.992	5.51E-09	1.97E-07	10.58	216543	centrosomal protein 68
Cep78	0.724	7.769	11.71	3.66E-11	2.92E-09	15.65	208518	centrosomal protein 78
Cep83	1.202	7.813	17.4	1.01E-14	4.48E-12	23.81	77048	centrosomal protein 83
Cep85	0.7529	7.313	8.838	7.52E-09	2.51E-07	10.27	70012	centrosomal protein 85
Cerk	1.032	9.445	11.4	6.19E-11	4.50E-09	15.12	223753	ceramide kinase
Cers5	0.7233	9.961	8.876	6.96E-09	2.37E-07	10.34	71949	ceramide synthase 5
Cers6	-1.676	8.203	-12.35	1.27E-11	1.21E-09	16.71	241447	ceramide synthase 6
Chaf1a	1.515	7.642	20.11	4.39E-16	5.38E-13	26.85	27221	chromatin assembly factor 1 subunit A (p150)

Chaf1b	1.499	8.099	13.7	1.53E-12	2.10E-10	18.83	110749	chromatin assembly factor 1 subunit B (p60)
Chek1	2.331	7.24	24.54	5.52E-18	1.96E-14	31	12649	checkpoint kinase 1
Chek2	0.9071	6.89	9.31	2.92E-09	1.15E-07	11.22	50883	checkpoint kinase 2
Chil5	-0.8519	5.738	-12.65	7.81E-12	8.14E-10	17.2	229687	chitinase-like 5
Chpf	-0.6337	7.264	-8.728	9.42E-09	3.03E-07	10.04	74241	chondroitin polymerizing factor
Chst10	-1.046	7.792	-10.78	1.84E-10	1.15E-08	14.02	98388	carbohydrate sulfotransferase 10
Chst2	-0.6555	6.995	-8.696	1.01E-08	3.21E-07	9.973	54371	carbohydrate sulfotransferase 2
Chtf18	0.9841	7.417	11.13	9.98E-11	6.75E-09	14.64	214901	CTF18 chromosome transmission fidelity factor 18
Ciita	-2.233	8.819	-11.81	3.06E-11	2.56E-09	15.82	12265	class II transactivator
Cit	1.608	7.656	12.98	4.64E-12	5.23E-10	17.72	12704	citron
Cited2	0.7837	10.24	8.334	2.13E-08	6.09E-07	9.214	17684	Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 2
Ckap2	1.956	6.677	15.74	8.43E-14	2.11E-11	21.71	80986	cytoskeleton associated protein 2
Ckap2l	1.749	7.456	16.69	2.46E-14	8.65E-12	22.93	70466	cytoskeleton associated protein 2-like
Ckap5	1.025	8.949	12.27	1.43E-11	1.34E-09	16.59	75786	cytoskeleton associated protein 5
Cks1b	2.19	8.752	16.39	3.62E-14	1.16E-11	22.55	54124	CDC28 protein kinase 1b
Cks2	1.824	8.346	13.39	2.45E-12	3.10E-10	18.36	66197	CDC28 protein kinase regulatory subunit 2
Clec7a	-1.638	7.21	-9.926	8.89E-10	4.25E-08	12.43	56644	C-type lectin domain family 7 member a
Clec9a	-1.904	6.41	-11.75	3.39E-11	2.77E-09	15.72	232414	C-type lectin domain family 9 member a

Clhc1	0.7471	7.955	10.05	7.07E-10	3.48E-08	12.66	69885	clathrin heavy chain linker domain containing 1
Cln8	-0.9842	6.176	-9.899	9.35E-10	4.44E-08	12.38	26889	ceroid-lipofuscinosis neuronal 8
Clspn	1.805	7.161	13.65	1.65E-12	2.23E-10	18.75	269582	claspin
Cmc2	1.465	9.083	10.62	2.45E-10	1.42E-08	13.73	66531	COX assembly mitochondrial protein 2
Cmss1	0.965	7.725	15.17	1.84E-13	3.89E-11	20.94	66497	cms small ribosomal subunit 1
Cmtm7	2.121	9.794	19.37	9.92E-16	8.82E-13	26.06	102545	CKLF-like MARVEL transmembrane domain containing 7
Cnbd2	-0.6665	5.839	-8.85	7.34E-09	2.47E-07	10.29	70873	cyclic nucleotide binding domain containing 2
Cnga1	-1.079	5.005	-9.988	7.91E-10	3.83E-08	12.55	12788	cyclic nucleotide gated channel alpha 1
Cnn2	-0.9594	11.11	-8.847	7.38E-09	2.48E-07	10.29	12798	calponin 2
Cnot6	0.5776	9.96	8.33	2.15E-08	6.13E-07	9.205	104625	CCR4-NOT transcription complex subunit 6
Cnr2	-1.647	8.443	-9.022	5.19E-09	1.88E-07	10.64	12802	cannabinoid receptor 2 (macrophage)
Cnrip1	1.147	7.725	9.819	1.09E-09	5.00E-08	12.22	380686	cannabinoid receptor interacting protein 1
Cntln	1.82	7.172	13.85	1.22E-12	1.75E-10	19.06	338349	centlein centrosomal protein
Col27a1	0.9383	8.031	11.75	3.40E-11	2.77E-09	15.72	373864	collagen type XXVII alpha 1
Coro7	1.001	10.04	8.861	7.17E-09	2.43E-07	10.31	78885	coronin 7
Cpeb2	-1.218	7.432	-9.627	1.58E-09	6.79E-08	11.85	231207	cytoplasmic polyadenylation element binding protein 2
Cplx2	2.074	7.274	13.13	3.63E-12	4.27E-10	17.97	12890	complexin 2
Cpne4	-1.98	6.985	-18.84	1.82E-15	1.35E-12	25.47	74020	copine IV

Cpsf2	0.9853	8.923	15.37	1.40E-13	3.15E-11	21.21	51786	cleavage and polyadenylation specific factor 2
Cr2	-3.112	9.406	-12.9	5.22E-12	5.80E-10	17.6	12902	complement receptor 2
Crbn	-0.9202	9.589	-8.266	2.46E-08	6.87E-07	9.067	58799	cereblon
Crebl2	-1.028	8.28	-12.46	1.05E-11	1.04E-09	16.9	232430	cAMP responsive element binding protein-like 2
Crebrf	-0.7623	9.053	-8.282	2.38E-08	6.68E-07	9.102	77128	CREB3 regulatory factor
Crip1	0.7059	11.12	8.834	7.59E-09	2.53E-07	10.26	12925	cysteine-rich protein 1 (intestinal)
Crtam	-1.133	6.643	-8.316	2.21E-08	6.29E-07	9.175	54698	cytotoxic and regulatory T cell molecule
Cse1l	0.5286	10.87	8.277	2.40E-08	6.72E-07	9.091	110750	chromosome segregation 1-like (S. cerevisiae)
Cspp1	0.8446	8.141	11.06	1.13E-10	7.48E-09	14.51	211660	centrosome and spindle pole associated protein 1
Cst7	-1.515	8.231	-8.619	1.18E-08	3.66E-07	9.812	13011	cystatin F (leukocystatin)
Cstf2	0.655	8.927	8.375	1.95E-08	5.68E-07	9.301	108062	cleavage stimulation factor 3 pre-RNA subunit 2
Cstf3	0.7002	7.965	10.82	1.72E-10	1.08E-08	14.09	228410	cleavage stimulation factor 3 pre-RNA subunit 3
Ctc1	0.5847	8.579	8.841	7.47E-09	2.50E-07	10.27	68964	CTS telomere maintenance complex component 1
Ctps	0.9373	7.83	10.24	4.92E-10	2.55E-08	13.03	51797	cytidine 5-triphosphate synthase
Ctss	-0.9437	10.22	-8.561	1.33E-08	4.04E-07	9.692	13040	cathepsin S
Ctsw	-2.383	8.275	-11.76	3.35E-11	2.76E-09	15.74	13041	cathepsin W
Cxcl10	-0.9311	6.694	-8.441	1.70E-08	5.04E-07	9.439	15945	chemokine (C-X-C motif) ligand 10

Cxcl16	-1.805	7.091	-10.66	2.27E-10	1.34E-08	13.8	66102	chemokine (C-X-C motif) ligand 16
Cxcl9	-2.092	7.62	-8.291	2.33E-08	6.56E-07	9.123	17329	chemokine (C-X-C motif) ligand 9
Cxcr3	-1.794	8.081	-11.85	2.88E-11	2.42E-09	15.89	12766	chemokine (C-X-C motif) receptor 3
Cxcr4	1.119	10.71	8.096	3.52E-08	9.45E-07	8.703	12767	chemokine (C-X-C motif) receptor 4
Cxcr5	-2.449	7.952	-9.433	2.30E-09	9.39E-08	11.47	12145	chemokine (C-X-C motif) receptor 5
Cxcr6	-1.821	6.373	-9.347	2.72E-09	1.08E-07	11.3	80901	chemokine (C-X-C motif) receptor 6
Cxx1c	-1.103	7.277	-8.682	1.03E-08	3.29E-07	9.945	72865	CAAX box 1C
Cyld	-0.6924	9.051	-9.374	2.58E-09	1.03E-07	11.35	74256	cylindromatosis (turban tumor syndrome)
Cyp2s1	-1.257	7.629	-8.947	6.03E-09	2.11E-07	10.49	74134	cytochrome P450 family 2 subfamily s polypeptide 1
Cyp51	0.8646	7.564	9.423	2.34E-09	9.49E-08	11.45	13121	cytochrome P450 family 51
Daam1	-1.072	7.092	-9.62	1.60E-09	6.86E-08	11.83	208846	dishevelled associated activator of morphogenesis 1
Dapk1	-1.167	7.164	-11.12	1.00E-10	6.76E-09	14.63	69635	death associated protein kinase 1
Dapl1	-4.048	8.748	-18.19	3.86E-15	2.25E-12	24.74	76747	death associated protein-like 1
Dbf4	1.513	8.334	16.19	4.68E-14	1.37E-11	22.29	27214	DBF4 homolog (S. cerevisiae)
Dbp	-1.092	8.099	-11.18	9.06E-11	6.25E-09	14.73	13170	D site albumin promoter binding protein
Dck	1.665	8.783	16.63	2.64E-14	9.04E-12	22.86	13178	deoxycytidine kinase
Dctpp1	0.7558	8.727	12.91	5.12E-12	5.71E-10	17.62	66422	dCTP pyrophosphatase 1

Ddah2	1.032	7.494	8.103	3.47E-08	9.32E-07	8.719	51793	dimethylarginine dimethylaminohydrolase 2
Ddc	2.595	6.72	16.23	4.46E-14	1.35E-11	22.34	13195	dopa decarboxylase
Ddias	1.138	6.94	14.68	3.68E-13	6.88E-11	20.25	74041	DNA damage-induced apoptosis suppressor
Ddr1	-0.9271	7.076	-8.163	3.06E-08	8.31E-07	8.847	12305	discoidin domain receptor family member 1
Ddx1	0.719	9.906	8.674	1.05E-08	3.33E-07	9.928	104721	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1
Ddx39	0.858	8.479	10.21	5.19E-10	2.66E-08	12.97	68278	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
Dennd2d	-1.957	8.908	-11.35	6.76E-11	4.88E-09	15.03	72121	DENN/MADD domain containing 2D
Depdc1a	1.933	5.638	16.7	2.43E-14	8.64E-12	22.94	76131	DEP domain containing 1a
Depdc1b	1.396	6.883	12.46	1.05E-11	1.04E-09	16.9	218581	DEP domain containing 1B
Depdc7	2.743	6.664	22.19	5.12E-17	1.14E-13	28.91	211896	DEP domain containing 7
Dera	0.6984	9.216	11.15	9.62E-11	6.54E-09	14.67	232449	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)
Desi1	0.7783	10.14	10.21	5.24E-10	2.67E-08	12.96	28075	desumoylating isopeptidase 1
Dhfr	1.717	7.577	14.8	3.10E-13	5.99E-11	20.42	13361	dihydrofolate reductase
Diap3	1.889	7.098	10.04	7.20E-10	3.53E-08	12.64	56419	diaphanous homolog 3 (Drosophila)
Dirc2	-1.049	8.806	-8.05	3.89E-08	1.03E-06	8.604	224132	disrupted in renal carcinoma 2 (human)
Dlg5	-0.5215	6.977	-8.904	6.58E-09	2.26E-07	10.4	71228	discs large homolog 5 (Drosophila)
Dlgap5	1.854	7.956	15.28	1.57E-13	3.45E-11	21.09	218977	discs large (Drosophila) homolog-associated protein 5

Dna2	1.536	7.918	15.31	1.51E-13	3.36E-11	21.13	327762	DNA replication helicase 2 homolog (yeast)
Dnajb2	-0.7903	7.644	-8.79	8.28E-09	2.71E-07	10.17	56812	DnaJ (Hsp40) homolog subfamily B member 2
Dnajc2	0.5029	8.331	9.623	1.59E-09	6.82E-08	11.84	22791	DnaJ (Hsp40) homolog subfamily C member 2
Dnajc21	0.903	8.419	10.96	1.33E-10	8.63E-09	14.35	78244	DnaJ (Hsp40) homolog subfamily C member 21
Dnmbp	-0.594	7.493	-8.309	2.24E-08	6.37E-07	9.16	71972	dynamin binding protein
Dnmt1	0.8185	9.694	8.634	1.14E-08	3.57E-07	9.845	13433	DNA methyltransferase (cytosine-5) 1
Dnph1	0.9289	7.559	11.73	3.55E-11	2.86E-09	15.68	381101	2-deoxynucleoside 5-phosphate N-hydrolase 1
Dpagt1	0.7374	8.425	9.608	1.63E-09	7.00E-08	11.81	13478	dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)
Dpp4	1.342	9.968	9.001	5.41E-09	1.95E-07	10.6	13482	dipeptidylpeptidase 4
Dpp7	-0.7116	7.812	-9.701	1.37E-09	6.02E-08	11.99	83768	dipeptidylpeptidase 7
Dscam	-0.9151	6.506	-8.67	1.06E-08	3.35E-07	9.919	13508	Down syndrome cell adhesion molecule
Dscc1	1.369	6.429	11.11	1.03E-10	6.93E-09	14.6	72107	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
Dse	-1.493	8.297	-8.558	1.34E-08	4.06E-07	9.686	212898	dermatan sulfate epimerase
Dsn1	1.11	7.707	10.41	3.58E-10	1.96E-08	13.35	66934	DSN1 MIND kinetochore complex component homolog (S. cerevisiae)

Dtl	2.177	7.766	18.26	3.56E-15	2.14E-12	24.82	76843	denticleless homolog (Drosophila)
Dtx1	-2.157	9.427	-11.99	2.29E-11	1.97E-09	16.12	14357	deltex 1 homolog (Drosophila)
Dusp10	-1.461	8.831	-8.205	2.80E-08	7.69E-07	8.937	63953	dual specificity phosphatase 10
Dusp6	1.325	10.63	12.76	6.56E-12	6.99E-10	17.37	67603	dual specificity phosphatase 6
Dut	0.849	7.732	12.79	6.24E-12	6.71E-10	17.42	110074	deoxyuridine triphosphatase
Dync2h1	0.9387	6.622	9.431	2.31E-09	9.39E-08	11.46	110350	dynein cytoplasmic 2 heavy chain 1
E2f1	1.007	7.625	9.378	2.56E-09	1.03E-07	11.36	13555	E2F transcription factor 1
E2f2	1.143	8.127	8.178	2.96E-08	8.08E-07	8.879	242705	E2F transcription factor 2
E2f3	1.414	7.769	17.5	8.89E-15	4.22E-12	23.93	13557	E2F transcription factor 3
E2f7	1.463	7.329	11.53	4.94E-11	3.74E-09	15.34	52679	E2F transcription factor 7
E2f8	2.121	8.105	14.65	3.83E-13	7.05E-11	20.21	108961	E2F transcription factor 8
Ebf1	1.259	9.281	9.194	3.68E-09	1.40E-07	10.99	13591	early B cell factor 1
Ect2	2.202	8.1	20.34	3.44E-16	4.58E-13	27.09	13605	ect2 oncogene
Eef2k	1.632	8.331	16.54	2.98E-14	9.81E-12	22.74	13631	eukaryotic elongation factor-2 kinase
Efnb1	-0.7012	7.274	-9.108	4.36E-09	1.62E-07	10.82	13641	ephrin B1
Eid2	-0.502	7.296	-9.566	1.77E-09	7.52E-08	11.73	386655	EP300 interacting inhibitor of differentiation 2
Eif2a	0.7117	9.188	8.569	1.31E-08	3.99E-07	9.709	229317	eukaryotic translation initiation factor 2A
Eif3b	0.6184	10.31	8.159	3.08E-08	8.36E-07	8.84	27979	eukaryotic translation initiation factor 3 subunit B
Eif4e	0.6456	9.259	11.76	3.37E-11	2.77E-09	15.73	13684	eukaryotic translation initiation factor 4E
Eif4h	0.5904	10.57	8.031	4.04E-08	1.07E-06	8.564	22384	eukaryotic translation initiation factor 4H

Ell3	-1.539	7.527	-8.892	6.74E-09	2.31E-07	10.38	269344	elongation factor RNA polymerase II-like 3
Elof1	0.8249	8.062	8.512	1.47E-08	4.42E-07	9.59	66126	elongation factor 1 homolog (ELF1 S. cerevisiae)
Elovl7	-0.897	5.894	-8.557	1.34E-08	4.07E-07	9.684	74559	ELOVL family member 7 elongation of long chain fatty acids (yeast)
Eme1	1.508	7.151	15.09	2.07E-13	4.32E-11	20.82	268465	essential meiotic endonuclease 1 homolog 1 (S. pombe)
Emp1	1.792	8.443	8.99	5.53E-09	1.97E-07	10.58	13730	epithelial membrane protein 1
Eng	1.772	8.949	8.28	2.39E-08	6.70E-07	9.098	13805	endoglin
Enkd1	0.7787	7.24	10	7.72E-10	3.75E-08	12.57	102124	enkurin domain containing 1
Eno3	-1.065	8.657	-8.783	8.41E-09	2.75E-07	10.15	13808	enolase 3 beta muscle
Enpp1	-1.723	8.228	-8.007	4.26E-08	1.11E-06	8.511	18605	ectonucleotide pyrophosphatase/phosphodiesterase 1
Enpp4	-1.414	7.929	-14.53	4.54E-13	8.04E-11	20.04	224794	ectonucleotide pyrophosphatase/phosphodiesterase 4
Enpp5	-1.531	7.143	-9.589	1.69E-09	7.23E-08	11.77	83965	ectonucleotide pyrophosphatase/phosphodiesterase 5
Eogt	-0.921	7.855	-9.972	8.15E-10	3.94E-08	12.51	101351	EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase
Eomes	-1.58	7.254	-10.99	1.28E-10	8.35E-09	14.39	13813	eomesodermin homolog (Xenopus laevis)
Epb4.1l4b	1.38	6.929	8.697	1.00E-08	3.21E-07	9.975	54357	erythrocyte protein band 4.1-like 4b

Epb4.1l5	1.535	6.962	11.93	2.51E-11	2.13E-09	16.02	226352	erythrocyte protein band 4.1-like 5
Epha2	1.897	7.361	13.02	4.32E-12	4.95E-10	17.79	13836	Eph receptor A2
Ephx1	-1.704	8.895	-8.867	7.10E-09	2.41E-07	10.33	13849	epoxide hydrolase 1 microsomal
Ercc6l	1.162	6.999	13.03	4.27E-12	4.91E-10	17.8	236930	excision repair cross-complementing rodent repair deficiency complementation group 6 like
Erg	2.809	8.049	20.29	3.61E-16	4.58E-13	27.04	13876	avian erythroblastosis virus E-26 (v-ets) oncogene related
Erh	0.9664	9.067	11.15	9.65E-11	6.55E-09	14.67	13877	enhancer of rudimentary homolog (Drosophila)
Esco2	2.307	7.525	10.8	1.79E-10	1.12E-08	14.05	71988	establishment of cohesion 1 homolog 2 (S. cerevisiae)
Espl1	1.651	7.183	13.55	1.93E-12	2.55E-10	18.6	105988	extra spindle pole bodies 1 (S. cerevisiae)
Esyt2	-0.9812	9.355	-9.768	1.20E-09	5.44E-08	12.12	52635	extended synaptotagmin-like protein 2
Ethe1	0.8406	7.516	9.287	3.06E-09	1.19E-07	11.18	66071	ethylmalonic encephalopathy 1
Etv5	1.928	7.733	13.5	2.07E-12	2.69E-10	18.53	104156	ets variant 5
Exo1	1.762	7.168	17.4	1.01E-14	4.48E-12	23.8	26909	exonuclease 1
Exoc6b	-1.391	8.05	-14.15	7.81E-13	1.20E-10	19.5	75914	exocyst complex component 6B
Exosc9	0.5524	8.743	8.151	3.13E-08	8.48E-07	8.822	50911	exosome component 9
Eya2	-0.927	6.655	-10.35	4.04E-10	2.17E-08	13.22	14049	eyes absent 2 homolog (Drosophila)
Ezh2	1.708	9.703	17.78	6.31E-15	3.30E-12	24.26	14056	enhancer of zeste homolog 2 (Drosophila)
F2r	-1.203	8.181	-19.04	1.44E-15	1.14E-12	25.7	14062	coagulation factor II (thrombin) receptor

Faah	-1.644	7.739	-10.27	4.69E-10	2.46E-08	13.07	14073	fatty acid amide hydrolase
Fam102a	-1.5	9.671	-9.783	1.17E-09	5.31E-08	12.15	98952	family with sequence similarity 102 member A
Fam105a	-1.956	8.253	-9.719	1.32E-09	5.87E-08	12.03	223433	family with sequence similarity 105 member A
Fam129a	-1.413	7.886	-8.113	3.40E-08	9.16E-07	8.74	63913	family with sequence similarity 129 member A
Fam169b	-2.223	8.499	-11.32	7.15E-11	5.11E-09	14.97	434197	family with sequence similarity 169 member B
Fam198a	1.112	6.703	9.11	4.35E-09	1.62E-07	10.82	245050	family with sequence similarity 198 member A
Fam216a	0.6789	8.035	10.71	2.08E-10	1.26E-08	13.9	68948	family with sequence similarity 216 member A
Fam26f	-1.474	7.317	-10.27	4.68E-10	2.46E-08	13.07	215900	family with sequence similarity 26 member F
Fam46c	-1.906	9.647	-8.383	1.92E-08	5.60E-07	9.318	74645	family with sequence similarity 46 member C
Fam49a	-0.8522	9.621	-7.984	4.47E-08	1.16E-06	8.462	76820	family with sequence similarity 49 member A
Fam60a	0.7062	10.36	9.574	1.75E-09	7.42E-08	11.74	56306	family with sequence similarity 60 member A
Fam64a	1.893	7.49	14.69	3.60E-13	6.77E-11	20.27	109212	family with sequence similarity 64 member A
Fam65a	0.607	8.389	8.474	1.59E-08	4.75E-07	9.509	75687	family with sequence similarity 65 member A
Fam69a	-1.175	9.614	-11.55	4.75E-11	3.64E-09	15.38	67266	family with sequence similarity 69 member A
Fam72a	1.324	5.292	10.41	3.61E-10	1.96E-08	13.34	108900	family with sequence similarity 72 member A

Fam83d	1.02	6.49	12.52	9.55E-12	9.62E-10	17	71878	family with sequence similarity 83 member D
Fancb	0.8412	6.725	8.167	3.03E-08	8.25E-07	8.856	237211	Fanconi anemia complementation group B
Fancd2	1.586	7.096	13.85	1.23E-12	1.76E-10	19.05	211651	Fanconi anemia complementation group D2
Fanci	1.079	7.008	9.299	2.99E-09	1.17E-07	11.2	208836	Fanconi anemia complementation group I
Fancm	0.9832	7.687	10.6	2.54E-10	1.46E-08	13.69	104806	Fanconi anemia complementation group M
Farp2	-0.7524	6.473	-8.904	6.58E-09	2.26E-07	10.4	227377	FERM RhoGEF and pleckstrin domain protein 2
Fas	-1.433	6.886	-10.8	1.79E-10	1.12E-08	14.05	14102	Fas (TNF receptor superfamily member 6)
Fbxl19	0.7937	7.555	10.9	1.49E-10	9.60E-09	14.23	233902	F-box and leucine-rich repeat protein 19
Fbxl21	-0.5186	5.218	-8.295	2.31E-08	6.52E-07	9.131	213311	F-box and leucine-rich repeat protein 21
Fbxo5	1.241	8.144	10.89	1.51E-10	9.71E-09	14.22	67141	F-box protein 5
Fbxw4	-0.6343	8.217	-8.662	1.08E-08	3.39E-07	9.904	30838	F-box and WD-40 domain protein 4
Fcgrt	-1.466	8.657	-13.72	1.48E-12	2.06E-10	18.87	14132	Fc receptor IgG alpha chain transporter
Fchsd2	-1.476	9.638	-12.31	1.35E-11	1.28E-09	16.65	207278	FCH and double SH3 domains 2
Fcrl6	1.563	6.548	11.18	9.09E-11	6.25E-09	14.73	677296	Fc receptor-like 6
Fen1	1.132	8.041	9.595	1.68E-09	7.18E-08	11.79	14156	flap structure specific endonuclease 1
Fgd6	1.163	7.469	12.02	2.17E-11	1.89E-09	16.17	13998	FYVE RhoGEF and PH domain containing 6

Fignl1	1.466	6.241	20.61	2.58E-16	3.82E-13	27.36	60530	fidgetin-like 1
Flt3	-1.254	7.511	-10.85	1.64E-10	1.04E-08	14.13	14255	FMS-like tyrosine kinase 3
Flt3l	-1.234	8.44	-8.874	6.99E-09	2.38E-07	10.34	14256	FMS-like tyrosine kinase 3 ligand
Fmnl2	-1.392	6.939	-10.45	3.33E-10	1.84E-08	13.42	71409	formin-like 2
Fmo5	-1.178	7.676	-10.52	2.95E-10	1.65E-08	13.54	14263	flavin containing monooxygenase 5
Foxm1	1.678	7.658	14.17	7.68E-13	1.19E-10	19.52	14235	forkhead box M1
Frg1	0.7566	9.107	16.93	1.80E-14	6.90E-12	23.23	14300	FSHD region gene 1
Fscn1	-2.527	8.909	-12.6	8.48E-12	8.72E-10	17.11	14086	fascin homolog 1 actin bundling protein (Strongylocentrotus purpuratus)
Fut8	1.083	8.734	8.857	7.24E-09	2.44E-07	10.31	53618	fucosyltransferase 8
Fxn	0.5866	7.956	8.422	1.77E-08	5.22E-07	9.399	14297	frataxin
G2e3	0.8535	7.667	8.685	1.03E-08	3.28E-07	9.95	217558	G2/M-phase specific E3 ubiquitin ligase
Galm	-1.512	6.916	-8.803	8.07E-09	2.66E-07	10.2	319625	galactose mutarotase
Galnt14	1.828	6.305	14.48	4.84E-13	8.35E-11	19.98	71685	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14
Gar1	0.8156	8.783	10.78	1.85E-10	1.15E-08	14.01	68147	GAR1 ribonucleoprotein homolog (yeast)
Gas2l3	3.36	8.197	18.28	3.49E-15	2.14E-12	24.84	237436	growth arrest-specific 2 like 3
Gbp8	-1.587	7.901	-8.807	8.02E-09	2.65E-07	10.2	76074	guanylate-binding protein 8
Gclc	1.263	9.526	11.55	4.80E-11	3.67E-09	15.37	14629	glutamate-cysteine ligase catalytic subunit
Gemin6	0.5588	7.475	9.02	5.21E-09	1.88E-07	10.64	67242	gem (nuclear organelle) associated protein 6

Gen1	1.74	7.151	17.27	1.18E-14	4.99E-12	23.65	209334	Gen homolog 1 endonuclease (Drosophila)
Gimap7	-1.422	7.689	-8.345	2.08E-08	6.00E-07	9.237	231932	GTPase IMAP family member 7
Gins1	1.984	7.211	21.27	1.29E-16	2.17E-13	28.03	69270	GINS complex subunit 1 (Psf1 homolog)
Gins2	1.148	8.067	11.7	3.68E-11	2.93E-09	15.64	272551	GINS complex subunit 2 (Psf2 homolog)
Gltp	-0.5571	10.3	-9.078	4.64E-09	1.71E-07	10.76	56356	glycolipid transfer protein
Gm10212	-1.248	7.004	-8.202	2.81E-08	7.73E-07	8.931	---	predicted pseudogene 10212
Gm10384	2.262	6.224	9.413	2.39E-09	9.65E-08	11.43	100038735	predicted gene 10384
Gm10673	-2.636	6.734	-15.38	1.39E-13	3.14E-11	21.22	100038559	predicted gene 10673
Gm12260	1.252	9.119	11.25	8.03E-11	5.64E-09	14.85	---	predicted gene 12260
Gm12387	1.836	5.898	9.304	2.96E-09	1.16E-07	11.21	---	predicted gene 12387
Gm12474	-1.184	7.295	-8.416	1.80E-08	5.27E-07	9.386	545557	predicted gene 12474
Gm12957	1.489	9.153	8.106	3.45E-08	9.28E-07	8.726	---	predicted gene 12957
Gm13160	1.465	10.5	13.44	2.28E-12	2.92E-10	18.43	---	predicted gene 13160
Gm13212	-1.072	5.724	-9.763	1.21E-09	5.48E-08	12.11	433801	predicted gene 13212
Gm13238	0.5202	9.823	8.778	8.49E-09	2.77E-07	10.14	236069	carnitine deficiency-associated gene expressed in ventricle 3 pseudogene
Gm13310	1.034	7.729	9.505	2.00E-09	8.29E-08	11.61	---	predicted gene 13310
Gm14150	0.8938	10.86	8.779	8.48E-09	2.77E-07	10.15	---	predicted gene 14150
Gm15697	1.977	5.814	9.726	1.30E-09	5.81E-08	12.04	---	predicted gene 15697
Gm16379	0.8738	10.95	8.064	3.77E-08	1.01E-06	8.635	---	predicted pseudogene 16379
Gm16494	0.9817	10.68	11.45	5.65E-11	4.22E-09	15.21	---	predicted gene 16494
Gm17296	2.124	8.308	24.17	7.75E-18	2.51E-14	30.69	212728	predicted gene 17296
Gm22303	1.287	8.074	10.61	2.53E-10	1.46E-08	13.7	---	predicted gene 22303
Gm22806	1.355	6.526	10.53	2.87E-10	1.62E-08	13.57	---	predicted gene 22806
Gm23406	1.159	5.189	8.95	5.99E-09	2.10E-07	10.5	---	predicted gene 23406

Gm23421	1.212	4.43	8.776	8.53E-09	2.78E-07	10.14	---	predicted gene 23421
Gm24357	0.986	10.53	8.094	3.54E-08	9.48E-07	8.699	---	predicted gene 24357
Gm24412	1.085	9.027	11.59	4.46E-11	3.44E-09	15.45	---	predicted gene 24412
Gm25188	0.857	9.207	10.01	7.53E-10	3.67E-08	12.6	---	predicted gene 25188
Gm3851	0.6045	11.42	8.99	5.53E-09	1.97E-07	10.58	---	predicted gene 3851
Gm525	2.462	8.399	10.03	7.30E-10	3.58E-08	12.63	217071	predicted gene 525
Gm527	-0.9968	6.933	-8.008	4.25E-08	1.11E-06	8.513	217648	predicted gene 527
Gm6625	0.6858	10.58	10.05	7.02E-10	3.46E-08	12.67	625801	predicted gene 6625
Gm6901	0.6731	9.471	8.772	8.61E-09	2.80E-07	10.13	628648	predicted gene 6901
Gm8587	0.678	7.816	8.205	2.80E-08	7.69E-07	8.937	667350	predicted pseudogene 8587
Gmds	1.167	8.359	10.07	6.74E-10	3.35E-08	12.71	218138	GDP-mannose 4 6-dehydratase
Gmnn	1.066	6.227	12.86	5.54E-12	6.08E-10	17.54	57441	geminin
Gnb4	1.303	8.596	8.99	5.53E-09	1.97E-07	10.58	14696	guanine nucleotide binding protein (G protein) beta 4
Gpd1l	0.911	9.266	9.432	2.30E-09	9.39E-08	11.46	333433	glycerol-3-phosphate dehydrogenase 1-like
Gpr146	-1.044	8	-9.22	3.49E-09	1.34E-07	11.04	80290	G protein-coupled receptor 146
Gpr156	-0.8866	6.676	-9.58	1.73E-09	7.34E-08	11.76	239845	G protein-coupled receptor 156
Gpr183	-1.566	8.699	-8.21	2.76E-08	7.62E-07	8.949	321019	G protein-coupled receptor 183
Gpr56	3.336	9.087	14.49	4.81E-13	8.35E-11	19.98	14766	G protein-coupled receptor 56
Gpr84	1.075	6.253	9.555	1.81E-09	7.66E-08	11.71	80910	G protein-coupled receptor 84
Gpr97	3.065	8.424	15.81	7.68E-14	1.98E-11	21.8	54672	G protein-coupled receptor 97
Gpsm2	1.027	6.971	8.253	2.52E-08	7.02E-07	9.042	76123	G-protein signalling modulator 2 (AGS3-like C. elegans)
Gramd1b	-1.353	8.302	-8.169	3.01E-08	8.21E-07	8.862	235283	GRAM domain containing 1B
Grap2	-2.354	9.615	-10.87	1.57E-10	9.98E-09	14.18	17444	GRB2-related adaptor protein 2
Grip1	0.8672	5.907	9.452	2.22E-09	9.08E-08	11.5	74053	glutamate receptor interacting protein 1

Gstk1	-1.253	7.664	-8.935	6.18E-09	2.15E-07	10.47	76263	glutathione S-transferase kappa 1
Gtf2e2	0.6825	8.257	8.335	2.12E-08	6.09E-07	9.216	68153	general transcription factor II E polypeptide 2 (beta subunit)
Gtf3c5	0.7791	7.935	19.02	1.48E-15	1.15E-12	25.67	70239	general transcription factor IIIC polypeptide 5
Gtse1	2.116	7.695	16.93	1.80E-14	6.90E-12	23.23	29870	G two S phase expressed protein 1
H2-Aa	-1.829	9.736	-9.48	2.10E-09	8.62E-08	11.56	14960	histocompatibility 2 class II antigen A alpha
H2-Ab1	-1.787	10.84	-9.331	2.81E-09	1.11E-07	11.26	14961	histocompatibility 2 class II antigen A beta 1
H2-DMa	-1.774	9.377	-9.142	4.08E-09	1.52E-07	10.89	14998	histocompatibility 2 class II locus DMa
H2-DMb2	-2.487	9.904	-10.58	2.65E-10	1.52E-08	13.65	15000	histocompatibility 2 class II locus Mb2
H2-Ea-ps	-4.019	9.745	-11.2	8.71E-11	6.05E-09	14.77	100504404	histocompatibility 2 class II antigen E alpha pseudogene
H2-Eb1	-2.948	8.856	-9.671	1.45E-09	6.33E-08	11.93	14969	histocompatibility 2 class II antigen E beta
H2-M2	-2.546	7.764	-11.34	6.85E-11	4.92E-09	15.01	14990	histocompatibility 2 M region locus 2
H2afv	0.7572	9.73	8.674	1.05E-08	3.33E-07	9.928	77605	H2A histone family member V
H2afx	1.7	9.074	19.35	1.02E-15	8.82E-13	26.04	15270	H2A histone family member X
H2afy	0.8452	10.84	12.36	1.25E-11	1.20E-09	16.72	26914	H2A histone family member Y
H2afz	0.7923	10.52	10.38	3.78E-10	2.05E-08	13.29	51788	H2A histone family member Z
Haus6	0.8721	7.951	8.021	4.13E-08	1.09E-06	8.542	230376	HAUS augmin-like complex subunit 6

Havcr1	-1.593	6.705	-10.06	6.95E-10	3.44E-08	12.68	171283	hepatitis A virus cellular receptor 1
Hcrtr2	-0.8727	5.275	-8.941	6.10E-09	2.13E-07	10.48	387285	hypocretin (orexin) receptor 2
Hdac6	0.5245	7.835	7.994	4.38E-08	1.14E-06	8.484	15185	histone deacetylase 6
Hdac8	0.9923	7.688	8.624	1.17E-08	3.63E-07	9.823	70315	histone deacetylase 8
Hdgfrp3	-0.8995	6.315	-10.66	2.28E-10	1.34E-08	13.8	29877	hepatoma-derived growth factor related protein 3
Hectd2	-0.775	5.281	-10.01	7.63E-10	3.72E-08	12.58	226098	HECT domain containing 2
Hells	1.86	7.66	14.84	2.93E-13	5.72E-11	20.48	15201	helicase lymphoid specific
Herc3	-0.9392	8.296	-8.32	2.19E-08	6.25E-07	9.184	73998	hect domain and RLD 3
Hid1	-1.19	7.556	-8.53	1.42E-08	4.29E-07	9.626	217310	HID1 domain containing
Hint3	-0.922	7.921	-8.98	5.64E-09	2.00E-07	10.56	66847	histidine triad nucleotide binding protein 3
Hira	0.7424	8.473	10.25	4.87E-10	2.53E-08	13.04	15260	histone cell cycle regulation defective homolog A (S. cerevisiae)
Hirip3	1.18	7.487	11.44	5.74E-11	4.27E-09	15.19	233876	HIRA interacting protein 3
Hist1h1a	1.993	10.11	14.67	3.71E-13	6.90E-11	20.24	80838	histone cluster 1 H1a
Hist1h1b	1.819	10.15	10.99	1.27E-10	8.34E-09	14.39	56702	histone cluster 1 H1b
Hist1h2aa	0.743	8.374	10.05	7.08E-10	3.48E-08	12.66	319163	histone cluster 1 H2aa
Hist1h2ab	2.468	9.145	12	2.24E-11	1.93E-09	16.14	319172	histone cluster 1 H2ab
Hist1h2ae	1.374	5.336	9.953	8.45E-10	4.08E-08	12.48	319166	histone cluster 1 H2ae
Hist1h2ak	1.148	8.855	10.42	3.57E-10	1.95E-08	13.35	319169	histone cluster 1 H2ak
Hist1h2ao	1.541	11.15	15.91	6.75E-14	1.80E-11	21.93	665433	histone cluster 1 H2ao
Hist1h2ba	1.346	7.992	8.871	7.04E-09	2.40E-07	10.33	319177	histone cluster 1 H2ba
Hist1h2bb	1.675	10.19	10.12	6.13E-10	3.09E-08	12.8	319178	histone cluster 1 H2bb
Hist1h2bf	1.089	12.18	9.648	1.51E-09	6.59E-08	11.89	319180	histone cluster 1 H2bf
Hist1h2bg	1.685	9.036	11.44	5.77E-11	4.28E-09	15.19	319181	histone cluster 1 H2bg
Hist1h2bh	1.375	7.681	8.021	4.13E-08	1.09E-06	8.542	319182	histone cluster 1 H2bh

Hist1h2bm	1.64	10.73	11.73	3.50E-11	2.83E-09	15.69	319186	histone cluster 1 H2bm
Hist1h2bn	1.532	10.67	10.65	2.33E-10	1.37E-08	13.78	319187	histone cluster 1 H2bn
Hist1h2bp	0.7611	6.156	8.197	2.84E-08	7.79E-07	8.921	319188	histone cluster 1 H2bp
Hist1h2bq	1.084	12.18	9.836	1.06E-09	4.87E-08	12.25	665596	histone cluster 1 H2bq
Hist1h3a	1.323	12.57	10.39	3.73E-10	2.02E-08	13.31	360198	histone cluster 1 H3a
Hist1h3e	1.299	12.54	10.33	4.16E-10	2.22E-08	13.2	319151	histone cluster 1 H3e
Hist1h3f	1.294	12.61	10.39	3.74E-10	2.03E-08	13.3	260423	histone cluster 1 H3f
Hist1h4a	0.8151	9.407	11.73	3.51E-11	2.83E-09	15.69	326619	histone cluster 1 H4a
Hist1h4c	1.2	9.142	11.79	3.21E-11	2.66E-09	15.78	319155	histone cluster 1 H4c
Hist1h4d	0.9111	12.26	10.35	4.06E-10	2.18E-08	13.22	319156	histone cluster 1 H4d
Hist1h4f	1.159	10.9	9.296	3.01E-09	1.18E-07	11.19	319157	histone cluster 1 H4f
Hist1h4h	0.8629	12.64	10.74	2.00E-10	1.22E-08	13.94	69386	histone cluster 1 H4h
Hist1h4j	1.526	8.13	11.71	3.65E-11	2.92E-09	15.65	319159	histone cluster 1 H4j
Hist1h4m	0.8168	10.28	11.67	3.91E-11	3.09E-09	15.58	100041230	histone cluster 1 H4m
Hist2h2aa1	0.821	11.62	10.74	1.97E-10	1.21E-08	13.95	15267	histone cluster 2 H2aa1
Hist2h2ab	0.8821	12.33	10.02	7.39E-10	3.61E-08	12.61	621893	histone cluster 2 H2ab
Hist2h2bb	1.065	9.166	11.98	2.34E-11	2.00E-09	16.1	319189	histone cluster 2 H2bb
Hist2h3b	1.784	5.779	10.51	3.02E-10	1.69E-08	13.52	319154	histone cluster 2 H3b
Hist2h3c2	1.343	12.56	10.25	4.83E-10	2.52E-08	13.04	97114	histone cluster 2 H3c2
Hist2h4	1.056	11.17	10.33	4.18E-10	2.22E-08	13.19	97122	histone cluster 2 H4
Hist3h2bb-ps	1.033	8.004	10.5	3.06E-10	1.71E-08	13.5	382522	histone cluster 3 H2bb pseudogene
Hist4h4	0.9667	9.893	8.763	8.76E-09	2.85E-07	10.11	320332	histone cluster 4 H4
Hjurp	1.143	8.364	10.67	2.24E-10	1.33E-08	13.82	381280	Holliday junction recognition protein
Hlcs	-0.9469	7.554	-10.25	4.86E-10	2.53E-08	13.04	110948	holocarboxylase synthetase (biotin-[propriony-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)

Hmga1	0.8687	9.473	10.05	7.09E-10	3.48E-08	12.66	15361	high mobility group AT-hook 1
Hmgb1	0.7567	11.39	12.32	1.33E-11	1.26E-09	16.66	15289	high mobility group box 1
Hmgb2	1.696	10.03	16.66	2.55E-14	8.90E-12	22.89	97165	high mobility group box 2
Hmgb3	1.663	8.062	15.49	1.19E-13	2.75E-11	21.37	15354	high mobility group box 3
Hmgcll1	3.524	6.605	21.81	7.44E-17	1.56E-13	28.55	208982	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1
Hmgn2	0.8608	10.48	11.42	6.03E-11	4.42E-09	15.14	15331	high mobility group nucleosomal binding domain 2
Hmgn2-ps1	0.6882	9.029	9.078	4.64E-09	1.71E-07	10.76	---	high mobility group nucleosomal binding domain 2 pseudogene 1
Hmgn3	1.239	7.108	9.113	4.32E-09	1.61E-07	10.83	94353	high mobility group nucleosomal binding domain 3
Hmmr	2.218	7.013	16.12	5.11E-14	1.45E-11	22.21	15366	hyaluronan mediated motility receptor (RHAMM)
Hnrnpab	0.5473	10.47	9.07	4.71E-09	1.73E-07	10.74	15384	heterogeneous nuclear ribonucleoprotein A/B
Homer3	0.5709	7.421	8.679	1.04E-08	3.30E-07	9.938	26558	homer homolog 3 (Drosophila)
Hpcal1	-0.7852	8.438	-9.335	2.78E-09	1.10E-07	11.27	53602	hippocalcin-like 1
Hpgds	-1.549	6.988	-9.172	3.85E-09	1.46E-07	10.95	54486	hematopoietic prostaglandin D synthase
Icos	-2.019	7.987	-8.542	1.38E-08	4.18E-07	9.653	54167	inducible T cell co-stimulator
Ids	-1.01	8.753	-11.43	5.87E-11	4.34E-09	15.17	15931	iduronate 2-sulfatase
Iffo2	-0.7025	6.444	-10.3	4.39E-10	2.32E-08	13.14	212632	intermediate filament family orphan 2
Ifnar2	-0.9451	9.923	-10.41	3.60E-10	1.96E-08	13.34	15976	interferon (alpha and beta) receptor 2
Ift122	0.9007	6.54	10.59	2.61E-10	1.50E-08	13.67	81896	intraflagellar transport 122

Ift22	0.9273	8.982	14.21	7.18E-13	1.14E-10	19.58	67286	intraflagellar transport 22
Igf1r	-1.385	7.367	-12.49	9.99E-12	1.00E-09	16.95	16001	insulin-like growth factor I receptor
Igll1	5.301	8.871	21.71	8.23E-17	1.63E-13	28.46	16136	immunoglobulin lambda-like polypeptide 1
Ikzf2	-0.8565	7.388	-8.161	3.07E-08	8.34E-07	8.844	22779	IKAROS family zinc finger 2
Il10rb	-1.498	9.175	-13.89	1.16E-12	1.68E-10	19.11	16155	interleukin 10 receptor beta
Il18r1	-2.555	7.309	-15.32	1.49E-13	3.34E-11	21.15	16182	interleukin 18 receptor 1
Il1rl2	-1.682	6.648	-11.34	6.90E-11	4.95E-09	15.01	107527	interleukin 1 receptor-like 2
Il21r	-2.039	9.574	-9.431	2.31E-09	9.39E-08	11.46	60504	interleukin 21 receptor
Il23r	-0.7764	5.186	-8.053	3.86E-08	1.02E-06	8.612	209590	interleukin 23 receptor
Il27ra	-2.101	9.324	-9.387	2.51E-09	1.01E-07	11.38	50931	interleukin 27 receptor alpha
Il2rb	-2.087	8.659	-9.93	8.83E-10	4.23E-08	12.43	16185	interleukin 2 receptor beta chain
Il6st	-2.072	9.467	-15.84	7.46E-14	1.94E-11	21.83	16195	interleukin 6 signal transducer
Ilf2	0.9819	8.817	10.83	1.68E-10	1.06E-08	14.11	67781	interleukin enhancer binding factor 2
Ilf3	0.6158	9.242	8.181	2.94E-08	8.03E-07	8.887	16201	interleukin enhancer binding factor 3
Impdh2	0.6871	9.015	9.391	2.49E-09	1.00E-07	11.38	23918	inosine 5-phosphate dehydrogenase 2
Incenp	1.422	8.179	15.44	1.28E-13	2.92E-11	21.3	16319	inner centromere protein
Inip	0.4535	8.574	8.484	1.56E-08	4.67E-07	9.529	66209	INTS3 and NABP interacting protein
Inpp4a	-1.432	8.068	-9.115	4.30E-09	1.60E-07	10.83	269180	inositol polyphosphate-4-phosphatase type I
Inpp4b	-2.353	8.531	-16.29	4.09E-14	1.27E-11	22.43	234515	inositol polyphosphate-4-phosphatase type II

Inpp5d	0.8993	10.81	8.941	6.10E-09	2.13E-07	10.48	16331	inositol polyphosphate-5-phosphatase D
Inpp5f	-1.521	7.423	-9.885	9.61E-10	4.53E-08	12.35	101490	inositol polyphosphate-5-phosphatase F
Ipmk	1.833	9.703	14.94	2.53E-13	5.08E-11	20.62	69718	inositol polyphosphate multikinase
Ipo11	0.6881	8.249	9.277	3.12E-09	1.22E-07	11.16	76582	importin 11
Ipo5	0.8965	9.292	8.996	5.47E-09	1.96E-07	10.59	70572	importin 5
Ipo7	0.659	9.239	8.351	2.05E-08	5.94E-07	9.25	233726	importin 7
Ipo9	0.5913	9.341	8.032	4.04E-08	1.07E-06	8.564	226432	importin 9
Iqgap2	-1.861	8.031	-14.58	4.23E-13	7.60E-11	20.11	544963	IQ motif containing GTPase activating protein 2
Iqgap3	1.412	7.137	12.53	9.50E-12	9.60E-10	17	404710	IQ motif containing GTPase activating protein 3
Irak2	-1.408	8.23	-9.716	1.33E-09	5.88E-08	12.02	108960	interleukin-1 receptor-associated kinase 2
Ireb2	0.4277	8.738	8.001	4.31E-08	1.13E-06	8.499	64602	iron responsive element binding protein 2
Itfg3	-1.158	8.075	-10.57	2.70E-10	1.54E-08	13.63	106581	integrin alpha FG-GAP repeat containing 3
Itga6	-1.244	8.654	-12.88	5.37E-12	5.93E-10	17.57	16403	integrin alpha 6
Itgae	-1.457	6.942	-8.628	1.16E-08	3.61E-07	9.832	16407	integrin alpha E epithelial-associated
Itgb7	-2.284	8.823	-13.5	2.06E-12	2.69E-10	18.53	16421	integrin beta 7
Itk	-3.454	9.083	-15.84	7.43E-14	1.94E-11	21.84	16428	IL2 inducible T cell kinase
Itm2c	-0.9353	9.576	-8.869	7.06E-09	2.40E-07	10.33	64294	integral membrane protein 2C
Itpa	0.5412	9.44	8.701	9.94E-09	3.19E-07	9.984	16434	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)

Jade3	0.662	7.954	8.211	2.76E-08	7.62E-07	8.95	382207	jade family PHD finger 3
Jam2	-1.899	7.762	-7.984	4.48E-08	1.16E-06	8.46	67374	junction adhesion molecule 2
Kansl1l	1.77	7.578	14.23	6.95E-13	1.11E-10	19.62	68691	KAT8 regulatory NSL complex subunit 1-like
Kbtbd11	-1.189	8.174	-8.98	5.64E-09	2.00E-07	10.56	74901	kelch repeat and BTB (POZ) domain containing 11
Kcnq5	0.9039	8.019	12.82	5.95E-12	6.45E-10	17.47	226922	potassium voltage-gated channel subfamily Q member 5
Kctd3	0.942	8.598	15.73	8.60E-14	2.14E-11	21.69	226823	potassium channel tetramerisation domain containing 3
Kdm1a	0.4507	8.797	9.033	5.07E-09	1.84E-07	10.67	99982	lysine (K)-specific demethylase 1A
Kif11	2.534	8.523	17.38	1.03E-14	4.53E-12	23.78	16551	kinesin family member 11
Kif14	1.92	6.725	14.15	7.91E-13	1.21E-10	19.49	381293	kinesin family member 14
Kif15	2.232	7.774	17.95	5.15E-15	2.83E-12	24.46	209737	kinesin family member 15
Kif18a	1.401	7.185	12.87	5.48E-12	6.03E-10	17.55	228421	kinesin family member 18A
Kif18b	2.089	8.017	16.2	4.58E-14	1.37E-11	22.31	70218	kinesin family member 18B
Kif1b	-1.48	7.989	-13.29	2.85E-12	3.50E-10	18.21	16561	kinesin family member 1B
Kif20a	2.087	7.932	15.29	1.57E-13	3.45E-11	21.1	19348	kinesin family member 20A
Kif20b	1.521	7.267	14.47	4.92E-13	8.45E-11	19.96	240641	kinesin family member 20B
Kif22	1.929	7.689	15.26	1.62E-13	3.50E-11	21.06	110033	kinesin family member 22
Kif23	1.753	8.18	18.6	2.40E-15	1.68E-12	25.2	71819	kinesin family member 23
Kif24	1.525	6.792	14.92	2.61E-13	5.19E-11	20.59	109242	kinesin family member 24
Kif2a	1.287	9.023	15.77	8.10E-14	2.07E-11	21.75	16563	kinesin family member 2A
Kif2c	2.31	7.52	18.38	3.10E-15	1.97E-12	24.96	73804	kinesin family member 2C
Kif4	2.309	7.061	15.59	1.04E-13	2.47E-11	21.51	16571	kinesin family member 4
Klf12	-1.249	6.886	-9.745	1.26E-09	5.64E-08	12.08	16597	Kruppel-like factor 12
Klf3	-1.481	9.047	-10.08	6.70E-10	3.34E-08	12.71	16599	Kruppel-like factor 3 (basic)

Klhl3	-0.9849	7.012	-8.054	3.85E-08	1.02E-06	8.613	100503085	kelch-like 3
Klhl6	0.9643	9.958	8.065	3.76E-08	1.00E-06	8.638	239743	kelch-like 6
Klkb1	-0.6812	6.6	-9.173	3.84E-09	1.45E-07	10.95	16621	kallikrein B plasma 1
Klra10	-1.13	4.599	-9.717	1.32E-09	5.88E-08	12.02	16628	killer cell lectin-like receptor subfamily A member 10
Klra3	-1.239	6.193	-12.13	1.82E-11	1.64E-09	16.35	16634	killer cell lectin-like receptor subfamily A member 3
Klrc1	-1.784	6.036	-13.77	1.39E-12	1.96E-10	18.93	16641	killer cell lectin-like receptor subfamily C member 1
Klri2	-1.646	5.317	-9.674	1.44E-09	6.31E-08	11.94	320407	killer cell lectin-like receptor family I member 2
Klrk1	-1.686	5.877	-10.36	3.92E-10	2.11E-08	13.25	27007	killer cell lectin-like receptor subfamily K member 1
Knstrn	1.425	8.039	13.27	2.93E-12	3.59E-10	18.18	51944	kinetochore-localized astrin/SPAG5 binding
Kntc1	1.794	6.606	13.35	2.59E-12	3.25E-10	18.3	208628	kinetochore associated 1
Kpna2	1.523	9.625	16.19	4.70E-14	1.37E-11	22.29	16647	karyopherin (importin) alpha 2
Kpna3	0.825	9.784	8.447	1.68E-08	4.98E-07	9.453	16648	karyopherin (importin) alpha 3
Ksr1	-0.6285	7.687	-9.513	1.97E-09	8.18E-08	11.62	16706	kinase suppressor of ras 1
Kti12	0.6173	9.994	9.694	1.38E-09	6.10E-08	11.98	100087	KTI12 homolog chromatin associated (S. cerevisiae)
Kynu	-2.397	7.72	-14.18	7.52E-13	1.18E-10	19.54	70789	kynureninase (L-kynurenine hydrolase)
Lacc1	-1.504	7.299	-9.148	4.03E-09	1.51E-07	10.9	210808	laccase (multicopper oxidoreductase) domain containing 1
Lair1	-1.359	7.722	-10.14	5.92E-10	3.00E-08	12.84	52855	leukocyte-associated Ig-like receptor 1

Lamp3	-0.7562	4.776	-8.451	1.67E-08	4.94E-07	9.461	239739	lysosomal-associated membrane protein 3
Lancl2	1.306	8.158	11.42	5.98E-11	4.40E-09	15.15	71835	LanC (bacterial lantibiotic synthetase component C)-like 2
Larp7	0.6529	8.826	8.848	7.36E-09	2.48E-07	10.29	28036	La ribonucleoprotein domain family member 7
Lat	-2.406	8.828	-12.83	5.87E-12	6.42E-10	17.48	16797	linker for activation of T cells
Lbr	0.7975	10.26	8.963	5.85E-09	2.06E-07	10.52	98386	lamin B receptor
Lck	-2.258	9.869	-8.801	8.10E-09	2.66E-07	10.19	16818	lymphocyte protein tyrosine kinase
Lcp2	-1.319	10.02	-10.74	1.98E-10	1.21E-08	13.94	16822	lymphocyte cytosolic protein 2
Lgals9	1.688	10.46	12.71	7.07E-12	7.46E-10	17.3	16859	lectin galactose binding soluble 9
Lgr5	3.17	6.967	14.13	8.14E-13	1.23E-10	19.46	14160	leucine rich repeat containing G protein coupled receptor 5
Lhx2	1.88	7.291	11.79	3.21E-11	2.66E-09	15.78	16870	LIM homeobox protein 2
Lig1	1.441	8.418	12.56	9.03E-12	9.20E-10	17.05	16881	ligase I DNA ATP-dependent
Lin9	1.123	6.895	8.02	4.14E-08	1.09E-06	8.539	72568	lin-9 homolog (C. elegans)
Lincpint	-1.92	8.948	-7.96	4.71E-08	1.21E-06	8.409	232685	long intergenic non-protein coding RNA Trp53 induced transcript
Lipa	-0.7348	9.846	-8.444	1.69E-08	5.01E-07	9.445	16889	lysosomal acid lipase A
Lmnb1	1.714	9.095	13.5	2.07E-12	2.69E-10	18.53	16906	lamin B1
Lmnb2	0.7786	7.481	8.601	1.22E-08	3.77E-07	9.776	16907	lamin B2
LOC102635075	0.6673	11.46	8.957	5.92E-09	2.08E-07	10.51	102635075	high mobility group protein B1-like
LOC102640615	0.7453	11.06	9.325	2.84E-09	1.12E-07	11.25	102640615	non-histone chromosomal protein HMG-17-like
LOC102640809	1.004	5.51	7.969	4.62E-08	1.19E-06	8.428	102640809	uncharacterized LOC102640809

Lonp2	-0.6394	9.074	-8.324	2.17E-08	6.20E-07	9.192	66887	lon peptidase 2 peroxisomal
Lpcat2	-1.724	7.796	-8.497	1.51E-08	4.55E-07	9.558	270084	lysophosphatidylcholine acyltransferase 2
Lphn2	2.9	5.607	11.62	4.24E-11	3.30E-09	15.5	99633	latrophilin 2
Lrig1	-1.568	7.123	-14.14	8.00E-13	1.22E-10	19.48	16206	leucine-rich repeats and immunoglobulin-like domains 1
Lrmp	1.22	9.427	11.64	4.11E-11	3.21E-09	15.53	16970	lymphoid-restricted membrane protein
Lrr1	1.802	6.085	9.823	1.08E-09	4.97E-08	12.23	69706	leucine rich repeat protein 1
Lrrc49	0.9846	7.109	8.519	1.45E-08	4.36E-07	9.604	102747	leucine rich repeat containing 49
Lrrc59	0.7289	10.13	8.257	2.50E-08	6.98E-07	9.05	98238	leucine rich repeat containing 59
Lrrc61	-1.218	8.844	-11.13	9.92E-11	6.72E-09	14.64	243371	leucine rich repeat containing 61
Lrrn4	1.546	6.401	9.539	1.87E-09	7.86E-08	11.68	320974	leucine rich repeat neuronal 4
Lsm2	0.6827	7.102	9.506	1.99E-09	8.29E-08	11.61	27756	LSM2 homolog U6 small nuclear RNA associated (S. cerevisiae)
Lxn	2.437	7.589	12.15	1.75E-11	1.59E-09	16.39	17035	latexin
Ly6d	-1.637	9.184	-10.07	6.84E-10	3.39E-08	12.69	17068	lymphocyte antigen 6 complex locus D
Lypd6b	-0.91	6.533	-8.008	4.25E-08	1.11E-06	8.512	71897	LY6/PLAUR domain containing 6B
Lysmd2	-0.7668	6.648	-8.299	2.29E-08	6.49E-07	9.139	70082	LysM putative peptidoglycan-binding domain containing 2
Mad2l1	1.372	9.202	13.95	1.05E-12	1.54E-10	19.2	56150	MAD2 mitotic arrest deficient-like 1

Malt1	-1.167	9.381	-8.617	1.18E-08	3.67E-07	9.809	240354	mucosa associated lymphoid tissue lymphoma translocation gene 1
Maml3	1.141	8.196	11.43	5.93E-11	4.37E-09	15.16	433586	mastermind like 3 (Drosophila)
Man1c1	-1.428	7.887	-8.845	7.42E-09	2.49E-07	10.28	230815	mannosidase alpha class 1C member 1
Mapk12	-0.8129	7.482	-9.423	2.34E-09	9.49E-08	11.45	29857	mitogen-activated protein kinase 12
Mapre3	-0.6549	7.291	-10.11	6.28E-10	3.16E-08	12.78	100732	microtubule-associated protein RP/EB family member 3
Marveld1	-1.239	8.486	-16.84	2.01E-14	7.45E-12	23.12	277010	MARVEL (membrane-associating) domain containing 1
Mastl	1.959	6.398	13.96	1.04E-12	1.53E-10	19.22	67121	microtubule associated serine/threonine kinase-like
Mboat1	-1.722	7.21	-8.471	1.60E-08	4.77E-07	9.504	218121	membrane bound O-acyltransferase domain containing 1
Mcm10	1.822	7.67	15.85	7.33E-14	1.93E-11	21.85	70024	minichromosome maintenance deficient 10 (S. cerevisiae)
Mcm2	1.338	9.5	13	4.47E-12	5.10E-10	17.76	17216	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)
Mcm3	1.442	8.881	14.44	5.13E-13	8.70E-11	19.92	17215	minichromosome maintenance deficient 3 (S. cerevisiae)
Mcm4	1.034	9.225	11.8	3.16E-11	2.62E-09	15.79	17217	minichromosome maintenance deficient 4 homolog (S. cerevisiae)

Mcm5	1.079	9.356	10.73	2.02E-10	1.23E-08	13.92	17218	minichromosome maintenance deficient 5 cell division cycle 46 (S. cerevisiae)
Mcm6	1.798	8.998	16.45	3.34E-14	1.09E-11	22.63	17219	minichromosome maintenance deficient 6 (MIS5 homolog S. pombe) (S. cerevisiae)
Mcm7	1.379	9.739	12.95	4.86E-12	5.45E-10	17.67	17220	minichromosome maintenance deficient 7 (S. cerevisiae)
Mcm8	0.8507	6.684	10.91	1.46E-10	9.47E-09	14.25	66634	minichromosome maintenance deficient 8 (S. cerevisiae)
Mctp2	-2.583	7.02	-18.46	2.83E-15	1.90E-12	25.05	244049	multiple C2 domains transmembrane 2
Mdm1	0.6285	7.286	8.57	1.30E-08	3.99E-07	9.711	17245	transformed mouse 3T3 cell double minute 1
Med10	0.7756	9.547	12.92	5.05E-12	5.65E-10	17.63	28077	mediator complex subunit 10
Melk	1.47	6.924	11.62	4.24E-11	3.30E-09	15.5	17279	maternal embryonic leucine zipper kinase
Memo1	0.8741	7.924	10.37	3.87E-10	2.09E-08	13.27	76890	mediator of cell motility 1
Mesdc1	0.5391	7.272	8.829	7.65E-09	2.55E-07	10.25	80889	mesoderm development candidate 1
Mex3a	0.9498	6.702	8.348	2.07E-08	5.98E-07	9.242	72640	mex3 homolog A (C. elegans)
Mfhas1	-1.759	8.259	-18.54	2.57E-15	1.76E-12	25.14	52065	malignant fibrous histiocytoma amplified sequence 1
Mical2	-0.7215	6.612	-8.858	7.21E-09	2.44E-07	10.31	320878	microtubule associated monooxygenase calponin and LIM domain containing 2
Mif	0.8906	10.02	8.849	7.36E-09	2.48E-07	10.29	17319	macrophage migration inhibitory factor
Mif4gd	-1.574	8.95	-13.37	2.54E-12	3.19E-10	18.32	69674	MIF4G domain containing

Mipol1	-0.6032	6.441	-9.084	4.58E-09	1.69E-07	10.77	73490	mirror-image polydactyly gene 1 homolog (human)
Mir181b-1	1.303	5.963	8.807	8.00E-09	2.64E-07	10.2	723890	microRNA 181b-1
Mir568	-1.38	6.752	-10.78	1.85E-10	1.15E-08	14.01	100124467	microRNA 568
Mis18a	0.8016	8.301	8.539	1.39E-08	4.21E-07	9.645	66578	MIS18 kinetochore protein homolog A (S. pombe)
Mis18bp1	2.429	7.276	14.95	2.50E-13	5.08E-11	20.63	217653	MIS18 binding protein 1
Mki67	1.973	9.703	9.885	9.62E-10	4.53E-08	12.35	17345	antigen identified by monoclonal antibody Ki 67
Mmp11	1.208	7.754	16.81	2.09E-14	7.58E-12	23.09	17385	matrix metallopeptidase 11
Mms22l	1.616	7.392	15.68	9.21E-14	2.26E-11	21.62	212377	MMS22-like DNA repair protein
Mnd1	1.589	5.878	15.98	6.14E-14	1.71E-11	22.02	76915	meiotic nuclear divisions 1 homolog (S. cerevisiae)
Mns1	1.407	7.175	14.25	6.81E-13	1.10E-10	19.64	17427	meiosis-specific nuclear structural protein 1
Mpp1	0.7497	9.161	9.136	4.13E-09	1.54E-07	10.87	17524	membrane protein palmitoylated
Mrpl23	0.9266	9.697	11.75	3.43E-11	2.78E-09	15.71	19935	mitochondrial ribosomal protein L23
Ms4a1	-2.715	10.52	-11.42	6.00E-11	4.41E-09	15.15	12482	membrane-spanning 4-domains subfamily A member 1
Ms4a4b	-3.868	8.131	-17.69	7.09E-15	3.55E-12	24.15	60361	membrane-spanning 4-domains subfamily A member 4B
Ms4a4c	-2.809	8.931	-17.59	7.97E-15	3.83E-12	24.03	64380	membrane-spanning 4-domains subfamily A member 4C
Ms4a6b	-1.931	10.12	-11.16	9.39E-11	6.42E-09	14.7	69774	membrane-spanning 4-domains subfamily A member 6B
Msh6	0.8206	7.683	12.08	1.97E-11	1.76E-09	16.27	17688	mutS homolog 6 (E. coli)
Msi2	0.7313	9.47	8.726	9.44E-09	3.04E-07	10.04	76626	musashi RNA-binding protein 2

Msl3	0.4823	9.604	9.345	2.73E-09	1.08E-07	11.29	17692	male-specific lethal 3 homolog (Drosophila)
Mtbp	0.8721	7.736	8.292	2.32E-08	6.55E-07	9.124	105837	Mdm2 transformed 3T3 cell double minute p53 binding protein
Mtdh	0.9921	10.61	8.063	3.78E-08	1.01E-06	8.633	67154	metadherin
Mtf2	0.6828	9.152	11.4	6.17E-11	4.50E-09	15.12	17765	metal response element binding transcription factor 2
Mtfr2	1.649	6.965	24.69	4.82E-18	1.91E-14	31.13	71804	mitochondrial fission regulator 2
Mtor	1.432	9.215	14.17	7.59E-13	1.19E-10	19.53	56717	mechanistic target of rapamycin (serine/threonine kinase)
Mtss1	0.7951	9.866	9.051	4.89E-09	1.79E-07	10.7	211401	metastasis suppressor 1
Mtss1l	-0.6952	6.825	-12.98	4.59E-12	5.20E-10	17.73	244654	metastasis suppressor 1-like
Mxra8	-1.232	7.836	-9.22	3.49E-09	1.34E-07	11.04	74761	matrix-remodelling associated 8
Myb	3.17	9.137	34	3.75E-21	1.33E-16	37.54	17863	myeloblastosis oncogene
Mybl2	1.663	8.194	11.25	8.04E-11	5.64E-09	14.85	17865	myeloblastosis oncogene-like 2
Myo1e	-2.357	8.818	-13.75	1.41E-12	2.00E-10	18.91	71602	myosin IE
Myo7a	1.567	8.094	17.74	6.60E-15	3.38E-12	24.22	17921	myosin VIIA
Myof	-1.695	7.081	-10.64	2.38E-10	1.40E-08	13.76	226101	myoferlin
Myzap	-0.8983	6.529	-8.258	2.50E-08	6.97E-07	9.051	102371	myocardial zonula adherens protein
Mzb1	1.636	9.864	10.54	2.83E-10	1.61E-08	13.58	69816	marginal zone B and B1 cell-specific protein 1
N4bp2	1.062	8.765	10.81	1.73E-10	1.09E-08	14.08	333789	NEDD4 binding protein 2
Nasp	1.203	8.158	10.71	2.07E-10	1.26E-08	13.9	50927	nuclear autoantigenic sperm protein (histone-binding)
Nav1	-1.479	7.366	-11.59	4.50E-11	3.46E-09	15.44	215690	neuron navigator 1

Ncapd2	1.65	8.662	14.17	7.65E-13	1.19E-10	19.52	68298	non-SMC condensin I complex subunit D2
Ncapg	2.411	7.47	14.35	5.89E-13	9.69E-11	19.78	54392	non-SMC condensin I complex subunit G
Ncapg2	1.998	7.292	11.25	8.06E-11	5.64E-09	14.85	76044	non-SMC condensin II complex subunit G2
Ncaph	2.168	8.332	17.94	5.24E-15	2.83E-12	24.44	215387	non-SMC condensin I complex subunit H
Ncaph2	0.5809	8.835	8.183	2.93E-08	8.01E-07	8.89	52683	non-SMC condensin II complex subunit H2
Ncr1	-2.346	7.063	-13.21	3.21E-12	3.87E-10	18.09	17086	natural cytotoxicity triggering receptor 1
Ndc1	1.482	8.337	13.88	1.18E-12	1.70E-10	19.09	72787	NDC1 transmembrane nucleoporin
Ndc80	1.485	7.583	12.18	1.66E-11	1.53E-09	16.44	67052	NDC80 homolog kinetochore complex component (S. cerevisiae)
Ndrg2	-1.872	7.485	-9.669	1.45E-09	6.35E-08	11.93	29811	N-myc downstream regulated gene 2
Neil3	2.179	7.424	12.76	6.55E-12	6.99E-10	17.37	234258	nei like 3 (E. coli)
Nek2	1.906	7.602	15.27	1.61E-13	3.49E-11	21.07	18005	NIMA (never in mitosis gene a)-related expressed kinase 2
Nek7	-0.6441	9.843	-10.63	2.43E-10	1.41E-08	13.74	59125	NIMA (never in mitosis gene a)-related expressed kinase 7
Nfatc2	-2.011	7.877	-14.15	7.85E-13	1.20E-10	19.5	18019	nuclear factor of activated T cells cytoplasmic calcineurin dependent 2
Nfic	-0.95	8.253	-8.823	7.76E-09	2.58E-07	10.24	18029	nuclear factor I/C

Nkg7	-2.254	9.071	-9.452	2.21E-09	9.08E-08	11.51	72310	natural killer cell group 7 sequence
Nmral1	0.9761	7.508	11.25	7.99E-11	5.64E-09	14.86	67824	NmrA-like family domain containing 1
Nod1	-1.564	7.849	-14.01	9.69E-13	1.44E-10	19.29	107607	nucleotide-binding oligomerization domain containing 1
Nop16	0.8383	9.049	10.09	6.48E-10	3.25E-08	12.75	28126	NOP16 nucleolar protein
Nop58	0.8357	9.314	8.557	1.34E-08	4.07E-07	9.683	55989	NOP58 ribonucleoprotein
Nop9	0.7775	8.419	8.799	8.14E-09	2.67E-07	10.19	67842	NOP9 nucleolar protein
Notch2	-1.702	9.371	-12.06	2.03E-11	1.79E-09	16.24	18129	notch 2
Npr2	-1.171	5.955	-10.25	4.85E-10	2.53E-08	13.04	230103	natriuretic peptide receptor 2
Nr3c1	-0.6806	9.09	-9.047	4.93E-09	1.80E-07	10.69	14815	nuclear receptor subfamily 3 group C member 1
Nrp1	-1.985	7.439	-8.647	1.11E-08	3.48E-07	9.872	18186	neuropilin 1
Nsg2	-1.278	7.099	-8.676	1.05E-08	3.32E-07	9.931	18197	neuron specific gene family member 2
Nsl1	1.13	7.378	9.886	9.59E-10	4.53E-08	12.35	381318	NSL1 MIND kinetochore complex component homolog (S. cerevisiae)
Nt5c2	0.6844	9.059	9.83	1.07E-09	4.92E-08	12.24	76952	5-nucleotidase cytosolic II
Nt5dc2	1.866	8.584	9.619	1.60E-09	6.86E-08	11.83	70021	5-nucleotidase domain containing 2
Nudcd2	0.8962	7.932	10.63	2.42E-10	1.41E-08	13.74	52653	NudC domain containing 2
Nudt21	0.6392	9.726	10.93	1.41E-10	9.18E-09	14.29	68219	nudix (nucleoside diphosphate linked moiety X)-type motif 21
Nuf2	2.202	7.044	18.1	4.29E-15	2.42E-12	24.64	66977	NUF2 NDC80 kinetochore complex component homolog (S. cerevisiae)

Nup107	0.6147	8.232	8.372	1.97E-08	5.71E-07	9.294	103468	nucleoporin 107
Nup133	0.5919	8.45	8.352	2.05E-08	5.94E-07	9.251	234865	nucleoporin 133
Nup155	0.8073	8.945	7.983	4.48E-08	1.16E-06	8.46	170762	nucleoporin 155
Nup205	0.8754	9.271	9.194	3.68E-09	1.40E-07	10.99	70699	nucleoporin 205
Nup210l	0.9774	6.664	8.91	6.50E-09	2.24E-07	10.41	77595	nucleoporin 210-like
Nup37	0.642	7.952	9.119	4.27E-09	1.59E-07	10.84	69736	nucleoporin 37
Nup43	0.5812	7.782	8.354	2.04E-08	5.92E-07	9.255	69912	nucleoporin 43
Nup50	0.549	10.28	8.614	1.19E-08	3.69E-07	9.803	18141	nucleoporin 50
Nup62-il4i1	-1.756	7.78	-8.841	7.48E-09	2.50E-07	10.27	100328588	Nup62-Il4i1 protein
Nup88	0.4955	9.277	9.346	2.72E-09	1.08E-07	11.29	19069	nucleoporin 88
Nup93	0.8889	8.651	10.08	6.66E-10	3.33E-08	12.72	71805	nucleoporin 93
Nusap1	1.895	8.165	10.37	3.86E-10	2.09E-08	13.27	108907	nucleolar and spindle associated protein 1
Nxt1	0.4711	8.279	8.573	1.29E-08	3.97E-07	9.718	56488	NTF2-related export protein 1
Oip5	2.091	6.209	13.16	3.48E-12	4.13E-10	18.01	70645	Opa interacting protein 5
Ola1	0.5976	8.889	8.698	1.00E-08	3.20E-07	9.978	67059	Obg-like ATPase 1
Orc1	1.581	6.327	12.62	8.21E-12	8.48E-10	17.15	18392	origin recognition complex subunit 1
Orc6	0.8196	8.373	9.716	1.33E-09	5.88E-08	12.02	56452	origin recognition complex subunit 6
Osbpl3	-0.9323	6.905	-8.494	1.52E-08	4.58E-07	9.552	71720	oxysterol binding protein-like 3
Otub2	1.812	7.845	14.44	5.12E-13	8.70E-11	19.92	68149	OTU domain ubiquitin aldehyde binding 2
Pa2g4	0.9185	10.06	9.369	2.60E-09	1.04E-07	11.34	18813	proliferation-associated 2G4
Pacs1	-1.131	9.041	-9.858	1.01E-09	4.71E-08	12.3	107975	phosphofurin acidic cluster sorting protein 1
Palld	-0.767	6.434	-9.824	1.08E-09	4.97E-08	12.23	72333	palladin cytoskeletal associated protein

Papss2	-1.852	7.033	-8.466	1.62E-08	4.81E-07	9.492	23972	3-phosphoadenosine 5-phosphosulfate synthase 2
Pard3b	-0.6612	6.595	-8.331	2.14E-08	6.12E-07	9.208	72823	par-3 family cell polarity regulator beta
Parpbp	1.615	6.439	13.2	3.30E-12	3.96E-10	18.06	75317	PARP1 binding protein
Pask	1.359	6.874	16.25	4.30E-14	1.33E-11	22.38	269224	PAS domain containing serine/threonine kinase
Paxip1	0.7658	8.702	8.62	1.18E-08	3.66E-07	9.815	55982	PAX interacting (with transcription-activation domain) protein 1
Pbk	2.15	7	13.7	1.54E-12	2.11E-10	18.83	52033	PDZ binding kinase
Pcna	0.7063	11.25	8.071	3.71E-08	9.91E-07	8.651	18538	proliferating cell nuclear antigen
Pdcd4	-1.202	10.7	-8.664	1.07E-08	3.38E-07	9.907	18569	programmed cell death 4
Pde10a	1.669	7.066	8.582	1.27E-08	3.90E-07	9.736	23984	phosphodiesterase 10A
Pde2a	2.174	10.56	22.27	4.72E-17	1.12E-13	28.98	207728	phosphodiesterase 2A cGMP-stimulated
Pdgfb	-0.5861	7.21	-8.028	4.07E-08	1.07E-06	8.557	18591	platelet derived growth factor B polypeptide
Pdk3	0.5711	8.138	10.17	5.59E-10	2.84E-08	12.9	236900	pyruvate dehydrogenase kinase isoenzyme 3
Pdlim4	-0.6984	7.186	-9.546	1.84E-09	7.79E-08	11.69	30794	PDZ and LIM domain 4
Pdss1	1.05	7.188	9.586	1.71E-09	7.27E-08	11.77	56075	prenyl (solanesyl) diphosphate synthase subunit 1
Pelo	0.7884	7.614	8.407	1.83E-08	5.35E-07	9.368	105083	pelota homolog (Drosophila)
Pfas	0.8289	8.278	8.586	1.26E-08	3.87E-07	9.745	237823	phosphoribosylformylglycinamidine synthase (FGAR amidotransferase)

Pgap1	-1.22	6.226	-10.1	6.46E-10	3.24E-08	12.75	241062	post-GPI attachment to proteins 1
Phf1	-1.241	8.692	-10.53	2.89E-10	1.62E-08	13.56	21652	PHD finger protein 1
Phf19	1.075	7.404	12.31	1.35E-11	1.28E-09	16.64	74016	PHD finger protein 19
Phf5a	0.8619	8.82	8.417	1.79E-08	5.26E-07	9.389	68479	PHD finger protein 5A
Pif1	1.317	6.51	14.61	4.03E-13	7.32E-11	20.16	208084	PIF1 5-to-3 DNA helicase homolog (S. cerevisiae)
Pik3cb	-1.507	7.883	-9.154	3.98E-09	1.50E-07	10.91	74769	phosphatidylinositol 3-kinase catalytic beta polypeptide
Pitpnc1	-1.273	8.876	-9.771	1.19E-09	5.42E-08	12.13	71795	phosphatidylinositol transfer protein cytoplasmic 1
Pkib	-0.7787	6.897	-8.815	7.88E-09	2.61E-07	10.22	18768	protein kinase inhibitor beta cAMP dependent testis specific
Pkig	0.9194	7.96	10.7	2.14E-10	1.29E-08	13.87	18769	protein kinase inhibitor gamma
Plac8	1.286	10.07	8.474	1.59E-08	4.75E-07	9.508	231507	placenta-specific 8
Plbd1	-1.854	9.878	-8.031	4.05E-08	1.07E-06	8.562	66857	phospholipase B domain containing 1
Pld2	-0.8739	7.225	-7.975	4.56E-08	1.18E-06	8.441	18806	phospholipase D2
Plekha1	-1.024	8.31	-9.81	1.11E-09	5.08E-08	12.2	101476	pleckstrin homology domain containing family A (phosphoinositide binding specific) member 1
Plk1	2.258	9.004	18.14	4.12E-15	2.36E-12	24.68	18817	polo-like kinase 1
Plk4	1.319	7.521	8.914	6.45E-09	2.23E-07	10.42	20873	polo-like kinase 4
Plp2	0.7659	11.25	8.868	7.08E-09	2.40E-07	10.33	18824	proteolipid protein 2
Plscr3	1.637	8.358	25.4	2.58E-18	1.31E-14	31.71	70310	phospholipid scramblase 3
Pmf1	1.039	8.003	11.49	5.27E-11	3.98E-09	15.28	67037	polyamine-modulated factor 1
Pnp	2.581	9.302	20.62	2.54E-16	3.82E-13	27.38	18950	purine-nucleoside phosphorylase

Pnp2	2.66	10.26	23.3	1.73E-17	4.74E-14	29.93	667034	purine-nucleoside phosphorylase 2
Poc1a	1.014	6.943	14.21	7.16E-13	1.14E-10	19.59	70235	POC1 centriolar protein homolog A (Chlamydomonas)
Pola1	1.431	7.894	12.39	1.19E-11	1.15E-09	16.78	18968	polymerase (DNA directed) alpha 1
Pola2	0.8378	8.718	9.242	3.35E-09	1.29E-07	11.09	18969	polymerase (DNA directed) alpha 2
Pole	1.675	8.164	12.33	1.31E-11	1.25E-09	16.68	18973	polymerase (DNA directed) epsilon
Pole2	1.221	7.877	15.97	6.26E-14	1.72E-11	22.01	18974	polymerase (DNA directed) epsilon 2 (p59 subunit)
Polq	1.309	6.927	10.09	6.58E-10	3.29E-08	12.73	77782	polymerase (DNA directed) theta
Pop1	0.9355	6.878	8.904	6.57E-09	2.26E-07	10.4	67724	processing of precursor 1 ribonuclease P/MRP family (S. cerevisiae)
Pou2af1	0.8098	10.84	9.734	1.28E-09	5.74E-08	12.06	18985	POU domain class 2 associating factor 1
Pou6f1	-1.192	7.671	-9.863	1.00E-09	4.67E-08	12.31	19009	POU domain class 6 transcription factor 1
Ppfibp2	-1.136	7.33	-9.439	2.27E-09	9.28E-08	11.48	19024	PTPRF interacting protein binding protein 2 (liprin beta 2)
Ppil1	1.43	7.788	12.18	1.67E-11	1.53E-09	16.44	68816	peptidylprolyl isomerase (cyclophilin)-like 1
Ppm1e	1.483	7.515	19.78	6.35E-16	7.28E-13	26.49	320472	protein phosphatase 1E (PP2C domain containing)
Ppm1h	-1.644	7.555	-14.18	7.47E-13	1.18E-10	19.54	319468	protein phosphatase 1H (PP2C domain containing)

Ppp1cc	0.3856	11.1	8.751	8.97E-09	2.90E-07	10.09	19047	protein phosphatase 1 catalytic subunit gamma isoform
Ppp1r13b	-1.373	8.723	-8.292	2.32E-08	6.55E-07	9.125	21981	protein phosphatase 1 regulatory (inhibitor) subunit 13B
Ppp1r14b	0.9968	9.237	9.86	1.01E-09	4.70E-08	12.3	18938	protein phosphatase 1 regulatory (inhibitor) subunit 14B
Ppp2r4	0.516	9.592	10.21	5.19E-10	2.66E-08	12.97	110854	protein phosphatase 2A activator regulatory subunit B
Ppt2	-0.7093	7.626	-9	5.42E-09	1.95E-07	10.6	54397	palmitoyl-protein thioesterase 2
Prc1	2.022	7.708	14.61	4.07E-13	7.34E-11	20.15	233406	protein regulator of cytokinesis 1
Prep	1.204	10.15	11.68	3.83E-11	3.04E-09	15.6	19072	prolyl endopeptidase
Prf1	-1.402	8.109	-10.61	2.49E-10	1.44E-08	13.71	18646	perforin 1 (pore forming protein)
Prim1	1.451	8.189	15.1	2.03E-13	4.28E-11	20.84	19075	DNA primase p49 subunit
Prim2	1.418	8.772	16.1	5.23E-14	1.48E-11	22.18	19076	DNA primase p58 subunit
Prkag2	-0.8814	7.614	-8.155	3.11E-08	8.43E-07	8.83	108099	protein kinase AMP-activated gamma 2 non-catalytic subunit
Prkch	-2.693	8.433	-12.02	2.17E-11	1.89E-09	16.17	18755	protein kinase C eta
Prkcq	-2.894	9.132	-11.28	7.59E-11	5.39E-09	14.91	18761	protein kinase C theta
Prkcsh	0.5169	9.043	8.281	2.38E-08	6.68E-07	9.101	19089	protein kinase C substrate 80K-H
Prm1	0.7594	6.454	9.569	1.76E-09	7.47E-08	11.74	19118	protamine 1
Prmt1	0.778	8.923	10.02	7.40E-10	3.61E-08	12.61	15469	protein arginine N-methyltransferase 1
Procr	-0.9825	7.005	-8.804	8.05E-09	2.66E-07	10.2	19124	protein C receptor endothelial
Prr11	2.32	7.306	19.24	1.15E-15	9.30E-13	25.92	270906	proline rich 11
Prr5l	-1.36	6.143	-10.69	2.17E-10	1.30E-08	13.85	72446	proline rich 5 like

Psat1	1.309	8.621	9.989	7.90E-10	3.83E-08	12.55	107272	phosphoserine aminotransferase 1
Psmc1	0.5536	9.072	8.882	6.88E-09	2.35E-07	10.36	19179	protease (prosome macropain) 26S subunit ATPase 1
Psmd1	0.5846	9.618	8.013	4.21E-08	1.10E-06	8.524	70247	proteasome (prosome macropain) 26S subunit non-ATPase 1
Ptgr1	3.974	7.922	18.64	2.28E-15	1.65E-12	25.26	67103	prostaglandin reductase 1
Ptma	0.6015	11.99	10.13	6.03E-10	3.04E-08	12.82	19231	prothymosin alpha
Ptp4a3	0.7962	10.14	9.859	1.01E-09	4.70E-08	12.3	19245	protein tyrosine phosphatase 4a3
Ptpn14	-1.574	8.551	-10.64	2.36E-10	1.39E-08	13.77	19250	protein tyrosine phosphatase non-receptor type 14
Ptpn21	-0.6397	6.31	-9.194	3.68E-09	1.40E-07	10.99	24000	protein tyrosine phosphatase non-receptor type 21
Ptpn9	0.7028	8.248	10.6	2.53E-10	1.46E-08	13.7	56294	protein tyrosine phosphatase non-receptor type 9
Pttg1	1.199	7.804	11.54	4.88E-11	3.71E-09	15.36	30939	pituitary tumor-transforming gene 1
Pus10	0.7338	8.222	10.75	1.96E-10	1.21E-08	13.95	74467	pseudouridylate synthase 10
Pxdc1	-2.246	8.317	-9.186	3.74E-09	1.42E-07	10.97	66895	PX domain containing 1
Rab11fip4	-1.121	7.327	-11.44	5.75E-11	4.27E-09	15.19	268451	RAB11 family interacting protein 4 (class II)
Rab30	-1.923	7.888	-9.22	3.49E-09	1.34E-07	11.04	75985	RAB30 member RAS oncogene family
Rab37	-1.159	7.752	-8.817	7.85E-09	2.60E-07	10.22	58222	RAB37 member RAS oncogene family
Rabgef1	-0.4804	8.601	-8.006	4.27E-08	1.12E-06	8.508	56715	RAB guanine nucleotide exchange factor (GEF) 1

Racgap1	1.818	8.364	13.41	2.38E-12	3.04E-10	18.39	26934	Rac GTPase-activating protein 1
Rad51	1.351	7.009	16.15	4.95E-14	1.42E-11	22.24	19361	RAD51 homolog
Rad51ap1	1.368	6.145	13.37	2.53E-12	3.19E-10	18.33	19362	RAD51 associated protein 1
Rad51b	0.9546	6.166	9.677	1.43E-09	6.28E-08	11.95	19363	RAD51 homolog B
Rad54b	1.654	6.272	14.81	3.03E-13	5.89E-11	20.44	623474	RAD54 homolog B (S. cerevisiae)
Rad54l	1.8	7.187	15.92	6.68E-14	1.80E-11	21.94	19366	RAD54 like (S. cerevisiae)
Raet1d	1.476	5.374	8.757	8.87E-09	2.88E-07	10.1	56554	retinoic acid early transcript delta
Rag1	4.928	7.731	26.64	8.90E-19	7.91E-15	32.69	19373	recombination activating gene 1
Rag2	2.956	5.386	21.28	1.28E-16	2.17E-13	28.03	19374	recombination activating gene 2
Ran	0.8093	9.383	8.46	1.64E-08	4.86E-07	9.48	19384	RAN member RAS oncogene family
Ranbp1	0.779	10.17	10.53	2.91E-10	1.64E-08	13.55	19385	RAN binding protein 1
Rapgef2	-0.6507	8.27	-8.283	2.37E-08	6.67E-07	9.104	76089	Rap guanine nucleotide exchange factor (GEF) 2
Raph1	-1.226	6.729	-8.592	1.24E-08	3.83E-07	9.757	77300	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
Rarg	-1.062	7.629	-13	4.51E-12	5.12E-10	17.75	19411	retinoic acid receptor gamma
Rasal1	-0.7831	7.41	-8.104	3.46E-08	9.31E-07	8.721	19415	RAS protein activator like 1 (GAP1 like)
Rasgef1a	-0.7996	6.259	-8.005	4.28E-08	1.12E-06	8.507	70727	RasGEF domain family member 1A
Rasgef1b	-2.247	7.741	-10.53	2.87E-10	1.62E-08	13.57	320292	RasGEF domain family member 1B
Rasgrp3	-3.097	9.066	-15.27	1.61E-13	3.49E-11	21.07	240168	RAS guanyl releasing protein 3
Raver2	-1.554	7.022	-11.48	5.39E-11	4.06E-09	15.26	242570	ribonucleoprotein PTB-binding 2

Rbbp8	1.186	7.796	9.503	2.00E-09	8.31E-08	11.61	225182	retinoblastoma binding protein 8
Rbl2	-0.8735	9.047	-11.05	1.13E-10	7.51E-09	14.51	19651	retinoblastoma-like 2
Rbm17	0.5917	8.273	8.119	3.35E-08	9.05E-07	8.753	76938	RNA binding motif protein 17
Rbmxl1	0.9821	10.72	13.4	2.43E-12	3.08E-10	18.37	19656	RNA binding motif protein X linked-like-1
Rcc1	0.9054	8.365	10.57	2.68E-10	1.54E-08	13.64	100088	regulator of chromosome condensation 1
Rcc2	1.089	10.04	10.88	1.55E-10	9.88E-09	14.19	108911	regulator of chromosome condensation 2
Rcn3	-1.5	7.024	-8.211	2.76E-08	7.62E-07	8.951	52377	reticulocalbin 3 EF-hand calcium binding domain
Rdh12	1.17	7.938	9.477	2.11E-09	8.66E-08	11.55	77974	retinol dehydrogenase 12
Recql4	0.8191	6.819	10.11	6.35E-10	3.19E-08	12.77	79456	RecQ protein-like 4
Relb	-0.8035	7.916	-8.305	2.26E-08	6.42E-07	9.152	19698	avian reticuloendotheliosis viral (v-rel) oncogene related B
Rfc3	1.375	7.984	14.44	5.14E-13	8.70E-11	19.92	69263	replication factor C (activator 1) 3
Rfc4	1.143	8.765	16.93	1.81E-14	6.90E-12	23.23	106344	replication factor C (activator 1) 4
Rfwd3	0.8968	9.226	11.8	3.11E-11	2.59E-09	15.81	234736	ring finger and WD repeat domain 3
Rgs13	-2.552	5.864	-9.056	4.84E-09	1.77E-07	10.71	246709	regulator of G-protein signaling 13
Rgs16	1.712	8.343	8.337	2.12E-08	6.08E-07	9.22	19734	regulator of G-protein signaling 16
Rgs3	-0.6395	6.713	-8.89	6.77E-09	2.32E-07	10.37	50780	regulator of G-protein signaling 3

Rhno1	0.7676	8.3	10.21	5.21E-10	2.66E-08	12.97	72440	RAD9-HUS1-RAD1 interacting nuclear orphan 1
Rhof	-1.314	8.724	-8.868	7.08E-09	2.40E-07	10.33	23912	ras homolog gene family member f
Rinl	-1.355	8.138	-8.957	5.91E-09	2.08E-07	10.51	320435	Ras and Rab interactor-like
Rnase12	1.626	5.865	8.08	3.65E-08	9.74E-07	8.669	497106	ribonuclease RNase A family 12 (non-active)
Rnaseh2b	0.7331	7.453	8.016	4.18E-08	1.10E-06	8.53	67153	ribonuclease H2 subunit B
Rnd3	-1.457	7.198	-9.592	1.69E-09	7.21E-08	11.78	74194	Rho family GTPase 3
Rnf157	1.247	8.484	12	2.24E-11	1.93E-09	16.14	217340	ring finger protein 157
Rnf26	0.7759	8.728	12.01	2.22E-11	1.93E-09	16.15	213211	ring finger protein 26
Rnf43	-1.026	7.356	-12.2	1.60E-11	1.48E-09	16.48	207742	ring finger protein 43
Rnmt	0.5352	7.932	8.44	1.71E-08	5.04E-07	9.437	67897	RNA (guanine-7-) methyltransferase
Rora	-1.501	7.012	-13.17	3.42E-12	4.06E-10	18.03	19883	RAR-related orphan receptor alpha
Rpa2	0.746	8.574	8.413	1.81E-08	5.30E-07	9.38	19891	replication protein A2
Rps6ka3	-0.8719	9.314	-9.291	3.03E-09	1.19E-07	11.19	110651	ribosomal protein S6 kinase polypeptide 3
Rqcd1	0.6581	9.609	9.257	3.25E-09	1.26E-07	11.12	58184	rcd1 (required for cell differentiation) homolog 1 (S. pombe)
Rras	-1.223	9.385	-8.891	6.75E-09	2.31E-07	10.38	20130	Harvey rat sarcoma oncogene subgroup R
Rrm1	1.456	9.522	14.95	2.51E-13	5.08E-11	20.63	20133	ribonucleotide reductase M1
Rrm2	2.152	9.233	14.52	4.60E-13	8.06E-11	20.03	20135	ribonucleotide reductase M2
Rtca	0.5587	8.923	9.743	1.26E-09	5.65E-08	12.08	66368	RNA 3-terminal phosphate cyclase
Rtkn2	0.9644	5.625	11.31	7.21E-11	5.14E-09	14.96	170799	rhotekin 2

Ruvbl2	0.7303	8.471	9.148	4.03E-09	1.51E-07	10.9	20174	RuvB-like protein 2
S1pr1	-1.32	9.15	-8.145	3.17E-08	8.57E-07	8.809	13609	sphingosine-1-phosphate receptor 1
Sae1	1.282	9.848	10.57	2.69E-10	1.54E-08	13.63	56459	SUMO1 activating enzyme subunit 1
Samd3	-1.043	6.149	-9.152	4.00E-09	1.50E-07	10.91	268288	sterile alpha motif domain containing 3
Samhd1	-0.9525	10.72	-8.669	1.06E-08	3.35E-07	9.918	56045	SAM domain and HD domain 1
Sap30	1.44	7.767	10.89	1.52E-10	9.72E-09	14.21	60406	sin3 associated polypeptide
Sapcd2	0.633	7.763	9.231	3.42E-09	1.32E-07	11.07	72080	suppressor APC domain containing 2
Sass6	1.108	8.108	10.78	1.85E-10	1.15E-08	14.01	72776	spindle assembly 6 homolog (C. elegans)
Satb2	2.621	6.816	10.31	4.35E-10	2.31E-08	13.15	212712	special AT-rich sequence binding protein 2
Scaper	-0.8444	8.471	-8.055	3.84E-08	1.02E-06	8.616	244891	S phase cyclin A-associated protein in the ER
Scn11a	1.353	6.036	11.19	8.85E-11	6.12E-09	14.76	24046	sodium channel voltage-gated type XI alpha
Scn1b	-0.7197	7.075	-9.376	2.57E-09	1.03E-07	11.36	20266	sodium channel voltage-gated type I beta
Scn4b	2.274	7.163	8.601	1.22E-08	3.77E-07	9.776	399548	sodium channel type IV beta
Sdc4	0.9817	9.668	8.555	1.34E-08	4.08E-07	9.679	20971	syndecan 4
Sema3g	1.004	6.994	8.946	6.05E-09	2.11E-07	10.49	218877	sema domain immunoglobulin domain (Ig) short basic domain secreted (semaphorin) 3G
Sema4f	-1.359	6.717	-9.033	5.07E-09	1.84E-07	10.67	20355	sema domain immunoglobulin domain (Ig) TM domain and short cytoplasmic domain

Sephs1		0.9312	8.931	10.72	2.04E-10	1.25E-08	13.91	109079	selenophosphate synthetase 1
	4-Sep	-0.876	6.426	-8.205	2.80E-08	7.69E-07	8.937	18952	septin 4
Serpinb9		-1.736	7.534	-9.8	1.13E-09	5.16E-08	12.18	20723	serine (or cysteine) peptidase inhibitor clade B member 9
Sf3a3		0.6463	9.28	7.976	4.55E-08	1.18E-06	8.445	75062	splicing factor 3a subunit 3
Sfxn5		-1.183	7.567	-7.979	4.52E-08	1.17E-06	8.451	94282	sideroflexin 5
Sgol1		1.892	7.278	14.25	6.80E-13	1.10E-10	19.64	72415	shugoshin-like 1 (S. pombe)
Sgol2		1.661	7.371	13.05	4.15E-12	4.81E-10	17.83	68549	shugoshin-like 2 (S. pombe)
Sh2b2		-1.471	8.081	-9.225	3.46E-09	1.33E-07	11.05	23921	SH2B adaptor protein 2
Sh2d1a		-2.094	6.676	-11.28	7.57E-11	5.39E-09	14.91	20400	SH2 domain protein 1A
Shank1		-1.041	6.618	-11.17	9.27E-11	6.36E-09	14.71	243961	SH3/ankyrin domain gene 1
Shcbp1		2.59	6.459	21.6	9.21E-17	1.72E-13	28.35	20419	Shc SH2-domain binding protein 1
She		-0.5785	6.804	-8.508	1.48E-08	4.45E-07	9.581	214547	src homology 2 domain-containing transforming protein E
Sidt1		-3.103	8.554	-18.42	2.96E-15	1.95E-12	25	320007	SID1 transmembrane family member 1
Siglech		-2.235	8.19	-9.407	2.42E-09	9.75E-08	11.42	233274	sialic acid binding Ig-like lectin H
Siva1		0.6513	7.862	8.336	2.12E-08	6.09E-07	9.218	30954	SIVA1 apoptosis-inducing factor
Ska1		1.072	6.378	8.655	1.09E-08	3.43E-07	9.888	66468	spindle and kinetochore associated complex subunit 1
Ska2		0.9834	8.165	10.23	5.05E-10	2.61E-08	13	66140	spindle and kinetochore associated complex subunit 2
Ska3		2.121	7.094	12.82	5.94E-12	6.45E-10	17.47	219114	spindle and kinetochore associated complex subunit 3
Skap1		-2.239	8.013	-8.916	6.43E-09	2.23E-07	10.43	78473	src family associated phosphoprotein 1

Ski	-1.015	9.284	-10.62	2.44E-10	1.42E-08	13.73	20481	ski sarcoma viral oncogene homolog (avian)
Skp2	1.192	7.658	12.11	1.87E-11	1.68E-09	16.32	27401	S-phase kinase-associated protein 2 (p45)
Slamf1	-1.17	7.755	-8.611	1.20E-08	3.71E-07	9.796	27218	signaling lymphocytic activation molecule family member 1
Slbp	0.8131	8.59	10.87	1.56E-10	9.93E-09	14.19	20492	stem-loop binding protein
Slc10a7	1.406	8.792	17.14	1.38E-14	5.72E-12	23.49	76775	solute carrier family 10 (sodium/bile acid cotransporter family) member 7
Slc16a5	-1.751	7.185	-9.627	1.58E-09	6.79E-08	11.85	217316	solute carrier family 16 (monocarboxylic acid transporters) member 5
Slc16a7	-1.769	6.728	-8.089	3.58E-08	9.57E-07	8.688	20503	solute carrier family 16 (monocarboxylic acid transporters) member 7
Slc25a13	1.686	7.401	17.07	1.52E-14	6.20E-12	23.4	50799	solute carrier family 25 (mitochondrial carrier adenine nucleotide translocator) member 13
Slc2a9	0.9538	7.927	9.85	1.03E-09	4.75E-08	12.28	117591	solute carrier family 2 (facilitated glucose transporter) member 9
Slc38a2	0.8113	11.03	8.342	2.09E-08	6.04E-07	9.231	67760	solute carrier family 38 member 2
Slc39a6	0.8299	8.571	9.64	1.54E-09	6.67E-08	11.87	106957	solute carrier family 39 (metal ion transporter) member 6
Slc43a3	1.33	10.05	8.267	2.45E-08	6.85E-07	9.071	58207	solute carrier family 43 member 3

Slc46a3	-1.313	8.919	-9.583	1.72E-09	7.30E-08	11.76	71706	solute carrier family 46 member 3
Slc4a7	1.021	9.117	8.958	5.90E-09	2.08E-07	10.51	218756	solute carrier family 4 sodium bicarbonate cotransporter member 7
Slc6a19	3.337	6.523	19.49	8.68E-16	8.81E-13	26.19	74338	solute carrier family 6 (neurotransmitter transporter) member 19
Slc7a6	0.9426	9.054	8.684	1.03E-08	3.28E-07	9.948	330836	solute carrier family 7 (cationic amino acid transporter y+ system) member 6
Slco3a1	-1.585	8.081	-12.23	1.54E-11	1.43E-09	16.52	108116	solute carrier organic anion transporter family member 3a1
Slco4a1	1.643	7.127	8.399	1.86E-08	5.44E-07	9.35	108115	solute carrier organic anion transporter family member 4a1
Slco5a1	-0.8535	6.102	-8.111	3.41E-08	9.19E-07	8.736	240726	solute carrier organic anion transporter family member 5A1
Smarca2	-1.004	9.048	-9.373	2.58E-09	1.03E-07	11.35	67155	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily a member 2
Smarca4	1.524	10.36	23.59	1.33E-17	3.94E-14	30.18	20586	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily a member 4
Smarcc1	0.9944	9.48	17.44	9.59E-15	4.48E-12	23.85	20588	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily c member 1

Smarce1	0.4856	9.948	8.442	1.70E-08	5.02E-07	9.442	57376	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily e member 1
Smc2	1.608	8.409	14.56	4.34E-13	7.76E-11	20.08	14211	structural maintenance of chromosomes 2
Smc3	0.6828	9.486	8.723	9.51E-09	3.05E-07	10.03	13006	structural maintenance of chromosomes 3
Smpd4	0.8506	8.315	8.895	6.70E-09	2.30E-07	10.38	77626	sphingomyelin phosphodiesterase 4
Smpdl3a	-1.775	9.139	-10.67	2.23E-10	1.33E-08	13.83	57319	sphingomyelin phosphodiesterase acid-like 3A
Smtn	2.272	8.15	24.81	4.34E-18	1.91E-14	31.23	29856	smoothelin
Smurf1	-0.7573	8.195	-10.27	4.71E-10	2.47E-08	13.07	75788	SMAD specific E3 ubiquitin protein ligase 1
Snhg5	1.138	8.569	10.23	5.00E-10	2.59E-08	13.01	72655	small nucleolar RNA host gene 5
Snrk	-0.8056	9.608	-10.72	2.06E-10	1.25E-08	13.91	20623	SNF related kinase
Snrpa1	0.7725	8.806	9.146	4.05E-09	1.51E-07	10.89	68981	small nuclear ribonucleoprotein polypeptide A
Snrpf	0.7967	8.709	8.86	7.20E-09	2.43E-07	10.31	69878	small nuclear ribonucleoprotein polypeptide F
Snx2	0.5814	10.82	8.054	3.85E-08	1.02E-06	8.614	67804	sorting nexin 2
Sorcs2	1.703	7.833	8.216	2.73E-08	7.54E-07	8.962	81840	sortilin-related VPS10 domain containing receptor 2
Sox4	2.511	8.439	25.44	2.49E-18	1.31E-14	31.74	20677	SRY (sex determining region Y)-box 4
Spag5	2.229	7.405	14.91	2.64E-13	5.21E-11	20.58	54141	sperm associated antigen 5
Spata7	0.7329	5.486	9.865	9.98E-10	4.66E-08	12.31	104871	spermatogenesis associated 7

Spc24	0.9493	7.095	8.907	6.53E-09	2.25E-07	10.41	67629	SPC24 NDC80 kinetochore complex component homolog (S. cerevisiae)
Spc25	1.738	7.258	12.74	6.71E-12	7.12E-10	17.35	66442	SPC25 NDC80 kinetochore complex component homolog (S. cerevisiae)
Spef2	1.57	5.601	11.41	6.05E-11	4.43E-09	15.14	320277	sperm flagellar 2
Spint2	-1.228	8.276	-8.481	1.57E-08	4.69E-07	9.523	20733	serine protease inhibitor Kunitz type 2
Spp1	2.115	6.596	9.043	4.97E-09	1.81E-07	10.69	20750	secreted phosphoprotein 1
Spred1	2.052	8.379	13.69	1.56E-12	2.13E-10	18.81	114715	sprouty protein with EVH-1 domain 1 related sequence
Spred2	1.496	8.456	16.84	2.01E-14	7.45E-12	23.13	114716	sprouty-related EVH1 domain containing 2
Sqle	1.294	8.037	10.47	3.23E-10	1.79E-08	13.45	20775	squalene epoxidase
Sqrdl	-1.451	7.101	-8.564	1.32E-08	4.02E-07	9.699	59010	sulfide quinone reductase-like (yeast)
Srbd1	0.5384	8.355	9.282	3.09E-09	1.20E-07	11.17	78586	S1 RNA binding domain 1
Srd5a1	0.7492	6.281	8.745	9.10E-09	2.93E-07	10.07	78925	steroid 5 alpha-reductase 1
Srd5a3	-0.8104	9.33	-7.978	4.53E-08	1.17E-06	8.449	57357	steroid 5 alpha-reductase 3
St3gal6	1.882	9.709	9.984	7.97E-10	3.86E-08	12.54	54613	ST3 beta-galactoside alpha-2 3-sialyltransferase 6
St8sia1	-2.132	7.312	-12.63	8.09E-12	8.39E-10	17.16	20449	ST8 alpha-N-acetyl-neuraminide alpha-2 8-sialyltransferase 1
St8sia6	-2.227	8.071	-11.65	4.06E-11	3.18E-09	15.54	241230	ST8 alpha-N-acetyl-neuraminide alpha-2 8-sialyltransferase 6
Stambpl1	1.512	9.702	12.07	1.99E-11	1.77E-09	16.26	76630	STAM binding protein like 1
Stard5	-1.031	9.139	-12.02	2.17E-11	1.89E-09	16.17	170460	StAR-related lipid transfer (START) domain containing 5

Stc2	-1.028	7.477	-11	1.24E-10	8.11E-09	14.42	20856	stanniocalcin 2
Steap3	1.062	7.505	11.54	4.89E-11	3.72E-09	15.35	68428	STEAP family member 3
Stil	2.256	7.106	16.19	4.65E-14	1.37E-11	22.3	20460	Scl/Tal1 interrupting locus
Stk3	1.32	8.625	10.27	4.63E-10	2.44E-08	13.09	56274	serine/threonine kinase 3
Stk39	-1.794	7.146	-13.09	3.88E-12	4.54E-10	17.9	53416	serine/threonine kinase 39
Stmn1	2.02	9.917	14.98	2.39E-13	4.90E-11	20.68	16765	stathmin 1
Ston1	1.466	6.649	14.43	5.25E-13	8.80E-11	19.9	77057	stonin 1
Stx11	-0.7376	8.401	-9.258	3.24E-09	1.26E-07	11.12	74732	syntaxin 11
Stxbp1	1.489	8.316	8.791	8.27E-09	2.71E-07	10.17	20910	syntaxin binding protein 1
Susd1	1.768	9.016	12.67	7.59E-12	7.93E-10	17.23	634731	sushi domain containing 1
Suv39h1	0.9685	8.511	10.26	4.75E-10	2.49E-08	13.06	20937	suppressor of variegation 3-9 homolog 1 (Drosophila)
Swap70	-1.867	9.35	-15.03	2.22E-13	4.60E-11	20.75	20947	SWA-70 protein
Syce2	1.008	7.7	12.08	1.98E-11	1.77E-09	16.26	71846	synaptonemal complex central element protein 2
Synpo2	-0.9785	6.475	-9.385	2.52E-09	1.01E-07	11.37	118449	synaptopodin 2
Sytl2	-1.232	6.508	-7.96	4.71E-08	1.21E-06	8.409	83671	synaptotagmin-like 2
Tacc3	1.571	7.493	14.16	7.71E-13	1.19E-10	19.51	21335	transforming acidic coiled-coil containing protein 3
Tada2a	0.7931	7.617	9.147	4.04E-09	1.51E-07	10.9	217031	transcriptional adaptor 2A
Taf1d	1.19	10.41	13.55	1.91E-12	2.53E-10	18.61	75316	TATA box binding protein (Tbp)-associated factor RNA polymerase I D
Taf9	0.7667	8.762	12.13	1.80E-11	1.62E-09	16.36	108143	TAF9 RNA polymerase II TATA box binding protein (TBP)-associated factor
Tanc2	-0.677	6.201	-11.65	4.07E-11	3.19E-09	15.54	77097	tetratricopeptide repeat ankyrin repeat and coiled-coil containing 2

Tank	-0.9954	9.516	-9.487	2.07E-09	8.53E-08	11.57	21353	TRAF family member-associated Nf-kappa B activator
Tapbpl	-0.9919	8.084	-8.479	1.57E-08	4.70E-07	9.52	213233	TAP binding protein-like
Tapt1	1.019	9.675	9.426	2.33E-09	9.46E-08	11.45	231225	transmembrane anterior posterior transformation 1
Tbc1d2b	-1.791	8.601	-11.81	3.08E-11	2.57E-09	15.82	67016	TBC1 domain family member 2B
Tbc1d31	1.221	7.975	10.44	3.44E-10	1.89E-08	13.39	210544	TBC1 domain family member 31
Tbc1d8	-1.168	7.799	-9.155	3.98E-09	1.50E-07	10.91	54610	TBC1 domain family member 8
Tbx21	-1.259	7.553	-11.47	5.46E-11	4.09E-09	15.24	57765	T-box 21
Tcf3	0.8216	10.01	12.83	5.89E-12	6.42E-10	17.48	21423	transcription factor 3
Tcf4	0.9224	9.862	9.496	2.03E-09	8.40E-08	11.59	21413	transcription factor 4
Tcf7	-2.418	8.995	-11.88	2.72E-11	2.29E-09	15.94	21414	transcription factor 7 T cell specific
Tcf7l2	1.418	7.964	8.569	1.30E-08	3.99E-07	9.709	21416	transcription factor 7 like 2 T cell specific HMG box
Tcrg-C4	-1.656	6.098	-9.758	1.23E-09	5.53E-08	12.1	---	T cell receptor gamma constant 4
Tdg	1.278	9.041	13.52	2.00E-12	2.63E-10	18.56	21665	thymine DNA glycosylase
Tdrkh	-0.9955	5.581	-11.75	3.39E-11	2.77E-09	15.72	72634	tudor and KH domain containing protein
Tdrp	-1.721	7.739	-11.77	3.32E-11	2.74E-09	15.74	72148	testis development related protein
Terc	0.943	10.02	9.016	5.25E-09	1.90E-07	10.63	21748	telomerase RNA component
Tex30	1.292	7.603	9.417	2.37E-09	9.59E-08	11.44	75623	testis expressed 30
Tfdp1	1.462	9.761	12.45	1.07E-11	1.06E-09	16.88	21781	transcription factor Dp 1
Tfpi	-1.81	7.259	-10.89	1.52E-10	9.76E-09	14.21	21788	tissue factor pathway inhibitor
Tfrc	2.052	8.764	13.24	3.07E-12	3.76E-10	18.13	22042	transferrin receptor
Tgfbr3	-1.419	8.273	-12.06	2.03E-11	1.79E-09	16.24	21814	transforming growth factor beta receptor III

Tgoln1	-0.621	9.975	-8.381	1.93E-08	5.63E-07	9.312	22134	trans-golgi network protein
Themis	-2.834	7.462	-16.56	2.91E-14	9.66E-12	22.76	210757	thymocyte selection associated
Thoc6	0.8708	8.633	13.23	3.15E-12	3.82E-10	18.11	386612	THO complex 6 homolog (Drosophila)
Thop1	0.6673	7.281	9.783	1.17E-09	5.31E-08	12.15	50492	thimet oligopeptidase 1
Thy1	-2.389	8.458	-12.68	7.41E-12	7.78E-10	17.25	21838	thymus cell antigen 1 theta
Tia1	0.9695	8.906	12.16	1.73E-11	1.58E-09	16.4	21841	cytotoxic granule-associated RNA binding protein 1
Ticrr	2.285	7.606	19.39	9.71E-16	8.82E-13	26.08	77011	TOPBP1-interacting checkpoint and replication regulator
Tifa	1.558	8.095	9.727	1.30E-09	5.81E-08	12.04	211550	TRAF-interacting protein with forkhead-associated domain
Timm8a1	0.93	7.547	8.591	1.25E-08	3.84E-07	9.754	30058	translocase of inner mitochondrial membrane 8A1
Timp2	-2.131	8.425	-13.58	1.84E-12	2.45E-10	18.65	21858	tissue inhibitor of metalloproteinase 2
Tipin	1.151	8.533	17.42	9.84E-15	4.48E-12	23.83	66131	timeless interacting protein
Tk2	-0.6495	8.861	-8.422	1.77E-08	5.22E-07	9.4	57813	thymidine kinase 2 mitochondrial
Tln2	-0.618	6.251	-8.054	3.85E-08	1.02E-06	8.613	70549	talin 2
Tlr1	-2.193	8.978	-11.6	4.37E-11	3.38E-09	15.47	21897	toll-like receptor 1
Tlr12	-0.5359	6.28	-9.2	3.64E-09	1.39E-07	11	384059	toll-like receptor 12
Tmcc3	-0.8913	6.917	-9.627	1.57E-09	6.79E-08	11.85	319880	transmembrane and coiled coil domains 3
Tmem138	0.7776	7.256	8.415	1.80E-08	5.28E-07	9.385	72982	transmembrane protein 138
Tmem176b	-1.518	8.784	-8.193	2.86E-08	7.85E-07	8.913	65963	transmembrane protein 176B
Tmem231	-0.8961	7.054	-12.41	1.14E-11	1.11E-09	16.82	234740	transmembrane protein 231
Tmem255a	3.706	7.047	31.27	2.46E-20	3.55E-16	35.91	245386	transmembrane protein 255A
Tmem39b	0.6246	8.232	8.256	2.51E-08	6.99E-07	9.047	230770	transmembrane protein 39b

Tmem98	1.231	7.25	9.534	1.89E-09	7.90E-08	11.67	103743	transmembrane protein 98
Tmpo	0.7701	9.927	8.822	7.77E-09	2.58E-07	10.23	21917	thymopoietin
Tnfrsf19	2.564	7.624	11.35	6.78E-11	4.88E-09	15.02	29820	tumor necrosis factor receptor superfamily member 19
Tnfrsf1a	-1.588	8.024	-9.895	9.43E-10	4.46E-08	12.37	21937	tumor necrosis factor receptor superfamily member 1a
Tnfrsf25	-1.202	7.548	-9.852	1.02E-09	4.75E-08	12.28	85030	tumor necrosis factor receptor superfamily member 25
Tnfsf8	-1.578	6.557	-9.938	8.69E-10	4.18E-08	12.45	21949	tumor necrosis factor (ligand) superfamily member 8
Tnik	-2.1	7.906	-13.96	1.04E-12	1.53E-10	19.21	665113	TRAF2 and NCK interacting kinase
Tnip1	-0.9124	8.356	-9.638	1.54E-09	6.69E-08	11.87	57783	TNFAIP3 interacting protein 1
Tob1	-0.6316	9.741	-8.922	6.34E-09	2.20E-07	10.44	22057	transducer of ErbB-2.1
Top2a	2.493	9.039	14.07	8.84E-13	1.33E-10	19.38	21973	topoisomerase (DNA) II alpha
Topbp1	0.9066	9.487	15.49	1.19E-13	2.75E-11	21.37	235559	topoisomerase (DNA) II binding protein 1
Tor4a	-0.9601	8.474	-8.946	6.04E-09	2.11E-07	10.49	227612	torsin family 4 member A
Tox	-1.497	7.974	-8.334	2.13E-08	6.09E-07	9.213	252838	thymocyte selection-associated high mobility group box
Tpx2	2.128	7.932	15.65	9.62E-14	2.34E-11	21.58	72119	TPX2 microtubule-associated protein homolog (Xenopus laevis)
Traf1	-1.961	8.177	-12.44	1.09E-11	1.07E-09	16.86	22029	TNF receptor-associated factor 1
Traf5	-1.084	9.03	-8.842	7.46E-09	2.50E-07	10.27	22033	TNF receptor-associated factor 5
Traip	0.8762	6.701	11.65	4.02E-11	3.16E-09	15.55	22036	TRAF-interacting protein
Traj41	-2.268	7.713	-12.36	1.25E-11	1.20E-09	16.73	---	T cell receptor alpha joining 41

Traj44	-1.752	8.557	-11.31	7.21E-11	5.14E-09	14.96	---	T cell receptor alpha joining 44
Traj49	-3.477	5.976	-14.55	4.42E-13	7.86E-11	20.07	---	T cell receptor alpha joining 49
Traj57	-1.803	8.59	-9.917	9.04E-10	4.32E-08	12.41	---	T cell receptor alpha joining 57
Trat1	-3.019	6.411	-14.93	2.59E-13	5.17E-11	20.6	77647	T cell receptor associated transmembrane adaptor 1
Trav10	-2.33	5.938	-10.68	2.23E-10	1.33E-08	13.83	---	T cell receptor alpha variable 10
Trav12d-2	-1.514	8.334	-8.523	1.44E-08	4.33E-07	9.612	---	T cell receptor alpha variable 12D-2
Trav13n-4	-0.878	8.592	-8.613	1.19E-08	3.69E-07	9.801	---	T cell receptor alpha variable 13N-4
Trav14-1	-1.97	5.992	-9.252	3.28E-09	1.27E-07	11.11	---	T cell receptor alpha variable 14-1
Trav14d-2	-2.048	6.478	-8.754	8.93E-09	2.89E-07	10.09	---	T cell receptor alpha variable 14D-2
Trav15-1-dv6-1	-1.806	4.22	-12.96	4.73E-12	5.32E-10	17.7	---	T cell receptor alpha variable 15-1-DV6-1
Trav15n-1	-0.9398	7.299	-8.015	4.19E-08	1.10E-06	8.528	---	T cell receptor alpha variable 15N-1
Trav16d-dv11	-1.361	6.643	-11.95	2.44E-11	2.08E-09	16.05	---	T cell receptor alpha variable 16D-DV11
Trav19	-0.9062	6.99	-8.172	3.00E-08	8.17E-07	8.867	547428	T cell receptor alpha variable 19
Trav21-dv12	-1.879	6.86	-9.089	4.54E-09	1.68E-07	10.78	---	T cell receptor alpha variable 21-DV12
Trav5-4	-1.762	5.738	-8.225	2.68E-08	7.42E-07	8.981	21507	T cell receptor alpha variable 5-4
Trav6d-4	-1.821	6.016	-8.365	2.00E-08	5.79E-07	9.278	---	T cell receptor alpha variable 6D-4
Trav6n-5	-1.419	6.101	-8.383	1.92E-08	5.60E-07	9.317	---	T cell receptor alpha variable 6N-5

Trav6n-6	-1.805	8.395	-10.54	2.82E-10	1.60E-08	13.59	---	T cell receptor alpha variable 6N-6
Trav7-3	-2.094	7.268	-9.177	3.81E-09	1.44E-07	10.96	---	T cell receptor alpha variable 7-3
Trav7-4	-2.307	7.494	-12.05	2.07E-11	1.82E-09	16.22	386450	T cell receptor alpha variable 7-4
Trav8d-1	-1.548	8.995	-8.101	3.49E-08	9.36E-07	8.714	667476	T cell receptor alpha variable 8D-1
Trav8n-2	-2.251	5.229	-8.199	2.83E-08	7.76E-07	8.926	---	T cell receptor alpha variable 8n-2
Trav9-1	-2.157	8.578	-9.873	9.83E-10	4.61E-08	12.33	---	T cell receptor alpha variable 9-1
Trav9n-4	-1.475	8.786	-8.459	1.64E-08	4.87E-07	9.478	---	T cell receptor alpha variable 9N-4
Trbv1	-2.459	8.98	-10.79	1.81E-10	1.13E-08	14.03	621968	T cell receptor beta variable 1
Trbv29	-2.73	7.014	-9.166	3.89E-09	1.47E-07	10.93	---	T cell receptor beta variable 29
Trerf1	-0.8955	7.187	-11.95	2.44E-11	2.08E-09	16.05	224829	transcriptional regulating factor 1
Trim16	0.7057	7.299	8.278	2.40E-08	6.71E-07	9.093	94092	tripartite motif-containing 16
Trim28	0.7683	9.76	10.25	4.87E-10	2.53E-08	13.04	21849	tripartite motif-containing 28
Trim37	0.8412	8.43	9.739	1.27E-09	5.69E-08	12.07	68729	tripartite motif-containing 37
Trim7	-2.175	7.672	-13.72	1.49E-12	2.07E-10	18.85	94089	tripartite motif-containing 7
Trip13	1.778	6.947	16.86	1.98E-14	7.45E-12	23.14	69716	thyroid hormone receptor interactor 13
Troap	1.625	7.602	15.86	7.22E-14	1.92E-11	21.86	78733	trophinin associated protein
Trp53i11	0.835	11.48	8.729	9.40E-09	3.03E-07	10.04	277414	transformation related protein 53 inducible protein 11
Trp53i13	1.172	7.829	9.02	5.21E-09	1.88E-07	10.64	216964	transformation related protein 53 inducible protein 13

Trpt1	-0.5751	7.142	-10.83	1.68E-10	1.06E-08	14.11	107328	tRNA phosphotransferase 1
Tshz3	-0.8003	7.039	-12.39	1.19E-11	1.15E-09	16.77	243931	teashirt zinc finger family member 3
Tspan9	-0.6889	7.034	-8.471	1.60E-08	4.77E-07	9.502	109246	tetraspanin 9
Ttc26	0.9945	5.757	8.144	3.18E-08	8.59E-07	8.806	264134	tetratricopeptide repeat domain 26
Ttf2	0.7704	7.157	10.39	3.73E-10	2.02E-08	13.31	74044	transcription termination factor RNA polymerase II
Ttk	2.349	6.824	19.59	7.77E-16	8.13E-13	26.3	22137	Ttk protein kinase
Ttll12	1.172	8.827	12.54	9.29E-12	9.41E-10	17.02	223723	tubulin tyrosine ligase-like family member 12
Tuba1b	0.7225	12.27	9.305	2.95E-09	1.16E-07	11.21	22143	tubulin alpha 1B
Tuba1c	0.8043	12.38	9.642	1.53E-09	6.65E-08	11.88	22146	tubulin alpha 1C
Tubb4b	0.6593	10.16	8.04	3.97E-08	1.05E-06	8.582	227613	tubulin beta 4B class IVB
Tube1	0.965	6.811	8.485	1.55E-08	4.66E-07	9.533	71924	epsilon-tubulin 1
Txk	-2.435	7.859	-14.41	5.41E-13	9.03E-11	19.87	22165	TXK tyrosine kinase
Tyms	1.988	8.35	15.2	1.76E-13	3.75E-11	20.98	22171	thymidylate synthase
Tyms-ps	0.7342	6.369	8.751	8.99E-09	2.91E-07	10.09	22172	thymidylate synthase pseudogene
Uba2	0.6257	9.677	11.75	3.40E-11	2.77E-09	15.72	50995	ubiquitin-like modifier activating enzyme 2
Ube2c	1.538	8.275	9.501	2.01E-09	8.33E-08	11.6	68612	ubiquitin-conjugating enzyme E2C
Ube2e2	-1.444	6.903	-9.232	3.41E-09	1.32E-07	11.07	218793	ubiquitin-conjugating enzyme E2E 2
Ube2s	0.9883	9.577	13.59	1.80E-12	2.41E-10	18.66	77891	ubiquitin-conjugating enzyme E2S
Uchl1	2.318	6.802	9.395	2.48E-09	9.97E-08	11.39	22223	ubiquitin carboxy-terminal hydrolase L1

Uchl5	0.8728	8.747	9.115	4.30E-09	1.60E-07	10.83	56207	ubiquitin carboxyl-terminal esterase L5
Uhrf1	2.112	8.455	13.51	2.05E-12	2.69E-10	18.54	18140	ubiquitin-like containing PHD and RING finger domains 1
Umps	0.8779	8.691	11.48	5.42E-11	4.07E-09	15.25	22247	uridine monophosphate synthetase
Upf3b	0.5967	7.425	8.205	2.80E-08	7.69E-07	8.938	68134	UPF3 regulator of nonsense transcripts homolog B (yeast)
Urgcp	-0.4102	8.032	-8.594	1.24E-08	3.82E-07	9.761	72046	upregulator of cell proliferation
Usp44	1.339	5.522	8.866	7.11E-09	2.41E-07	10.32	327799	ubiquitin specific peptidase 44
Usp53	-0.9051	7.555	-12.19	1.65E-11	1.52E-09	16.45	99526	ubiquitin specific peptidase 53
Usp54	0.9033	7.146	12.17	1.69E-11	1.54E-09	16.42	78787	ubiquitin specific peptidase 54
Vangl2	0.7257	7.117	10.31	4.37E-10	2.32E-08	13.15	93840	vang-like 2 (van gogh Drosophila)
Vpreb1	3.037	7.953	16.15	4.94E-14	1.42E-11	22.24	22362	pre-B lymphocyte gene 1
Vpreb2	1.656	8.859	11.41	6.14E-11	4.48E-09	15.12	22363	pre-B lymphocyte gene 2
Vpreb3	3.105	10.05	31	3.00E-20	3.55E-16	35.73	22364	pre-B lymphocyte gene 3
Wdhd1	1.526	8.139	11.44	5.76E-11	4.27E-09	15.19	218973	WD repeat and HMG-box DNA binding protein 1
Wdr5	0.5383	8.545	8.243	2.58E-08	7.18E-07	9.019	140858	WD repeat domain 5
Wdr62	0.912	7.329	11.25	8.02E-11	5.64E-09	14.86	233064	WD repeat domain 62
Wdr76	0.725	8.165	7.959	4.72E-08	1.21E-06	8.407	241627	WD repeat domain 76
Wee1	1.514	7.972	16.3	4.05E-14	1.27E-11	22.43	22390	WEE 1 homolog 1 (S. pombe)
Whsc1	1.628	8.396	18.38	3.10E-15	1.97E-12	24.96	107823	Wolf-Hirschhorn syndrome candidate 1 (human)
Xcl1	-1.077	7.318	-11.04	1.17E-10	7.72E-09	14.48	16963	chemokine (C motif) ligand 1
Xkr5	0.8784	6.33	9.703	1.36E-09	6.01E-08	12	319581	X Kell blood group precursor-related family member 5

Xkrx	-1.98	6.506	-13.79	1.33E-12	1.90E-10	18.97	331524	X Kell blood group precursor related X linked
Xrcc6	1.225	7.468	11.26	7.85E-11	5.56E-09	14.88	14375	X-ray repair complementing defective repair in Chinese hamster cells 6
Ywhae	0.5978	10.59	8.925	6.30E-09	2.19E-07	10.45	22627	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon polypeptide
Zak	1.317	7.288	9.492	2.05E-09	8.47E-08	11.58	65964	sterile alpha motif and leucine zipper containing kinase AZK
Zap70	-2.052	7.844	-10.97	1.31E-10	8.57E-09	14.36	22637	zeta-chain (TCR) associated protein kinase
Zbtb20	-1.378	8.953	-8.912	6.47E-09	2.24E-07	10.42	---	zinc finger and BTB domain containing 20
Zbtb4	-0.9957	7.971	-12.59	8.63E-12	8.84E-10	17.1	75580	zinc finger and BTB domain containing 4
Zbtbd6	1.269	6.558	11.93	2.53E-11	2.14E-09	16.02	432879	kelch repeat and BTB (POZ) domain containing 6
Zc3h12c	-1.696	7.595	-9.716	1.33E-09	5.88E-08	12.02	244871	zinc finger CCCH type containing 12C
Zc3hav1l	1.083	7.092	10.22	5.15E-10	2.64E-08	12.98	209032	zinc finger CCCH-type antiviral 1-like
Zcchc2	0.7672	8.833	12.72	6.95E-12	7.35E-10	17.31	227449	zinc finger CCHC domain containing 2
Zdhhc23	-0.9232	7.884	-10.22	5.08E-10	2.62E-08	12.99	332175	zinc finger DHHC domain containing 23
Zfand4	0.8454	5.835	8.001	4.31E-08	1.13E-06	8.498	67492	zinc finger AN1-type domain 4
Zfp109	-0.6979	7.243	-9.3	2.98E-09	1.17E-07	11.2	56869	zinc finger protein 109

Zfp282	0.5208	7.817	8.336	2.12E-08	6.09E-07	9.218	101095	zinc finger protein 282
Zfp366	-0.8826	7.939	-11.91	2.59E-11	2.19E-09	15.99	238803	zinc finger protein 366
Zfp422	0.926	8.482	9.746	1.25E-09	5.64E-08	12.08	67255	zinc finger protein 422
Zfp516	-0.8921	7.222	-9.314	2.90E-09	1.14E-07	11.23	329003	zinc finger protein 516
Zfp606	0.5805	7.727	8.771	8.63E-09	2.81E-07	10.13	67370	zinc finger protein 606
Zfp69	1.241	8.211	14.06	8.98E-13	1.34E-10	19.36	381549	zinc finger protein 69
Zfp706	0.6601	9.22	8.296	2.31E-08	6.52E-07	9.132	68036	zinc finger protein 706
Zgrf1	0.879	6.552	10.34	4.11E-10	2.20E-08	13.21	71643	zinc finger GRF-type containing 1
Zik1	0.7248	5.882	8.814	7.89E-09	2.61E-07	10.22	22775	zinc finger protein interacting with K protein 1
Zkscan16	2.617	5.871	12.07	2.00E-11	1.78E-09	16.25	100041581	zinc finger with KRAB and SCAN domains 16
Zkscan17	1.488	8.536	19.37	9.99E-16	8.82E-13	26.06	268417	zinc finger with KRAB and SCAN domains 17
Zkscan7	-0.9873	5.686	-8.231	2.65E-08	7.35E-07	8.992	382118	zinc finger with KRAB and SCAN domains 7
Zmynd15	-0.9961	6.663	-11.12	1.02E-10	6.83E-09	14.62	574428	zinc finger MYND-type containing 15
Zmynd19	0.7552	8.658	9.345	2.73E-09	1.08E-07	11.29	67187	zinc finger MYND domain containing 19
Znrf3	-1.017	7.986	-9.229	3.44E-09	1.32E-07	11.06	407821	zinc and ring finger 3
Zranb3	0.6474	7.255	9.531	1.90E-09	7.94E-08	11.66	226409	zinc finger RAN-binding domain containing 3
Zrsr1	-0.8422	7.461	-9.035	5.06E-09	1.84E-07	10.67	22183	zinc finger (CCCH type) RNA binding motif and serine/arginine rich 1
Zwilch	1.762	7.113	17.06	1.53E-14	6.20E-12	23.39	68014	zwilch kinetochore protein
Zyx	-1.115	8.505	-10.74	1.97E-10	1.21E-08	13.95	22793	zyxin