

differential regulated mRNAs										
Gene Symbol	Gene ID	Gene Description	Fold Change(SS-5D)	style(SS-5D)	p-value(SS-5D)	FDR(SS-5D)	Fold Change(SS-10D)	style(SS-10D)	p-value(SS-10D)	FDR(SS-10D)
1110051M20Rik	228356	RIKEN cDNA 1110051M20 g	-1.705282	down	0.007901	0.125233	-2.25534	down	0.000183	0
1810043G02Rik	67884	RIKEN cDNA 1810043G02 g	-1.54504	down	0.004305	0.11779	-2.590456	down	0.002158	0.000207
2210408I21Rik	72371	RIKEN cDNA 2210408I21 ge	-1.957759	down	0.034747	0.187117	1.763055	up	0.001841	0.000207
2410016O06Rik	71952	RIKEN cDNA 2410016O06 g	-1.549855	down	0.005123	0.11779	-4.379099	down	0.001201	0
2810416G20Rik	100040353	RIKEN cDNA 2810416G20 g	-1.623436	down	0.009086	0.125233	-2.387587	down	0.002631	0.000207
2900011O08Rik	67254	RIKEN cDNA 2900011O08 g	-1.827502	down	0.017571	0.163377	9.168278	up	0.000205	0
2900055J20Rik	73001	RIKEN cDNA 2900055J20 ge	-1.720841	down	0.033007	0.187117	4.428067	up	0.000368	0
2900079G21Rik	620760	RIKEN cDNA 2900079G21 g	-1.685086	down	0.022409	0.163377	2.177582	up	0.000975	0
3110043O21Rik	73205	RIKEN cDNA 3110043O21 g	1.544284	up	0.022223	0.592628	-1.896434	down	0.001638	0.000207
3110052M02Rik	73229	RIKEN cDNA 3110052M02 g	-1.965699	down	0.033715	0.187117	-2.093043	down	0.007076	0.033721
3110073H01Rik	73201	RIKEN cDNA 3110073H01 g	1.595433	up	0.023538	0.592628	-5.210318	down	0.001797	0.000207
3632451O06Rik	67419	RIKEN cDNA 3632451O06 g	-1.83837	down	0.018461	0.163377	2.372111	up	0.004367	0.000207
4930431P19Rik	73886	RIKEN cDNA 4930431P19 g	-1.8150615	down	0.018515	0.1524535	-1.713417	down	0.015852	0.033721
4931428F04Rik	74356	RIKEN cDNA 4931428F04 g	-1.792664	down	0.027961	0.187117	-4.520246	down	0.00083	0
4933434E20Rik	99650	RIKEN cDNA 4933434E20 g	1.554535	up	0.046508	0.627255	-1.858505	down	0.002101	0.000207
5031425E22Rik	269630	RIKEN cDNA 5031425E22 g	1.727704	up	0.005795	0.511605	-2.18616	down	0.02295	0.033721
6430548M08Rik	234797	RIKEN cDNA 6430548M08 g	-1.687719	down	0.033389	0.187117	2.5062605	up	0.002113	0.000207
9430079G20Rik	77291	RIKEN cDNA 9430079G20 g	-1.548564	down	0.009511	0.125233	2.294413	up	0.001852	0.000207
A830010M20Rik	231570	RIKEN cDNA A830010M20 g	2.888446	up	0.000883	0.406743	3.302858	up	0.008018	0.033721
A830018L16Rik	320492	RIKEN cDNA A830018L16 g	2.516301	up	0.039264	0.627255	6.757716	up	0.012552	0.0168605
ATP6	17705	ATP synthase F0 subunit 6	1.904047	up	0.005517	0.511605	-4.619021	down	0.000938	0
Aard	239435	alanine and arginine rich do	-3.545321	down	0.039553	0.215669	5.76527	up	0.002053	0.000207
Aars	234734	alanyl-tRNA synthetase	-1.524747	down	0.005937	0.11779	-1.687317	down	0.000625	0
Abca1	11303	ATP-binding cassette, sub-	1.655337	up	0.02619	0.627255	-4.744747	down	0.002779	0.000207
Abhd13	68904	abhydrolase domain contain	1.590774	up	0.013493	0.560498	-1.67209	down	0.039131	0.033721
Acadsb	66885	acyl-Coenzyme A dehydrog	1.999457	up	0.005781	0.511605	-2.215271	down	0.041384	0.033721
Acbd5	74159	acyl-Coenzyme A binding d	1.809082	up	0.008927	0.511605	-6.831288	down	0.001905	0.000207
Ace2	70008	angiotensin I converting en	-2.060949	down	0.03676	0.215669	2.72377	up	0.005902	0.033721
Acp1	11431	acid phosphatase 1, soluble	-1.578782	down	0.013822	0.139517	-1.728793	down	0.006092	0.000207
Acvr2a	11480	activin receptor IIA	1.68218	up	0.023072	0.592628	1.717409	up	0.004292	0.000207
Adam11	11488	a disintegrin and metallope	-1.636314	down	0.046637	0.215669	3.596052	up	0.001326	0.000069
Adamts8	30806	a disintegrin-like and metal	-2.906512	down	0.008586	0.125233	3.7933005	up	0.021376	0.016964
Adarb1	110532	adenosine deaminase, RNA	-2.515866	down	0.039377	0.215669	3.173114	up	0.001008	0
Adcy9	11515	adenylate cyclase 9	-1.939715	down	0.048076	0.215669	2.547589	up	0.000436	0

Adcyap1	11516	adenylate cyclase activating	-1.662154	down	0.013432	0.139517	2.41082	up	0.00372	0.000207
Adcyap1r1	11517	adenylate cyclase activating	-1.583634	down	0.01276	0.139517	4.001942	up	0.001418	0
Ago3	214150	argonaute RISC catalytic su	-2.351617	down	0.035962	0.215669	-3.070476	down	0.003089	0.000207
Ahctf1	226747	AT hook containing transcri	1.754162	up	0.008064	0.511605	-4.447743	down	0.002107	0.000207
Aif1	11629	allograft inflammatory facto	-2.226271	down	0.022354	0.163377	1.768089	up	0.001204	0
Ak8	68870	adenylate kinase 8	-1.836844	down	0.032389	0.187117	1.58285	up	0.005146	0.000207
Alas1	11655	aminolevulinic acid synthas	-1.656302	down	0.020223	0.163377	-5.195924	down	0.000637	0
Aldh3b2	621603	aldehyde dehydrogenase 3	-2.690118	down	0.004201	0.11779	2.46474	up	0.033335	0.033721
Aldob	230163	aldolase B, fructose-bispho	-1.7928	down	0.042987	0.215669	2.4286935	up	0.007461	0.033721
Amd1	11702	S-adenosylmethionine decar	1.577608	up	0.014811	0.592628	-5.873108	down	0.000121	0
Amhr2	110542	anti-Mullerian hormone typ	-1.638065	down	0.022728	0.163377	-2.104561	down	0.006452	0.033721
Anapc16	52717	anaphase promoting comp	-1.692986	down	0.032702	0.187117	-2.094412	down	0.002193	0.000207
Ank1	11733	ankyrin 1, erythroid	-1.596763	down	0.005972	0.11779	3.4888685	up	0.00205	0.0001035
Ankmy2	217473	ankyrin repeat and MYND d	-1.694899	down	0.03031	0.187117	-1.808016	down	0.006319	0.033721
Ankra2	68558	ankyrin repeat, family A (RF	-1.595551	down	0.026053	0.187117	-6.401317	down	0.001585	0.0001035
Ankrd35	213121	ankyrin repeat domain 35	-1.87342	down	0.044434	0.215669	2.794766	up	0.001196	0
Ankrd40	71452	ankyrin repeat domain 40	1.57108	up	0.028951	0.627255	-3.035101	down	0.003393	0.000207
Anp32a	11737	acidic (leucine-rich) nuclear	2.06612	up	0.034375	0.627255	-7.952358	down	0.000836	0
Anxa11	11744	annexin A11	-1.814959	down	0.004724	0.11779	-5.166059	down	0.00009	0
Ap3m1	55946	adaptor-related protein cor	-1.69727	down	0.047511	0.215669	-3.299548	down	0.00208	0.000207
Ap4e1	108011	adaptor-related protein cor	-1.645454	down	0.02549	0.187117	-3.772925	down	0.000516	0
Aph1c	68318	aph1 homolog C, gamma s	-2.008117	down	0.021843	0.163377	2.887417	up	0.036646	0.033721
App	11820	amyloid beta (A4) precursor	1.901821	up	0.044122	0.627255	5.910658	up	0.003236	0.000207
Appbp2	66884	amyloid beta precursor pro	1.650935	up	0.010064	0.560498	-6.777494	down	0.002465	0.000207
Arf1	11840	ADP-ribosylation factor 1	1.535922	up	0.009472	0.560498	-2.613278	down	0.002712	0.000207
Arhgef10	234094	Rho guanine nucleotide exc	-1.640757	down	0.038751	0.215669	-2.029829	down	0.020239	0.033721
Arhgef6	73341	Rac/Cdc42 guanine nucleot	-1.841596	down	0.017411	0.163377	-3.376697	down	0.035658	0.033721
Arhgef9	236915	CDC42 guanine nucleotide	-1.640662	down	0.007551	0.125233	3.7257645	up	0.003073	0.000207
Arih1	23806	ariadne RBR E3 ubiquitin pr	-1.894022	down	0.00501	0.11779	-4.457601	down	0.001326	0.0001035
Arl15	218639	ADP-ribosylation factor-like	-2.160102	down	0.000904	0.092902	-9.300936	down	0.000332	0
Armxc1	78248	armadillo repeat containing	1.64462	up	0.007051	0.511605	-6.757045	down	0.000803	0
Arnt	11863	aryl hydrocarbon receptor r	1.70324	up	0.010731	0.560498	-4.505216	down	0.00114	0
Arpp19	59046	cAMP-regulated phosphop	1.958131	up	0.028568	0.627255	-2.6211	down	0.000092	0
Arpp21	74100	cyclic AMP-regulated phos	2.2740955	up	0.0245995	0.6099415	9.5920875	up	0.001013	0.0001035
Asb11	68854	ankyrin repeat and SOCS b	-1.807582	down	0.020334	0.163377	1.934879	up	0.006855	0.033721
Asic1	11419	acid-sensing (proton-gated	-1.518638	down	0.044313	0.215669	1.525934	up	0.025358	0.033721
Atat1	73242	alpha tubulin acetyltransfer	-1.59127	down	0.03539	0.187117	-2.14325	down	0.006634	0.033721
Atg12	67526	autophagy related 12	-1.644209	down	0.011194	0.139517	-4.080264	down	0.000323	0

Atg2b	76559	autophagy related 2B	1.738107	up	0.037934	0.627255	-2.457204	down	0.00601	0.000207
Atg7	74244	autophagy related 7	-2.37625	down	0.004208	0.11779	1.787387	up	0.008539	0.033721
Atp2b1	67972	ATPase, Ca++ transporting	-2.045682	down	0.04495	0.215669	-3.566658	down	0.002222	0.000207
Atp5f1	11950	ATP synthase, H+ transport	1.7601295	up	0.0071325	0.5098325	-3.027037	down	0.000518	0
Atp5l	27425	ATP synthase, H+ transport	-1.607922	down	0.020632	0.163377	-2.010166	down	0.001886	0.000207
Atp6v0a2	21871	ATPase, H+ transporting, ly	-1.633284	down	0.002139	0.103486	-3.225242	down	0.003693	0.0168605
Atpaf2	246782	ATP synthase mitochondria	-1.609989	down	0.007097	0.125233	-3.509651	down	0.002091	0.000207
Atxn7	246103	ataxin 7	-1.744315	down	0.016714	0.163377	-1.92439	down	0.005084	0.000207
Avl9	78937	AVL9 homolog (S. cerevisia	1.717532	up	0.019988	0.592628	-4.419054	down	0.00214	0.000207
B230311B06Rik	381914	RIKEN cDNA B230311B06 g	-1.742103	down	0.027021	0.187117	4.822221	up	0.000407	0
BC004004	80748	cDNA sequence BC004004	-2.134372	down	0.014384	0.139517	-1.509971	down	0.043267	0.033721
BC048507	408058	cDNA sequence BC048507	-1.755482	down	0.008228	0.125233	-3.236764	down	0.000519	0
BC089491	280621	cDNA sequence BC089491	-1.555077	down	0.01275	0.139517	2.870843	up	0.002987	0.000207
Bace2	56175	beta-site APP-cleaving enz	-2.099957	down	0.021831	0.163377	3.304735	up	0.005349	0.033721
Baiap2l2	207495	BAI1-associated protein 2-l	-2.420181	down	0.000377	0.069898	-1.547249	down	0.043664	0.033721
Banp	53325	BTG3 associated nuclear pr	-1.522797	down	0.027777	0.187117	-1.558232	down	0.002216	0.000207
Barhl1	54422	BarH-like 1 (Drosophila)	-2.339232	down	0.023587	0.163377	4.154065	up	0.000585	0
Bbip1	100503572	BBSome interacting protein	1.728782	up	0.002824	0.459167	-3.861652	down	0.008047	0.033721
Bbs2	67378	Bardet-Biedl syndrome 2 (h	1.809906	up	0.013747	0.560498	-1.530235	down	0.02892	0.033721
Bcl11a	14025	B cell CLL/lymphoma 11A (g	-2.861274	down	0.023592	0.163377	3.368265	up	0.001747	0.0001035
Blzf1	66352	basic leucine zipper nuclear	1.657183	up	0.044265	0.627255	-4.827111	down	0.00098	0
Bmp7	12162	bone morphogenetic prote	-1.865447	down	0.002881	0.103486	-2.021685	down	0.000138	0
Bola1	69168	bolA-like 1 (E. coli)	-1.527461	down	0.003847	0.11779	-3.650696	down	0.000336	0
Braf	109880	Braf transforming gene	-1.676003	down	0.005227	0.11779	1.709042	up	0.001081	0
Brox	71678	BRO1 domain and CAAX m	1.695108	up	0.014862	0.592628	-3.892086	down	0.005503	0.000207
Brwd1	93871	bromodomain and WD rep	1.563148	up	0.025338	0.627255	-2.213256	down	0.002095	0.000069
Bscl2	14705	Berardinelli-Seip congenita	1.787292	up	0.020846	0.592628	-3.697643	down	0.034464	0.033721
Btbd3	228662	BTB (POZ) domain containi	-1.590143	down	0.00885	0.125233	6.688413	up	0.000268	0
Btg4	56057	B cell translocation gene 4	-3.331476	down	0.011423	0.139517	5.235212	up	0.008618	0.033721
C1qtnf5	235312	C1q and tumor necrosis fac	-2.13159	down	0.000559	0.090608	1.8929525	up	0.002025	0.000207
C230088H06Rik	320691	RIKEN cDNA C230088H06 g	1.630704	up	0.047933	0.627255	-3.056899	down	0.008452	0.033721
C230091D08Rik	330544	RIKEN cDNA C230091D08 g	1.74804	up	0.03467	0.627255	-2.015375	down	0.031563	0.033721
Cacna2d4	319734	calcium channel, voltage-d	-2.793376	down	0.010816	0.139517	3.06085	up	0.002885	0.000207
Cacng2	12300	calcium channel, voltage-d	2.449279	up	0.013697	0.560498	1.867406	up	0.026956	0.033721
Camk2b	12323	calcium/calmodulin-depend	-2.036434	down	0.022989	0.163377	2.360766	up	0.000888	0
Camk4	12326	calcium/calmodulin-depend	-1.704431	down	0.018855	0.163377	3.06206	up	0.003247	0.000207
Cap2	67252	CAP, adenylate cyclase-ass	-1.98656	down	0.016158	0.139517	7.0463905	up	0.000186	0
Cbln2	12405	cerebellin 2 precursor prote	1.978912	up	0.020643	0.592628	4.4988525	up	0.001831	0.0001035

Cbx8	30951	chromobox 8	-1.656605	down	0.011803	0.139517	-2.166231	down	0.021536	0.033721
Cby1	73739	chibby homolog 1 (Drosophila)	-1.663895	down	0.011345	0.139517	-2.630255	down	0.000461	0
Ccdc153	270150	coiled-coil domain containing 153	-1.509734	down	0.015303	0.139517	2.731248	up	0.00104	0
Ccdc186	213993	coiled-coil domain containing 186	2.588227	up	0.011132	0.560498	-2.316549	down	0.002495	0.000207
Ccdc47	67163	coiled-coil domain containing 47	1.560842	up	0.030378	0.627255	-14.82347	down	0.000366	0
Ccdc6	76551	coiled-coil domain containing 6	1.718697	up	0.000822	0.406743	-3.26484	down	0.00404	0.000207
Ccdc81	70884	coiled-coil domain containing 81	-2.014994	down	0.029552	0.187117	2.371514	up	0.006096	0.033721
Ccdc93	70829	coiled-coil domain containing 93	1.58558	up	0.025223	0.627255	-1.565957	down	0.004456	0.000207
Ccdc96	66717	coiled-coil domain containing 96	-1.921835	down	0.008582	0.125233	1.774872	up	0.007071	0.033721
Ccnh	66671	cyclin H	1.902709	up	0.007999	0.511605	-3.29916	down	0.002544	0.0001035
Ccsap	73420	centriole, cilia and spindle apparatus	-1.552753	down	0.00153	0.093579	1.822285	up	0.015024	0.033721
Cdkn2aip	70925	CDKN2A interacting protein	-1.720576	down	0.021171	0.163377	-1.892466	down	0.001573	0
Cecr2	330409	cat eye syndrome chromosome 3	-1.574002	down	0.018771	0.163377	1.748771	up	0.003758	0.000207
Celf3	78784	CUGBP, Elav-like family member 3	-1.887626	down	0.019079	0.163377	14.19606	up	0.000884	0
Celf5	319586	CUGBP, Elav-like family member 5	-1.914727	down	0.001154	0.092902	3.384593	up	0.001084	0
Ces5a	67935	carboxylesterase 5A	-2.433313	down	0.015696	0.139517	2.50875	up	0.004265	0.000207
Chd5	269610	chromodomain helicase domain protein 5	-1.675863	down	0.036002	0.215669	2.133451	up	0.001728	0.000138
Chd6	71389	chromodomain helicase domain protein 6	-2.4237843	down	0.0151057	0.1474703	-1.740435	down	0.041105	0.033721
Cherp	27967	calcium homeostasis endoplasmic reticulum protein	-1.510864	down	0.002774	0.103486	-17.53073	down	0.000075	0
Chst11	58250	carbohydrate sulfotransferase 11	-1.606308	down	0.015142	0.139517	-2.038365	down	0.001452	0
Chst12	59031	carbohydrate sulfotransferase 12	-1.540046	down	0.011388	0.139517	-4.629677	down	0.00043	0
Ciart	229599	circadian associated repressor	-1.765356	down	0.014991	0.139517	-2.823638	down	0.001871	0.000207
Cir1	66935	corepressor interacting with	-1.596476	down	0.00797	0.125233	-2.971058	down	0.001992	0.000207
Cish	12700	cytokine inducible SH2-containing protein	-2.010854	down	0.001306	0.093579	-3.962999	down	0.001548	0
Cldnd1	224250	claudin domain containing 1	-1.620659	down	0.035458	0.187117	-7.064112	down	0.001433	0
Clgn	12745	calmegin	-1.730076	down	0.02728	0.187117	7.640051	up	0.001874	0.000207
Clmn	94040	calmin	-2.246218	down	0.000675	0.090608	2.438369	up	0.002727	0.000207
Cltc	67300	clathrin, heavy polypeptide	-1.54343	down	0.015617	0.139517	-7.59329	down	0.001452	0.0001035
Cnnm2	94219	cyclin M2	-1.78627	down	0.005675	0.11779	-2.02066	down	0.039951	0.033721
Col19a1	12823	collagen, type XIX, alpha 1	2.290103	up	0.010316	0.560498	2.847152	up	0.004279	0.000207
Col24a1	71355	collagen, type XXIV, alpha 1	-1.981371	down	0.033861	0.187117	3.278835	up	0.003067	0.000207
Col26a1	140709	collagen, type XXVI, alpha 1	-1.68711	down	0.021828	0.163377	5.482688	up	0.000589	0
Col3a1	12825	collagen, type III, alpha 1	1.944597	up	0.015832	0.592628	-3.479225	down	0.001651	0.000207
Col8a2	329941	collagen, type VIII, alpha 2	-1.804266	down	0.01559	0.139517	-1.54194	down	0.008408	0.033721
Col9a2	12840	collagen, type IX, alpha 2	-1.653635	down	0.00407	0.11779	1.60819	up	0.007008	0.033721
Commmd2	52245	COMM domain containing 2	-2.264627	down	0.001141	0.092902	-3.825615	down	0.004668	0.000207
Cops5	26754	COP9 signalosome subunit 5	1.578702	up	0.003068	0.459167	-3.763629	down	0.00014	0
Cops8	108679	COP9 signalosome subunit 8	1.771878	up	0.003265	0.459167	-2.484403	down	0.002852	0.000207

Coq10b	67876	coenzyme Q10B	1.547266	up	0.016056	0.592628	-3.068825	down	0.008215	0.033721
Coq4	227683	coenzyme Q4	-1.740085	down	0.001135	0.092902	-1.772039	down	0.000132	0
Cox19	68033	cytochrome c oxidase asser	-1.590141	down	0.021685	0.163377	2.164795	up	0.001258	0
Cox8b	12869	cytochrome c oxidase subu	-2.299323	down	0.01511	0.139517	2.863063	up	0.003081	0.000207
Cpne4	74020	copine IV	-2.01975	down	0.006916	0.125233	4.135453	up	0.002421	0.000138
Cpne9	211232	copine family member IX	-1.633501	down	0.020481	0.163377	6.245578	up	0.000476	0
Cpxm1	56264	carboxypeptidase X 1 (M14	-1.787312	down	0.037141	0.215669	-2.263868	down	0.003543	0.000207
Cpxm2	55987	carboxypeptidase X 2 (M14	-3.705769	down	0.00261	0.103486	2.6182265	up	0.008294	0.033721
Crb2	241324	crumbs family member 2	-1.602916	down	0.004574	0.11779	-2.024325	down	0.013171	0.033721
Crebl2	232430	cAMP responsive element b	-1.636627	down	0.019628	0.163377	-3.06927	down	0.000339	0
Crip3	114570	cysteine-rich protein 3	-1.584527	down	0.006601	0.11779	2.128494	up	0.001146	0
Csf3r	12986	colony stimulating factor 3	-3.590247	down	0.000801	0.092902	3.734951	up	0.004269	0.000207
Csnk1g3	70425	casein kinase 1, gamma 3	1.94274	up	0.003027	0.459167	-4.697646	down	0.002514	0.000207
Cspg4	121021	chondroitin sulfate proteog	-1.605528	down	0.005859	0.11779	-2.438832	down	0.008969	0.033721
Ctage5	217615	CTAGE family, member 5	-1.924136	down	0.021338	0.163377	-1.569411	down	0.030181	0.033721
Ctnnb1	12387	catenin (cadherin associated	1.553783	up	0.024825	0.627255	-2.201098	down	0.002042	0.0001035
Ctns	83429	cystinosis, nephropathic	-1.584315	down	0.000679	0.090608	-1.693899	down	0.005858	0.000207
Cts7	56092	cathepsin 7	-2.84116	down	0.022178	0.163377	4.98388	up	0.003208	0.000207
Cul5	75717	cullin 5	-1.656312	down	0.014152	0.139517	-2.89093	down	0.001256	0
Cul9	78309	cullin 9	-1.804749	down	0.003759	0.11779	2.15758	up	0.002576	0.000207
Cux2	13048	cut-like homeobox 2	-2.09925	down	0.028202	0.187117	3.969397	up	0.004457	0.016964
Cxxc4	319478	CXXC finger 4	1.580169	up	0.04156	0.627255	11.629177	up	0.000643	0
Cyhr1	54151	cysteine and histidine rich 1	-1.782444	down	0.044531	0.215669	1.948561	up	0.00241	0.000207
Cyp2d22	56448	cytochrome P450, family 2,	-2.263174	down	0.001086	0.092902	2.747266	up	0.006338	0.033721
Cyp2j13	230459	cytochrome P450, family 2,	-1.638245	down	0.026994	0.187117	1.99053	up	0.00833	0.033721
Cystm1	66060	cysteine-rich transmembran	-1.539887	down	0.026071	0.187117	-1.803859	down	0.004792	0.000207
Cyth1	19157	cytohesin 1	-1.52394	down	0.00414	0.11779	1.613406	up	0.002597	0.000207
D10Jhu81e	28295	DNA segment, Chr 10, John	1.793288	up	0.045673	0.627255	-2.657481	down	0.000539	0
D16Ertd472e	67102	DNA segment, Chr 16, ERA	-1.595473	down	0.012555	0.139517	-3.028492	down	0.002325	0.000207
D630039A03Rik	242484	RIKEN cDNA D630039A03 g	-3.43821	down	0.000092	0	1.980935	up	0.003823	0.000207
D830050J10Rik	352968	RIKEN cDNA D830050J10 g	-1.821498	down	0.011182	0.139517	-1.964291	down	0.004554	0.000207
Daam2	76441	dishevelled associated activ	-1.803205	down	0.009534	0.125233	1.81448	up	0.002706	0.000207
Dagla	269060	diacylglycerol lipase, alpha	-1.846028	down	0.009417	0.125233	2.471981	up	0.002483	0.000207
Dcaf7	71833	DDB1 and CUL4 associated	1.684672	up	0.03025	0.627255	-1.848348	down	0.001453	0
Dcdc2a	195208	doublecortin domain conta	-1.921716	down	0.013371	0.139517	1.768169	up	0.003344	0.000207
Ddhd2	72108	DDHD domain containing 2	-1.742226	down	0.004571	0.11779	-4.586391	down	0.002242	0.000207
Ddo	70503	D-aspartate oxidase	2.025137	up	0.030274	0.627255	2.949902	up	0.020066	0.033721
Ddx3y	26900	DEAD (Asp-Glu-Ala-Asp) b	1.960419	up	0.005051	0.459167	-1.742034	down	0.005143	0.000207

Def8	23854	differentially expressed in F	-1.588812	down	0.004051	0.11779	-1.714669	down	0.003245	0.000207
Dennd1a	227801	DENN/MADD domain cont	-1.706077	down	0.002422	0.103486	-1.574268	down	0.019164	0.033721
Dennd4a	102442	DENN/MADD domain cont	1.762263	up	0.047386	0.627255	-2.313143	down	0.002807	0.000207
Dennd4b	229541	DENN/MADD domain cont	-2.072507	down	0.00729	0.125233	-4.806064	down	0.000706	0
Dgcr2	13356	DiGeorge syndrome critical	1.637871	up	0.015298	0.592628	-1.984754	down	0.005007	0.0168605
Dhdds	67422	dehydrodolichyl diphospha	-1.539377	down	0.003298	0.103486	-1.771238	down	0.007599	0.033721
Dll3	13389	delta-like 3 (Drosophila)	-2.244238	down	0.008918	0.125233	1.686733	up	0.004782	0.000207
Dlx1	13390	distal-less homeobox 1	-1.510161	down	0.033836	0.187117	-3.392284	down	0.002882	0.000207
Dlx2	13392	distal-less homeobox 2	-2.95487	down	0.027861	0.187117	-3.589599	down	0.001829	0.000207
Dmtf1	23857	cyclin D binding myb-like t	1.527695	up	0.01568	0.592628	-3.033367	down	0.015758	0.016964
Dnah9	237806	dynein, axonemal, heavy ch	-1.741277	down	0.023763	0.163377	1.801023	up	0.004743	0.000207
Dnajb3	15504	DnaJ heat shock protein far	-2.200575	down	0.020154	0.163377	3.391387	up	0.003574	0.000207
Dnajc16	214063	DnaJ heat shock protein far	-1.763102	down	0.041015	0.215669	1.96044	up	0.001853	0.000207
Dnm3	103967	dynamins 3	-2.399724	down	0.041746	0.215669	9.151647	up	0.00113	0.0001035
Doc2a	13446	double C2, alpha	-2.157972	down	0.001295	0.093579	2.616094	up	0.00089	0
Donson	60364	downstream neighbor of SQ	1.630038	up	0.039321	0.627255	-4.378455	down	0.001923	0.000207
Dph3	105638	diphthamine biosynthesis 3	-1.617324	down	0.032121	0.187117	-2.429705	down	0.00386	0.000207
Drp2	13497	dystrophin related protein 2	-2.166004	down	0.015152	0.139517	3.083502	up	0.008225	0.033721
Dusp28	67446	dual specificity phosphatase	-1.56083	down	0.006068	0.11779	1.664883	up	0.002148	0.000207
Dvl1	13542	dishevelled segment polarit	-1.504834	down	0.009506	0.125233	-1.604161	down	0.015092	0.033721
Dydc2	71200	DPY30 domain containing 2	-2.286974	down	0.011038	0.139517	7.945526	up	0.000512	0
Dync1i2	13427	dynein cytoplasmic 1 intern	1.500122	up	0.007247	0.511605	-5.540961	down	0.000266	0
Dynll1	56455	dynein light chain LC8-type	-1.525925	down	0.005176	0.11779	-2.226322	down	0.002351	0.000207
Dynll2	68097	dynein light chain LC8-type	-1.780152	down	0.004176	0.11779	2.865228	up	0.001043	0
Dyrk3	226419	dual-specificity tyrosine-(Y)	-1.586064	down	0.005035	0.11779	-3.005079	down	0.010557	0.033721
E330037M01Rik	319775	RIKEN cDNA E330037M01 g	-2.225451	down	0.003316	0.103486	2.397447	up	0.008187	0.033721
Ece2	107522	endothelin converting enzy	-1.554099	down	0.023254	0.163377	-1.975672	down	0.003692	0.000207
Efcab6	77627	EF-hand calcium binding do	-2.772088	down	0.002007	0.093579	2.378479	up	0.004391	0.000207
Efna3	13638	ephrin A3	-1.511632	down	0.002567	0.103486	1.784836	up	0.004875	0.000207
Elavl1	15568	ELAV (embryonic lethal, abr	-1.511356	down	0.004662	0.11779	3.289053	up	0.000241	0
Elmo2	140579	engulfment and cell motility	1.612346	up	0.029358	0.627255	-1.539671	down	0.003633	0.000207
Elp6	72341	elongator acetyltransferase	-1.64782	down	0.003009	0.103486	-3.228864	down	0.001832	0.000207
Entpd2	12496	ectonucleoside triphosphat	-1.547474	down	0.02616	0.187117	1.871024	up	0.003596	0.000207
Eny2	223527	enhancer of yellow 2 homo	-1.678265	down	0.010164	0.125233	-2.35601	down	0.004417	0.000207
Epb41	269587	erythrocyte membrane prot	1.523619	up	0.038407	0.627255	-4.884968	down	0.000921	0
Epha5	13839	Eph receptor A5	1.703573	up	0.036484	0.627255	2.904739	up	0.002418	0.000207
Epn1	13854	epsin 1	-1.633886	down	0.027489	0.187117	1.791581	up	0.003001	0.000207
Erbb3	13867	erb-b2 receptor tyrosine kir	-2.245574	down	0.012842	0.139517	1.510965	up	0.000815	0

Ergic1	67458	endoplasmic reticulum-golgi	-1.877061	down	0.001293	0.093579	-4.40197	down	0.000214	0
Esrrb	26380	estrogen related receptor, beta	-2.069308	down	0.006784	0.125233	2.212487	up	0.003429	0.000207
Esyt2	52635	extended synaptotagmin-like	2.53441	up	0.017582	0.592628	1.939941	up	0.002772	0.000207
Esyt3	272636	extended synaptotagmin-like	-1.779059	down	0.026249	0.187117	1.878288	up	0.004366	0.000207
Eya1	14048	EYA transcriptional coactivator	-1.720039	down	0.01549	0.139517	-4.019986	down	0.001711	0.000207
Fam110b	242297	family with sequence similarity	-1.754025	down	0.007671	0.125233	7.157243	up	0.000213	0
Fam131b	76156	family with sequence similarity	-2.77597	down	0.000279	0.069898	1.755503	up	0.006487	0.033721
Fam135b	70363	family with sequence similarity	-2.829056	down	0.016844	0.163377	8.089351	up	0.00154	0
Fam151b	73942	family with sequence similarity	1.79671	up	0.017352	0.592628	1.528579	up	0.024124	0.033721
Fam161b	217705	family with sequence similarity	-1.846152	down	0.005879	0.11779	2.164725	up	0.001634	0
Fam163a	329274	family with sequence similarity	-1.735302	down	0.011867	0.139517	2.351563	up	0.000896	0
Fam171a2	217219	family with sequence similarity	-1.968627	down	0.001328	0.093579	1.53179	up	0.007298	0.033721
Fam189a1	70638	family with sequence similarity	-1.794788	down	0.036152	0.215669	1.874926	up	0.007479	0.033721
Fam19a1	320265	family with sequence similarity	-2.093067	down	0.040733	0.215669	2.5969537	up	0.014524	0.011378333
Fam228b	207921	family with sequence similarity	-2.070593	down	0.013443	0.139517	2.681358	up	0.005192	0.033721
Fam69a	67266	family with sequence similarity	1.586252	up	0.00217	0.406743	-3.968796	down	0.001677	0.000207
Fam84a	105005	family with sequence similarity	-1.976522	down	0.00375	0.11779	2.9623595	up	0.003832	0.000207
Fam92a	68099	family with sequence similarity	1.543162	up	0.009352	0.560498	-3.196641	down	0.000886	0
Fasn	14104	fatty acid synthase	-1.582964	down	0.027546	0.187117	-2.001448	down	0.002389	0.000207
Fbxl20	72194	F-box and leucine-rich repeats	-1.528072	down	0.022543	0.163377	-6.716108	down	0.00023	0
Fbxo46	243867	F-box protein 46	-1.815183	down	0.002222	0.103486	-1.620029	down	0.006157	0.000207
Fgf13	14168	fibroblast growth factor 13	1.73846	up	0.011647	0.560498	5.6235215	up	0.001954	0.0001035
Fgf9	14180	fibroblast growth factor 9	-1.517527	down	0.030646	0.187117	7.218262	up	0.001489	0.0001035
Fgfbp3	72514	fibroblast growth factor binding	-1.942035	down	0.015896	0.139517	-1.505803	down	0.017186	0.033721
Fhit	14198	fragile histidine triad gene	-1.708809	down	0.002817	0.103486	-1.861004	down	0.009539	0.033721
Fktn	246179	fukutin	1.913226	up	0.004993	0.459167	-1.767335	down	0.038292	0.033721
Fmn12	71409	formin-like 2	1.529178	up	0.012597	0.560498	-3.718865	down	0.002455	0.000207
Foxn3	71375	forkhead box N3	-2.146081	down	0.002392	0.103486	-4.167785	down	0.001085	0
Foxo6	329934	forkhead box O6	-1.708761	down	0.014757	0.139517	1.906863	up	0.00267	0.000207
Frat1	14296	frequently rearranged in adenocarcinoma	-1.9430555	down	0.0082165	0.1150625	-1.684123	down	0.018485	0.033721
Frmpd1	666060	FERM and PDZ domain containing	-1.746664	down	0.006176	0.11779	2.105345	up	0.002151	0.000207
Frzb	20378	frizzled-related protein	-1.611997	down	0.047761	0.215669	2.381692	up	0.009021	0.033721
Fstl5	213262	follicle-stimulating-like 5	-2.015434	down	0.035472	0.187117	9.0821665	up	0.003972	0.016964
Fyco1	17281	FYVE and coiled-coil domain	-1.653824	down	0.003056	0.103486	-3.55026	down	0.007709	0.011309333
Fzd9	14371	frizzled class receptor 9	-1.699174	down	0.010382	0.125233	4.78503	up	0.000169	0
Gabbr1	54393	gamma-aminobutyric acid receptor	-1.720057	down	0.010745	0.139517	2.201464	up	0.000477	0
Gabra4	14397	gamma-aminobutyric acid receptor	-3.516064	down	0.001707	0.093579	10.35264	up	0.000491	0
Gabrb3	14402	gamma-aminobutyric acid receptor	-2.099727	down	0.017684	0.163377	4.0530733	up	0.003373	0.011378333

Garnl3	99326	GTPase activating RANGAP	-2.07185	down	0.033944	0.187117	1.784654	up	0.002737	0.000207
Gata2	14461	GATA binding protein 2	-1.8872	down	0.000212	0.069898	-2.078078	down	0.012986	0.033721
Gemin2	66603	gem (nuclear organelle) ass	-1.622903	down	0.001195	0.092902	-1.960868	down	0.005262	0.000207
Gfap	14580	glial fibrillary acidic protein	1.549493	up	0.021721	0.592628	9.941525	up	0.000462	0
Ghitm	66092	growth hormone inducible	1.578948	up	0.038227	0.627255	-2.086366	down	0.001976	0.000207
Gjb2	14619	gap junction protein, beta 2	-2.00134	down	0.000073	0	2.938982	up	0.003663	0.000207
Gm10199	100049552	predicted gene 10199	-1.954019	down	0.02582	0.187117	2.295844	up	0.003644	0.000207
Gm11568	432600	predicted gene 11568	-1.844184	down	0.044224	0.215669	3.697976	up	0.002528	0.000207
Gm11627	100040792	predicted gene 11627	-1.901541	down	0.003032	0.103486	2.315891	up	0.000407	0
Gm14308	100043381	predicted gene 14308	1.660669	up	0.002037	0.406743	-3.527103	down	0.001495	0
Gm14435	100302432	KRAB box containing protei	1.891372	up	0.018994	0.592628	-13.514	down	0.001335	0
Gm16381	100042786	predicted gene 16381	-1.921367	down	0.012919	0.139517	-2.816906	down	0.002232	0.000207
Gm20033	100504048	predicted gene, 20033	-2.136593	down	0.023476	0.163377	-2.238998	down	0.004163	0.000207
Gm20747	434960	predicted gene, 20747	2.358489	up	0.036016	0.627255	2.389796	up	0.005185	0.033721
Gm2897	100040671	predicted gene 2897	1.728171	up	0.003744	0.459167	-2.554574	down	0.006676	0.033721
Gm3993	100042727	predicted gene 3993	1.561569	up	0.006134	0.511605	-2.534199	down	0.003304	0.000207
Gm6710	626832	predicted gene 6710	1.981273	up	0.012476	0.560498	-12.24612	down	0.002239	0.000207
Gmfb	63985	glia maturation factor, beta	1.906957	up	0.011999	0.560498	-4.893148	down	0.000066	0
Gmps	229363	guanine monophosphate s	-1.609547	down	0.032262	0.187117	-1.827289	down	0.014739	0.033721
Gpc3	14734	glypican 3	-2.253897	down	0.025756	0.187117	4.759927	up	0.002325	0.000207
Gpm6b	14758	glycoprotein m6b	-3.692788	down	0.00232	0.103486	24.41212	up	0.000124	0
Gpr182	11536	G protein-coupled receptor	-3.3003	down	0.00812	0.125233	4.247422	up	0.003554	0.000207
Gpr34	23890	G protein-coupled receptor	3.509259	up	0.018668	0.592628	4.249158	up	0.004751	0.000207
Gpr62	436090	G protein-coupled receptor	-2.31684	down	0.035772	0.215669	3.329409	up	0.001839	0.000207
Gpr83	14608	G protein-coupled receptor	-1.514793	down	0.008377	0.125233	-3.839907	down	0.001521	0
Gpt2	108682	glutamic pyruvate transami	-1.515849	down	0.009385	0.125233	-3.79494	down	0.000657	0
Gria4	14802	glutamate receptor, ionotro	-2.586136	down	0.015108	0.139517	3.4936837	up	0.005986	0.011378333
Grin2a	14811	glutamate receptor, ionotro	-1.914406	down	0.040689	0.215669	4.3331525	up	0.003164	0.0168605
Grpr	14829	gastrin releasing peptide re	-2.353934	down	0.028253	0.187117	2.612548	up	0.006368	0.033721
Grrp1	72690	glycine/arginine rich protei	-2.688479	down	0.002458	0.103486	5.453497	up	0.00086	0
Gucy1a3	60596	guanylate cyclase 1, soluble	-2.063819	down	0.024585	0.163377	6.7168928	up	0.002867	0.0085855
Hbb-b1	15129	hemoglobin, beta adult ma	1.982674	up	0.0316835	0.6099415	7.1305495	up	0.000766	0
Hbb-y	15135	hemoglobin Y, beta-like em	1.573748	up	0.039582	0.627255	1.524767	up	0.012188	0.033721
Heyl	56198	hairy/enhancer-of-split rela	-2.286315	down	0.001865	0.093579	2.069267	up	0.003384	0.000207
Hhatl	74770	hedgehog acyltransferase-l	-1.664033	down	0.030438	0.187117	2.720072	up	0.003195	0.000207
Hhip	15245	Hedgehog-interacting prot	-2.054577	down	0.00801	0.125233	2.025639	up	0.023339	0.033721
Hip1	215114	huntingtin interacting prote	-1.90335	down	0.032504	0.187117	-4.779181	down	0.00078	0
Hnrnpl	15388	heterogeneous nuclear ribc	-1.508819	down	0.007184	0.125233	-16.37332	down	0.000233	0

Hnrnpul1	232989	heterogeneous nuclear ribo	-1.864927	down	0.0048015	0.109406	-1.512734	down	0.016087	0.033721
Homez	239099	homeodomain leucine zipp	-1.633901	down	0.019897	0.163377	-3.239435	down	0.001985	0.000207
Hormad1	67981	HORMA domain containing	-2.509097	down	0.038903	0.215669	1.832442	up	0.011642	0.033721
Hpd1	242642	4-hydroxyphenylpyruvate d	-2.017469	down	0.015783	0.139517	-1.675969	down	0.016852	0.033721
Hs3st1	15476	heparan sulfate (glucosamin	-1.729135	down	0.00591	0.11779	-2.160361	down	0.002694	0.000207
Hsf5	327992	heat shock transcription fac	-2.120534	down	0.01697	0.163377	2.971291	up	0.003877	0.000207
Htr2a	15558	5-hydroxytryptamine (serot	2.031593	up	0.006493	0.511605	1.556438	up	0.032471	0.033721
Ido2	209176	indoleamine 2,3-dioxygena	-1.7699965	down	0.0129625	0.128478	1.630844	up	0.007836	0.033721
Igdcc4	56741	immunoglobulin superfamil	1.864637	up	0.004225	0.459167	2.410514	up	0.001669	0.000207
Igf1r	16001	insulin-like growth factor I	-1.88919	down	0.003776	0.11779	-4.995051	down	0.001625	0.000207
Igsf3	78908	immunoglobulin superfamil	-1.73807	down	0.015296	0.139517	-5.285474	down	0.000473	0
Il17d	239114	interleukin 17D	-1.519711	down	0.005065	0.11779	3.922924	up	0.002098	0.000207
Ins2	16334	insulin II	-1.651441	down	0.030778	0.187117	2.873942	up	0.001636	0.0001035
Insc	233752	inscuteable homolog (Dros	-2.488684	down	0.018888	0.163377	3.015355	up	0.003533	0.000207
Ippk	75678	inositol 1,3,4,5,6-pentakisph	-1.740747	down	0.016535	0.163377	-1.944273	down	0.025962	0.033721
Irak2	108960	interleukin-1 receptor-asso	-1.802282	down	0.006541	0.11779	-4.639715	down	0.001275	0
Ireb2	64602	iron responsive element bin	1.894438	up	0.000515	0.321897	-3.233141	down	0.00408	0.000207
Isca1	69046	iron-sulfur cluster assembly	1.614774	up	0.044357	0.627255	-2.831263	down	0.001596	0
Itfg1	71927	integrin alpha FG-GAP repe	2.874306	up	0.036261	0.627255	-6.470652	down	0.00108	0
Itga11	319480	integrin alpha 11	-1.721663	down	0.004925	0.11779	-1.932794	down	0.002257	0.000207
Itn2b	16432	integral membrane protein	1.842806	up	0.008726	0.511605	-3.730365	down	0.001069	0.0001035
Itpr1	16438	inositol 1,4,5-trisphosphate	1.932497	up	0.0019	0.406743	-1.738402	down	0.005335	0.000207
Kansl1	76719	KAT8 regulatory NSL compl	-1.542086	down	0.032619	0.187117	-2.816599	down	0.003735	0.000207
Kansl3	226976	KAT8 regulatory NSL compl	-1.790738	down	0.001518	0.093579	-3.623024	down	0.001215	0
Kazn	71529	kazrin, periplakin interacti	-1.758433	down	0.008924	0.125233	4.7275487	up	0.003594	0.011309333
Kcna2	16490	potassium voltage-gated ch	-1.587158	down	0.012747	0.139517	1.932515	up	0.002835	0.000207
Kcne1l	66240	potassium voltage-gated ch	-1.702651	down	0.031391	0.187117	5.414044	up	0.001188	0
Kcnip4	80334	Kv channel interacting prote	2.131833	up	0.03916	0.627255	6.5752305	up	0.007985	0.0168605
Kcnj9	16524	potassium inwardly-rectifyi	-1.857572	down	0.030086	0.187117	3.6032215	up	0.003004	0.0168605
Kcnv1	67498	potassium channel, subfam	1.890159	up	0.013	0.560498	3.456807	up	0.00255	0.000207
Kctd7	212919	potassium channel tetrame	-1.776722	down	0.0066365	0.1215115	-1.638794	down	0.028049	0.033721
Kif1b	16561	kinesin family member 1B	1.678151	up	0.038059	0.627255	-1.698853	down	0.002382	0.000207
Kif1bp	72320	KIF1 binding protein	1.60283	up	0.01161	0.560498	-3.232014	down	0.000724	0
Kif26a	668303	kinesin family member 26A	-1.929034	down	0.009307	0.125233	2.829965	up	0.025109	0.033721
Kirrel2	243911	kin of IRRE like 2 (Drosophil	-3.047361	down	0.000423	0.090608	2.803074	up	0.008648	0.033721
Klf2	16598	Kruppel-like factor 2 (lung)	-1.693678	down	0.006312	0.11779	-11.80241	down	0.000324	0
Klhl12	240756	kelch-like 12	-1.736921	down	0.040158	0.215669	-2.141883	down	0.004593	0.000207
Krt9	107656	keratin 9	-2.22616	down	0.009924	0.125233	2.045485	up	0.001611	0

Ksr1	16706	kinase suppressor of ras 1	-1.538103	down	0.005348	0.11779	1.7339	up	0.002019	0.000207
Lama4	16775	laminin, alpha 4	1.852811	up	0.015872	0.592628	2.231597	up	0.018087	0.033721
Lamtor3	56692	late endosomal/lysosomal a	1.578311	up	0.001365	0.406743	-2.607549	down	0.00169	0.000207
Larp1	73158	La ribonucleoprotein doma	-1.514935	down	0.019492	0.163377	-1.938264	down	0.005762	0.000207
Lct	226413	lactase	-1.66396	down	0.030101	0.187117	2.355609	up	0.00282	0.000207
Leprotl1	68192	leptin receptor overlapping	1.562105	up	0.028639	0.627255	-3.952054	down	0.001118	0
Lhx6	16874	LIM homeobox protein 6	-1.597131	down	0.024272	0.163377	1.53741	up	0.003079	0.000207
Limch1	77569	LIM and calponin homology	-2.47418	down	0.004541	0.11779	2.867086	up	0.003432	0.000207
Lingo1	235402	leucine rich repeat and Ig d	-1.735076	down	0.033348	0.187117	3.753787	up	0.000932	0
Lrfrn5	238205	leucine rich repeat and fibr	-1.728212	down	0.042657	0.215669	7.316016	up	0.000829	0
Lrp4	228357	low density lipoprotein rece	-1.648803	down	0.007284	0.125233	1.89679	up	0.00223	0.000207
Lrrc3	237387	leucine rich repeat containi	-2.105137	down	0.012606	0.139517	1.790914	up	0.004634	0.000207
Lrrc40	67144	leucine rich repeat containi	2.098152	up	0.00011	0.163377	-1.987287	down	0.011072	0.033721
Lrrc55	241528	leucine rich repeat containi	-1.896773	down	0.046244	0.215669	2.855686	up	0.004533	0.000207
Lrrtm4	243499	leucine rich repeat transme	-2.947614	down	0.017107	0.163377	7.937829	up	0.003272	0.000207
Lsm6	78651	LSM6 homolog, U6 small nu	-1.7629095	down	0.013022	0.1388625	-1.594275	down	0.012372	0.0168605
Luc7l2	192196	LUC7-like 2 (S. cerevisiae)	-1.674546	down	0.022648	0.163377	-2.318962	down	0.001899	0.0001035
Lum	17022	lumican	1.694681	up	0.003419	0.459167	-1.768354	down	0.007224	0.033721
Magel2	27385	melanoma antigen, family L	-1.635914	down	0.025001	0.163377	2.182596	up	0.023073	0.033721
Magi1	14924	membrane associated guan	-1.676506	down	0.032676	0.187117	3.612804	up	0.001666	0.000207
Map1a	17754	microtubule-associated pro	-2.22785	down	0.026269	0.187117	2.1101415	up	0.004402	0.016964
Map3k13	71751	mitogen-activated protein i	-1.941464	down	0.021526	0.163377	1.901514	up	0.044878	0.033721
Map4k5	399510	mitogen-activated protein i	1.537001	up	0.043257	0.627255	-12.41951	down	0.00093	0
Mapk10	26414	mitogen-activated protein i	2.441838	up	0.017368	0.592628	4.9348225	up	0.002014	0.0001035
Mapk4	225724	mitogen-activated protein i	-1.68986	down	0.028675	0.187117	4.3619	up	0.000407	0
Mat2b	108645	methionine adenosyltransfe	1.905712	up	0.010059	0.560498	-2.830346	down	0.001632	0.000207
Matr3	17184	matrin 3	1.651541	up	0.02889	0.627255	-8.05788	down	0.002401	0.000207
Mcam	84004	melanoma cell adhesion mc	-1.569593	down	0.046749	0.215669	-1.820035	down	0.003289	0.000207
Mcoln1	94178	mucolipin 1	-1.55944	down	0.004646	0.11779	-2.030571	down	0.00036	0
Mef2a	17258	myocyte enhancer factor 2A	-1.754595	down	0.025662	0.187117	1.543538	up	0.000862	0
Mesdc1	80889	mesoderm development ca	-1.826294	down	0.003005	0.103486	-3.673205	down	0.002844	0.0001035
Mesdc2	67943	mesoderm development ca	-2.773255	down	0.000985	0.092902	1.685187	up	0.014827	0.033721
Mettl6	67011	methyltransferase like 6	-1.542307	down	0.006903	0.125233	-1.606658	down	0.017662	0.033721
Mfsd6	98682	major facilitator superfamily	-1.653941	down	0.028041	0.187117	-2.535449	down	0.004911	0.000207
Mfsd7c	217721	major facilitator superfamily	-2.524162	down	0.007022	0.125233	3.462677	up	0.004572	0.000207
Mlec	109154	malectin	-1.673631	down	0.015915	0.139517	-2.904305	down	0.003095	0.011240333
Mmgt1	236792	membrane magnesium tran	-1.864392	down	0.001568	0.093579	-3.269403	down	0.005833	0.000207
Mobp	17433	myelin-associated oligoder	-2.249951	down	0.004726	0.11779	5.336633	up	0.001095	0.000069

Morc2b	240069	microrchidia 2B	-1.513779	down	0.02081	0.163377	1.615575	up	0.036568	0.033721
Mphosph8	75339	M-phase phosphoprotein 8	1.821466	up	0.009595	0.560498	-2.14631	down	0.018524	0.033721
Mrpl38	60441	mitochondrial ribosomal pr	-1.51786	down	0.018559	0.163377	-1.550607	down	0.002238	0.000207
Mrps21	66292	mitochondrial ribosomal pr	-1.618048	down	0.016361	0.163377	-2.172115	down	0.001154	0
Mrps33	14548	mitochondrial ribosomal pr	-1.534195	down	0.032976	0.187117	-8.663358	down	0.000566	0
Mterf4	69821	mitochondrial transcription	-1.565415	down	0.005339	0.11779	-2.284331	down	0.001534	0
Mtmr7	54384	myotubularin related protei	-2.434276	down	0.028289	0.187117	3.063394	up	0.003569	0.0168605
Mto1	68291	mitochondrial tRNA translat	-2.481346	down	0.016209	0.139517	-2.922934	down	0.004346	0.000207
Mtus1	102103	mitochondrial tumor suppress	-1.595057	down	0.009251	0.125233	-2.250353	down	0.002804	0.000207
Myh14	71960	myosin, heavy polypeptide	-1.8766635	down	0.0255795	0.170451	3.616611	up	0.00138	0
Myh4	17884	myosin, heavy polypeptide	-2.14308	down	0.009241	0.125233	2.25562	up	0.004644	0.016964
Myo16	244281	myosin XVI	-3.578665	down	0.011134	0.139517	4.205123	up	0.001466	0
Myo18b	74376	myosin XVIIIb	-2.055176	down	0.022515	0.163377	-1.910554	down	0.010991	0.033721
Myrip	245049	myosin VIIA and Rab interact	-1.905662	down	0.041625	0.215669	6.725811	up	0.006931	0.033721
ND4	17719	NADH dehydrogenase subu	1.797744	up	0.005812	0.511605	-3.995936	down	0.002951	0.000207
Nadk2	68646	NAD kinase 2, mitochondria	1.538272	up	0.02866	0.627255	-6.094974	down	0.001542	0
Naif1	71254	nuclear apoptosis inducing	-2.068309	down	0.000383	0.069898	-3.25185	down	0.000236	0
Nap1l4	17955	nucleosome assembly prote	5.516534	up	0.041132	0.627255	-2.11356	down	0.002698	0.000207
Ndfip2	76273	Nedd4 family interacting pr	1.70217	up	0.032371	0.627255	-4.238774	down	0.003976	0.000207
Ndufc1	66377	NADH dehydrogenase (ubiq	-1.517168	down	0.019889	0.163377	-4.351381	down	0.000314	0
Necab1	69352	N-terminal EF-hand calciu	2.005373	up	0.044805	0.627255	2.874846	up	0.0013	0
Negr1	320840	neuronal growth regulator	-2.589822	down	0.032807	0.187117	2.646928	up	0.00245	0.0001035
Nek7	59125	NIMA (never in mitosis gen	1.62198	up	0.006925	0.511605	-3.746744	down	0.000835	0
Nelfa	24116	negative elongation factor	-1.699974	down	0.006224	0.11779	-2.543842	down	0.001593	0
Nemf	66244	nuclear export mediator fac	1.681006	up	0.033829	0.627255	-1.600108	down	0.005127	0.000207
Nfasc	269116	neurofascin	-1.917424	down	0.017126	0.163377	2.431612	up	0.005563	0.033721
Nfia	18027	nuclear factor I/A	-1.567638	down	0.005344	0.11779	-1.705124	down	0.016658	0.033721
Nhsl1	215819	NHS-like 1	-1.584689	down	0.032731	0.187117	-7.344674	down	0.000392	0
Nkx2-1	21869	NK2 homeobox 1	-1.917284	down	0.009214	0.125233	3.33695	up	0.004442	0.000207
Nlrp6	101613	NLR family, pyrin domain co	-1.644237	down	0.014738	0.139517	2.824709	up	0.032882	0.033721
Nmb	68039	neuromedin B	-1.587815	down	0.002935	0.103486	3.410741	up	0.003085	0.000207
Nmnat2	226518	nicotinamide nucleotide ad	-1.770191	down	0.018247	0.163377	2.6868445	up	0.003174	0.000207
Nop16	28126	NOP16 nucleolar protein	-1.76123	down	0.021251	0.163377	-1.724593	down	0.00044	0
Notch3	18131	notch 3	-2.004625	down	0.000491	0.090608	-1.947623	down	0.000504	0
Npas4	225872	neuronal PAS domain prote	-2.122547	down	0.023778	0.163377	2.269819	up	0.027238	0.033721
Nprl3	17168	nitrogen permease regulato	-1.563657	down	0.011252	0.139517	-1.983824	down	0.005941	0.000207
Nr1i3	12355	nuclear receptor subfamily	-2.236327	down	0.049792	0.250777	2.118686	up	0.018085	0.033721
Nrcam	319504	neuronal cell adhesion mol	-2.992122	down	0.032434	0.187117	3.219776	up	0.001781	0.0001035

Nt5c3	107569	5'-nucleotidase, cytosolic II	1.876108	up	0.009246	0.560498	-1.97407	down	0.019288	0.033721
Ntsr1	18216	neurotensin receptor 1	-2.022279	down	0.004217	0.11779	2.180415	up	0.004805	0.000207
Nudt4	71207	nudix (nucleoside diphosph	1.580587	up	0.020365	0.592628	-4.467172	down	0.000314	0
Nup210	54563	nucleoporin 210	-1.587545	down	0.002381	0.103486	-8.342995	down	0.000211	0
Nupr1l	69034	nuclear protein transcription	-1.544995	down	0.045001	0.215669	-2.371995	down	0.001111	0
Obp1b	628991	odorant binding protein IB	-2.653782	down	0.019169	0.163377	5.037211	up	0.002324	0.000207
Ogg1	18294	8-oxoguanine DNA-glycos	-1.689356	down	0.008198	0.125233	-2.612062	down	0.001723	0.000207
Olfir135	258329	olfactory receptor 135	2.870712	up	0.012389	0.560498	2.049906	up	0.017068	0.033721
Olfir1355	257734	olfactory receptor 1355	-1.745154	down	0.031408	0.187117	1.522123	up	0.035807	0.033721
Opalin	226115	oligodendrocytic myelin pa	-2.206312	down	0.042685	0.215669	3.701071	up	0.003396	0.000207
Oprd1	18386	opioid receptor, delta 1	-2.748162	down	0.043274	0.215669	3.42483	up	0.039609	0.033721
Oprk1	18387	opioid receptor, kappa 1	-2.18466	down	0.041939	0.215669	3.385202	up	0.002816	0.000207
Orai3	269999	ORAI calcium release-activ	-1.588891	down	0.005868	0.11779	-4.004176	down	0.002288	0.000207
Otof	83762	otoferlin	-2.15903	down	0.004047	0.11779	1.86576	up	0.038817	0.033721
Otud6b	72201	OTU domain containing 6B	1.519378	up	0.014611	0.560498	-1.98899	down	0.001647	0.000207
Ovca2	246257	candidate tumor suppressor	-1.633247	down	0.008182	0.125233	-3.771199	down	0.000632	0
Ovgp1	12659	oviductal glycoprotein 1	1.857776	up	0.010682	0.560498	1.913224	up	0.004366	0.000207
Oxr1	170719	oxidation resistance 1	2.330642	up	0.002403	0.459167	-6.785073	down	0.001748	0.000207
P2ry1	18441	purinergic receptor P2Y, G-	1.86732	up	0.02615	0.627255	2.131283	up	0.049061	0.033721
Paqr5	74090	progesterone and adipoQ rece	-2.0559555	down	0.0151055	0.1453015	2.522212	up	0.002948	0.000207
Paqr6	68957	progesterone and adipoQ rece	-1.525253	down	0.031953	0.187117	1.770011	up	0.004753	0.000207
Parg	26430	poly (ADP-ribose) glycohyd	1.710247	up	0.012711	0.560498	-5.383047	down	0.000981	0
Pcdh13	93884	protocadherin beta 13	-3.079603	down	0.003073	0.103486	3.525173	up	0.038421	0.033721
Pcdh21	93892	protocadherin beta 21	-1.79785	down	0.005502	0.11779	-2.822809	down	0.000854	0
Pcdhga12	93724	protocadherin gamma subf	3.277837	up	0.010152	0.560498	2.373509	up	0.005574	0.033721
Pcgf3	69587	polycomb group ring finger	1.970298	up	0.003161	0.459167	-1.862976	down	0.01505	0.033721
Pcmt2	245867	protein-L-isoaspartate (D-a	1.905884	up	0.004907	0.459167	-9.457061	down	0.002937	0.000207
Pcyt1b	236899	phosphate cytidylyltransfer	-1.916115	down	0.020984	0.163377	-2.103719	down	0.002704	0.000207
Pde7b	29863	phosphodiesterase 7B	-2.076845	down	0.015634	0.139517	2.436772	up	0.020186	0.033721
Pdia6	71853	protein disulfide isomerase	-1.569025	down	0.030402	0.187117	-2.562552	down	0.001089	0
Pdlim3	53318	PDZ and LIM domain 3	-2.012252	down	0.022949	0.163377	2.006322	up	0.003394	0.000207
Pds5b	100710	PDS5 cohesin associated fac	1.983976	up	0.001931	0.406743	-4.108817	down	0.000286	0
Pex12	103737	peroxisomal biogenesis fac	1.52871	up	0.01137	0.560498	-1.689902	down	0.014961	0.033721
Pex13	72129	peroxisomal biogenesis fac	3.959895	up	0.023126	0.592628	-8.737114	down	0.001127	0
Pfdn4	109054	prefoldin 4	-1.742223	down	0.040569	0.215669	-1.726607	down	0.005616	0.000207
Pfkl	56421	phosphofructokinase, plate	-1.512771	down	0.023322	0.163377	-4.297062	down	0.00102	0
Pgap2	233575	post-GPI attachment to pro	-1.535546	down	0.016336	0.163377	-1.905983	down	0.004289	0.000207
Pgm2l1	70974	phosphoglucomutase 2-like	1.746095	up	0.040931	0.627255	-2.381961	down	0.012312	0.016964

Pgm3	109785	phosphoglucomutase 3	1.807055	up	0.003044	0.459167	-3.997356	down	0.002156	0.000207
Phactr2	215789	phosphatase and actin regu	-2.619724	down	0.004469	0.11779	2.737613	up	0.002077	0.000207
Phospho2	73373	phosphatase, orphan 2	1.510374	up	0.003813	0.459167	-2.137204	down	0.001653	0.000207
Pip5k1l	227733	phosphatidylinositol-4-pho	-1.70475	down	0.037091	0.215669	1.671553	up	0.024098	0.033721
Pisd-ps3	66776	phosphatidylserine decarbo	-1.9867	down	0.000313	0.069898	-2.410544	down	0.001739	0.000207
Pithd1	66193	PITH (C-terminal proteaso	1.628619	up	0.015848	0.592628	-1.55118	down	0.006594	0.033721
Pja2	224938	paja 2, RING-H2 motif con	2.1378	up	0.031059	0.627255	-7.161655	down	0.004483	0.000207
Plagl1	22634	pleiomorphic adenoma ger	1.69871	up	0.021129	0.592628	-6.324209	down	0.00167	0.000207
Plekha1	101476	pleckstrin homology domai	-1.8984065	down	0.0257755	0.170451	1.50563	up	0.030484	0.033721
Plekha7	233765	pleckstrin homology domai	1.966647	up	0.002119	0.406743	-1.79845	down	0.014077	0.033721
Plekha2	226971	pleckstrin homology domai	1.59063	up	0.002853	0.459167	-3.382585	down	0.003226	0.000207
Plekhd1	217682	pleckstrin homology domai	-1.700259	down	0.032029	0.187117	3.614502	up	0.000918	0
Plpp1	19012	phospholipid phosphatase	1.527525	up	0.047145	0.627255	-2.555949	down	0.001709	0.000207
Pm20d1	212933	peptidase M20 domain con	-2.143364	down	0.045031	0.215669	2.908367	up	0.009627	0.033721
Polr1b	20017	polymerase (RNA) I polype	-1.819122	down	0.000316	0.069898	-2.038085	down	0.003272	0.000207
Pon2	330260	paraaxonase 2	1.859326	up	0.004472	0.459167	-1.712346	down	0.025518	0.033721
Ppa2	74776	pyrophosphatase (inorgani	1.585703	up	0.027073	0.627255	-4.141825	down	0.000395	0
Ppara	19013	peroxisome proliferator act	-1.665488	down	0.025322	0.187117	1.892584	up	0.001576	0
Ppargc1a	19017	peroxisome proliferative act	1.677711	up	0.034915	0.627255	1.953797	up	0.00428	0.000207
Ppargc1b	170826	peroxisome proliferative act	-1.943247	down	0.04722	0.215669	-2.049369	down	0.007638	0.033721
Ppfia2	327814	protein tyrosine phosphatas	-1.779687	down	0.024797	0.163377	3.306812	up	0.001825	0.000207
Ppfia3	76787	protein tyrosine phosphatas	-1.601524	down	0.026211	0.187117	4.223768	up	0.000182	0
Ppid	67738	peptidylprolyl isomerase D	1.770726	up	0.002954	0.459167	-3.126136	down	0.00027	0
Ppnr	26930	per-pentamer repeat gene	-1.515786	down	0.006918	0.125233	-1.532395	down	0.012642	0.033721
Ppp1r3e	105651	protein phosphatase 1, regu	-1.762942	down	0.039843	0.215669	1.744252	up	0.04372	0.033721
Ppp1r7	66385	protein phosphatase 1, regu	1.673604	up	0.014678	0.560498	-2.361667	down	0.004936	0.000207
Ppp2ca	19052	protein phosphatase 2 (for	1.626536	up	0.025573	0.627255	-2.493413	down	0.000688	0
Ppp2r1b	73699	protein phosphatase 2, regu	3.139591	up	0.019561	0.592628	-1.709621	down	0.011817	0.033721
Ppp2r5e	26932	protein phosphatase 2, regu	1.604497	up	0.031508	0.627255	-2.539167	down	0.003864	0.000207
Ppp3cb	19056	protein phosphatase 3, cata	2.009244	up	0.041665	0.627255	1.853352	up	0.000848	0
Pqlc2	212555	PQ loop repeat containing	-1.905875	down	0.003973	0.11779	-1.642525	down	0.011778	0.033721
Prkcq	18761	protein kinase C, theta	-1.888743	down	0.00838	0.125233	2.6235485	up	0.015412	0.016964
Prlr	19116	prolactin receptor	-2.793659	down	0.019632	0.163377	4.740144	up	0.001792	0.000207
Prok2	50501	prokineticin 2	-3.228424	down	0.0076	0.125233	3.6114025	up	0.007956	0.033721
Prox1	19130	prospero homeobox 1	-1.588198	down	0.006563	0.11779	3.824981	up	0.002095	0.000207
Prr36	73072	proline rich 36	-1.649089	down	0.018404	0.163377	2.26415	up	0.001075	0
Prtg	235472	protogenin	-1.843738	down	0.004438	0.11779	-1.764411	down	0.001426	0
Psmc7	17463	proteasome (prosome, mac	-1.605194	down	0.029712	0.187117	-2.650715	down	0.004122	0.000207

Psmid9	67151	proteasome (prosome, mac	-1.888813	down	0.000538	0.090608	-2.064215	down	0.002001	0.000207
Pstk	214580	phosphoseryl-tRNA kinase	-1.778767	down	0.021164	0.163377	1.679368	up	0.001926	0.000207
Ptdss1	19210	phosphatidylserine synthase	1.565226	up	0.006748	0.511605	-4.525509	down	0.002205	0.000207
Ptger3	19218	prostaglandin E receptor 3	-1.812831	down	0.024217	0.163377	1.757222	up	0.025818	0.033721
Ptpdc1	218232	protein tyrosine phosphatase	-1.999323	down	0.015213	0.139517	-2.177875	down	0.008113	0.033721
Ptpn13	19249	protein tyrosine phosphatase	1.936238	up	0.010514	0.560498	-3.979211	down	0.001025	0
Ptprij	19271	protein tyrosine phosphatase	-1.548771	down	0.001071	0.092902	2.130096	up	0.002104	0.000207
Ptpnk	19272	protein tyrosine phosphatase	1.557606	up	0.030583	0.627255	-1.843859	down	0.008886	0.033721
Pwp2	110816	PWP2 periodic tryptophan	-1.548985	down	0.02484	0.163377	-2.048699	down	0.001938	0.000207
Pyurf	66459	Pigy upstream reading frame	-1.534417	down	0.032938	0.187117	-1.887053	down	0.019143	0.033721
Qk	19317	quaking	1.8317	up	0.006565	0.511605	3.067728	up	0.001974	0.000207
Qrfpr	229214	pyroglutamylated RFamide	2.157471	up	0.002641	0.459167	1.800965	up	0.039505	0.033721
Rab11fip4	268451	RAB11 family interacting pr	-2.528547	down	0.013902	0.139517	2.588176	up	0.004019	0.000207
Rab12	19328	RAB12, member RAS oncog	-2.318318	down	0.008692	0.125233	-2.004131	down	0.003736	0.000207
Rab42	242681	RAB42, member RAS oncog	-1.651982	down	0.01091	0.139517	1.882291	up	0.007844	0.033721
Rab6a	19346	RAB6A, member RAS oncog	1.661694	up	0.017185	0.592628	1.633928	up	0.004082	0.000207
Rabep1	54189	rabaptin, RAB GTPase bindi	1.576921	up	0.044208	0.627255	-5.701785	down	0.014541	0.0168605
Rabgef1	56715	RAB guanine nucleotide exc	-1.666771	down	0.0192	0.163377	-4.939491	down	0.001003	0
Rac1	19353	RAS-related C3 botulinum s	-1.685733	down	0.025374	0.187117	-9.246829	down	0.000973	0
Ralgapa1	56784	Ral GTPase activating prote	-2.291494	down	0.003206	0.103486	-3.024985	down	0.004095	0.000207
Rapgef6	192786	Rap guanine nucleotide exc	1.717052	up	0.002922	0.459167	-2.296925	down	0.018333	0.033721
Rasa1	19415	RAS protein activator like 1	-1.740475	down	0.00295	0.103486	2.469638	up	0.003948	0.000207
Rassf2	215653	Ras association (RalGDS/AF	-1.613374	down	0.000729	0.092902	-2.426311	down	0.007702	0.033721
Rbm18	67889	RNA binding motif protein	-1.858713	down	0.025714	0.187117	-8.446276	down	0.000639	0
Rbm26	74213	RNA binding motif protein	-1.685891	down	0.003599	0.103486	-4.709801	down	0.001437	0.0001035
Rbm39	170791	RNA binding motif protein	1.563676	up	0.043079	0.627255	-3.742045	down	0.002404	0.000207
Rcan1	54720	regulator of calcineurin 1	2.384404	up	0.016723	0.592628	-1.739071	down	0.008199	0.033721
Rel1	100532	RELT-like 1	-1.641404	down	0.019012	0.163377	-1.598445	down	0.014183	0.033721
Rftn2	74013	raftlin family member 2	-1.604613	down	0.029688	0.187117	2.481894	up	0.001045	0
Rfwd3	234736	ring finger and WD repeat	1.8081	up	0.003535	0.459167	-3.395762	down	0.002191	0.000207
Rgag4	331474	retrotransposon gag domai	-1.530138	down	0.047657	0.215669	2.975294	up	0.00029	0
Ric3	320360	RIC3 acetylcholine receptor	-1.770835	down	0.016198	0.139517	3.8876583	up	0.002605	0.000138
Rlim	19820	ring finger protein, LIM dom	-1.542494	down	0.014538	0.139517	-2.600664	down	0.001141	0
Rnf123	84585	ring finger protein 123	-1.575475	down	0.016546	0.163377	-1.617001	down	0.017584	0.033721
Rnf146	68031	ring finger protein 146	1.758469	up	0.012306	0.560498	-1.895896	down	0.005535	0.0168605
Rnf165	225743	ring finger protein 165	-2.780879	down	0.018278	0.163377	36.989296	up	0.000152	0
Rnf187	108660	ring finger protein 187	-1.601325	down	0.014741	0.139517	-1.530024	down	0.004752	0.000207
Rnf213	672511	ring finger protein 213	-1.547482	down	0.008352	0.125233	-3.881388	down	0.001678	0.000207

Rnf220	66743	ring finger protein 220	1.764111	up	0.011909	0.560498	1.615534	up	0.002102	0.000207
Rnf24	51902	ring finger protein 24	-1.510452	down	0.011947	0.139517	-1.739791	down	0.011652	0.033721
Rnmt	67897	RNA (guanine-7-) methyltr	2.227094	up	0.000908	0.406743	-2.895035	down	0.003556	0.000207
Robo4	74144	roundabout guidance recep	-2.138893	down	0.035062	0.187117	2.619491	up	0.001294	0
Rpgrip1	77945	retinitis pigmentosa GTPase	1.657806	up	0.042173	0.627255	-2.064869	down	0.003662	0.000207
Rpn1	103963	ribophorin I	-1.85865	down	0.02374	0.163377	-8.478547	down	0.000439	0
Rprd2	75137	regulation of nuclear pre-m	-1.748569	down	0.014783	0.139517	-2.883428	down	0.000567	0
Rps13	68052	ribosomal protein S13	-1.573619	down	0.027263	0.187117	-1.874972	down	0.002911	0.000207
Rraga	68441	Ras-related GTP binding A	-1.694629	down	0.013864	0.139517	-1.78325	down	0.001415	0
Rtn3	20166	rhotekin	-1.539107	down	0.01463	0.139517	-1.793811	down	0.001607	0.000207
Rtn3	20168	reticulon 3	-2.530767	down	0.00396	0.11779	5.035208	up	0.000564	0
Rtn4	68585	reticulon 4	1.8449805	up	0.02422	0.5938765	-1.743108	down	0.005216	0.000207
Ryr1	20190	ryanodine receptor 1, skelet	-2.47945	down	0.001342	0.093579	3.07379	up	0.002314	0.000207
Sacm1l	83493	SAC1 suppressor of actin m	1.73338	up	0.028232	0.627255	-2.486092	down	0.009285	0.033721
Sall3	20689	sal-like 3 (Drosophila)	-2.140822	down	0.019705	0.163377	3.455183	up	0.003032	0.000207
Samd5	320825	sterile alpha motif domain c	-2.410104	down	0.044621	0.215669	4.586924	up	0.003071	0.000207
Satb1	20230	special AT-rich sequence bi	-2.585856	down	0.01117	0.139517	3.2005135	up	0.003992	0.0168605
Scrn1	69938	secernin 1	1.661368	up	0.023216	0.592628	1.610937	up	0.002278	0.000207
Scrt1	170729	scratch family zinc finger 1	-2.185359	down	0.003465	0.103486	1.681766	up	0.002935	0.000207
Scyl2	213326	SCY1-like 2 (S. cerevisiae)	1.570058	up	0.022385	0.592628	-1.821557	down	0.013734	0.033721
Sdcbp	53378	syndecan binding protein	-1.500268	down	0.026532	0.187117	-12.15173	down	0.002115	0.000207
Sdhaf3	71238	succinate dehydrogenase c	1.914558	up	0.028444	0.627255	-3.249332	down	0.00235	0.000207
Sec23a	20334	SEC23 homolog A, COPII co	1.548213	up	0.029863	0.627255	-2.466366	down	0.01567	0.033721
Selt	69227	selenoprotein T	-1.563726	down	0.033651	0.187117	-4.408658	down	0.001697	0.000207
Sema3g	218877	sema domain, immunoglob	-1.616069	down	0.007699	0.125233	-1.519405	down	0.009397	0.033721
Senp8	71599	SUMO/sentrin specific pept	-1.536953	down	0.041844	0.215669	-2.738007	down	0.002761	0.000207
Sepsecs	211006	Sep (O-phosphoserine) tRN	-1.555324	down	0.006171	0.11779	-2.149696	down	0.003481	0.000207
Sept6	56526	septin 6	1.754733	up	0.015267	0.592628	2.687251	up	0.000602	0
Serping1	12258	serine (or cysteine) peptida	1.570733	up	0.01582	0.592628	2.397149	up	0.003334	0.000207
Setd1b	208043	SET domain containing 1B	-2.038332	down	0.010257	0.1275067	-3.866751	down	0.003044	0.011309333
Setd6	66083	SET domain containing 6	-1.537757	down	0.001647	0.093579	-3.871546	down	0.00553	0.000207
Sez6	20370	seizure related gene 6	-1.716156	down	0.000858	0.092902	3.6462915	up	0.001789	0.0001035
Sft2d3	67158	SFT2 domain containing 3	-1.633235	down	0.006183	0.11779	-2.695193	down	0.022261	0.0168605
Sftpc	20389	surfactant associated protei	-1.600917	down	0.036222	0.215669	2.238523	up	0.001301	0
Sgce	20392	sarcoglycan, epsilon	1.615392	up	0.03779	0.627255	-2.117689	down	0.003285	0.000207
Sgsh	27029	N-sulfoglucosamine sulfoh	-1.524588	down	0.010334	0.125233	-3.58366	down	0.001694	0.000207
Sh3gl2	20404	SH3-domain GRB2-like 2	-1.875572	down	0.02783	0.187117	3.134357	up	0.004746	0.000207
Sh3rf2	269016	SH3 domain containing ring	-2.000623	down	0.006489	0.11779	-1.659185	down	0.013562	0.033721

Shisa9	72555	shisa family member 9	-1.614587	down	0.045504	0.215669	1.702102	up	0.002397	0.000207
Siae	22619	sialic acid acetyltransferase	1.52045	up	0.034276	0.627255	-4.558201	down	0.000574	0
Sin3b	20467	transcriptional regulator, SIN3	-1.779918	down	0.008359	0.125233	-3.735889	down	0.003589	0.000207
Sipa1l3	74206	signal-induced proliferation	-1.749258	down	0.030004	0.187117	-1.550991	down	0.04218	0.033721
Sirt4	75387	sirtuin 4	-1.820801	down	0.00585	0.11779	-4.108424	down	0.001774	0.000207
Skor1	207667	SKI family transcriptional co	-3.000115	down	0.004968	0.11779	1.541262	up	0.010837	0.033721
Slc17a6	140919	solute carrier family 17 (sod	2.179543	up	0.006434	0.511605	2.631192	up	0.017631	0.033721
Slc18a2	214084	solute carrier family 18 (ves	1.64941	up	0.032442	0.627255	2.375743	up	0.027467	0.033721
Slc22a4	30805	solute carrier family 22 (org	-1.567411	down	0.004633	0.11779	-5.103945	down	0.001004	0
Slc22a6	18399	solute carrier family 22 (org	-1.710947	down	0.007897	0.125233	3.058805	up	0.00065	0
Slc23a3	22626	solute carrier family 23 (nuc	-1.704932	down	0.021862	0.163377	-2.17499	down	0.00246	0.000207
Slc25a12	78830	solute carrier family 25 (mit	3.018798	up	0.004094	0.459167	1.973487	up	0.005096	0.000207
Slc25a3	18674	solute carrier family 25 (mit	1.573316	up	0.004043	0.459167	-1.610003	down	0.000456	0
Slc25a30	67554	solute carrier family 25, mer	-1.612137	down	0.013476	0.139517	-1.988829	down	0.026783	0.033721
Slc25a40	319653	solute carrier family 25, mer	-1.646956	down	0.004378	0.11779	-1.951372	down	0.008082	0.033721
Slc25a51	230125	solute carrier family 25, mer	2.389585	up	0.010118	0.560498	-7.044215	down	0.000609	0
Slc26a2	13521	solute carrier family 26 (sulf	-1.527939	down	0.012464	0.139517	-2.092132	down	0.003911	0.000207
Slc31a2	20530	solute carrier family 31, mer	1.502842	up	0.020563	0.592628	-1.575482	down	0.004698	0.000207
Slc32a1	22348	solute carrier family 32 (GAT	1.914535	up	0.047018	0.627255	3.947735	up	0.001369	0
Slc35d1	242585	solute carrier family 35 (UD	1.535536	up	0.021241	0.592628	-1.506645	down	0.037912	0.033721
Slc35f3	210027	solute carrier family 35, mer	-1.640022	down	0.007967	0.125233	4.701922	up	0.001002	0
Slc35f6	74919	solute carrier family 35, mer	-1.541093	down	0.010282	0.125233	-1.79723	down	0.008518	0.033721
Slc38a11	320106	solute carrier family 38, mer	-2.210224	down	0.006875	0.125233	2.930673	up	0.001886	0.000207
Slc38a9	268706	solute carrier family 38, mer	-1.50218	down	0.036974	0.215669	-3.083704	down	0.003013	0.0001035
Slc4a8	59033	solute carrier family 4 (anion	-1.8015425	down	0.022995	0.1667295	2.320711	up	0.000511	0
Slc6a20a	102680	solute carrier family 6 (neur	-2.087254	down	0.027555	0.187117	8.673273	up	0.000825	0
Slc6a7	240332	solute carrier family 6 (neur	-1.996649	down	0.001122	0.092902	4.5560775	up	0.001393	0.0001035
Slc8a1	20541	solute carrier family 8 (sodium	2.084507	up	0.031184	0.627255	3.067864	up	0.017243	0.033721
Slc9a2	226999	solute carrier family 9 (sodium	-2.327312	down	0.000281	0.069898	2.941197	up	0.00168	0.000207
Slc9a4	110895	solute carrier family 9 (sodium	1.69821	up	0.034494	0.627255	-2.713933	down	0.009387	0.033721
Slf1	105377	SMC5-SMC6 complex local	1.518139	up	0.042908	0.627255	-2.545393	down	0.003566	0.000207
Smcp	17235	sperm mitochondria-associ	2.241508	up	0.008542	0.511605	8.030486	up	0.001255	0
Smim10l1	381820	small integral membrane pr	1.898174	up	0.002698	0.459167	-12.91911	down	0.001994	0.000207
Smpd3	58994	sphingomyelin phosphodie	-1.848997	down	0.020778	0.163377	2.16104	up	0.000982	0
Smpd4	77626	sphingomyelin phosphodie	-1.504739	down	0.010578	0.139517	-1.734385	down	0.002911	0.000207
Smug1	71726	single-strand selective mon	1.744044	up	0.019697	0.592628	-2.450443	down	0.001356	0
Snhg11	319317	small nucleolar RNA host g	-2.916502	down	0.0244775	0.154624	3.0150608	up	0.003211	0.006827
Snrpn	20646	small nuclear ribonucleop	-1.584758	down	0.038617	0.215669	9.958264	up	0.000249	0

Sntg2	268534	syntrophin, gamma 2	-2.125434	down	0.003645	0.103486	3.535628	up	0.001948	0.000207
Soga3	67412	SOGA family member 3	-1.688926	down	0.026457	0.187117	3.400802	up	0.005375	0.033721
Sorcs2	81840	sortilin-related VPS10 dom	-1.553373	down	0.049082	0.215669	1.52257	up	0.003764	0.000207
Sorl1	20660	sortilin-related receptor, LD	-2.64475	down	0.008073	0.125233	4.06687	up	0.002333	0.000207
Sowaha	237761	sosondowah ankyrin repeat	-2.808755	down	0.011534	0.139517	7.2214325	up	0.002078	0.0001035
Sox10	20665	SRY (sex determining region)	-1.700211	down	0.001078	0.092902	2.408729	up	0.001727	0.000207
Sox13	20668	SRY (sex determining region)	-1.954587	down	0.03392	0.187117	1.875132	up	0.001816	0.000207
Sox18	20672	SRY (sex determining region)	-2.168833	down	0.036896	0.215669	2.363845	up	0.00153	0
Sox21	223227	SRY (sex determining region)	-1.690472	down	0.020644	0.163377	2.908093	up	0.003061	0.000207
Sp5	64406	trans-acting transcription fa	-2.105575	down	0.014821	0.139517	1.893058	up	0.029291	0.033721
Spint2	20733	serine protease inhibitor, Ku	-1.502004	down	0.015761	0.139517	-3.255344	down	0.001341	0
Spsb4	211949	splA/ryanodine receptor do	-1.5533595	down	0.0430275	0.215669	1.74582	up	0.006083	0.033721
Srebf2	20788	sterol regulatory element bl	-1.541524	down	0.019477	0.163377	-2.319275	down	0.001932	0.000138
Srgap1	117600	SLIT-ROBO Rho GTPase act	-1.797303	down	0.006614	0.11779	11.178222	up	0.016084	0.0168605
Srrm3	58212	serine/arginine repetitive m	-1.724856	down	0.047492	0.215669	2.7969195	up	0.020513	0.033721
St6galnac3	20447	ST6 (alpha-N-acetyl-neural	-2.495223	down	0.004523	0.11779	2.583122	up	0.003339	0.000207
St8sia1	20449	ST8 alpha-N-acetyl-neural	-1.631719	down	0.017935	0.163377	4.357155	up	0.000911	0
Stk25	59041	serine/threonine kinase 25	-1.562858	down	0.039856	0.215669	3.090147	up	0.001033	0
Stk33	117229	serine/threonine kinase 33	-2.220111	down	0.004913	0.11779	1.883085	up	0.012143	0.033721
Sucla2	20916	succinate-Coenzyme A liga	1.568234	up	0.013243	0.576563	-5.781871	down	0.001518	0.0001035
Surf6	20935	surfeit gene 6	-1.908048	down	0.027948	0.187117	-1.953256	down	0.001157	0
Syne1	64009	spectrin repeat containing,	1.542034	up	0.030032	0.627255	5.0450315	up	0.001872	0.0001035
Synj2bp	24071	synaptojanin 2 binding prot	1.994857	up	0.000826	0.406743	-2.263072	down	0.018115	0.016964
Sys1	66460	SYS1 Golgi-localized integr	-1.553633	down	0.011933	0.139517	-3.45219	down	0.00106	0
Syt12	171180	synaptotagmin XII	-1.65345	down	0.0354455	0.201393	2.539113	up	0.001086	0
Szt2	230676	seizure threshold 2	-1.646871	down	0.001825	0.093579	-2.072662	down	0.001029	0
Tarsl2	272396	threonyl-tRNA synthetase-	1.522081	up	0.016741	0.592628	-3.718504	down	0.003953	0.000207
Tbc1d30	74694	TBC1 domain family, memb	-2.647228	down	0.001339	0.093579	3.25	up	0.000416	0
Tbccd1	70573	TBCC domain containing 1	-1.600812	down	0.008633	0.125233	-4.954749	down	0.000594	0
Tcap	21393	titin-cap	-1.582183	down	0.037071	0.215669	2.585494	up	0.001529	0
Tceb3	27224	transcription elongation fac	6.935978	up	0.028743	0.627255	-2.112121	down	0.020071	0.033721
Tcerg1l	70571	transcription elongation rec	-1.775548	down	0.042938	0.215669	3.204361	up	0.016797	0.0168605
Tcf15	21407	transcription factor 15	-2.492956	down	0.016215	0.139517	2.10124	up	0.005166	0.033721
Tcf20	21411	transcription factor 20	-1.621387	down	0.015081	0.139517	-2.767229	down	0.00017	0
Tdo2	56720	tryptophan 2,3-dioxygenase	-1.799764	down	0.029875	0.187117	1.858054	up	0.040785	0.033721
Tecpr2	104859	tectonin beta-propeller rep	1.602078	up	0.032128	0.627255	-2.637226	down	0.00077	0
Tenm4	23966	teneurin transmembrane pr	-1.540455	down	0.021829	0.163377	-4.260721	down	0.0047	0.0168605
Thbs4	21828	thrombospondin 4	-2.027631	down	0.013959	0.139517	3.2721435	up	0.005377	0.0168605

Timm13	30055	translocase of inner mitoch	-1.635235	down	0.027576	0.187117	-2.058453	down	0.002304	0.0001035
Tln2	70549	talin 2	-2.002674	down	0.008925	0.125233	-3.542102	down	0.002098	0.000207
Tmcc3	319880	transmembrane and coiled	-2.841977	down	0.01167	0.139517	3.188045	up	0.002235	0.000207
Tmed9	67511	transmembrane emp24 pro	-1.769601	down	0.001839	0.093579	-3.065261	down	0.000061	0
Tmem114	74720	transmembrane protein 114	-1.584171	down	0.034434	0.187117	1.695845	up	0.002857	0.000207
Tmem132d	243274	transmembrane protein 132	-2.352516	down	0.034355	0.187117	4.022546	up	0.004262	0.000207
Tmem144	70652	transmembrane protein 144	-1.857972	down	0.008634	0.125233	-1.532522	down	0.008642	0.033721
Tmem150c	231503	transmembrane protein 150	-2.616403	down	0.02204	0.163377	5.442798	up	0.012363	0.016964
Tmem161b	72745	transmembrane protein 161	-2.129884	down	0.002547	0.103486	-2.446971	down	0.0027	0.000207
Tmem184c	234463	transmembrane protein 184	1.506685	up	0.030343	0.627255	-3.296424	down	0.001122	0
Tmem209	72649	transmembrane protein 209	1.572476	up	0.042405	0.627255	-1.651756	down	0.007848	0.016964
Tmem256	69186	transmembrane protein 256	-1.512981	down	0.006544	0.11779	-1.781963	down	0.006031	0.000207
Tmem59	56374	transmembrane protein 59	1.675313	up	0.000922	0.406743	-1.716457	down	0.001038	0.0001035
Tmem88	67020	transmembrane protein 88	-1.788588	down	0.004919	0.11779	-1.515794	down	0.005977	0.000207
Tmod2	50876	tropomodulin 2	-2.231434	down	0.031467	0.187117	4.4128597	up	0.002378	0.000138
Tmtc2	278279	transmembrane and tetratri	-1.599091	down	0.020686	0.163377	3.915295	up	0.000679	0
Tmx2	66958	thioredoxin-related transme	2.037671	up	0.003771	0.459167	-1.844813	down	0.003075	0.000207
Tnfsf12	21944	tumor necrosis factor (ligan	-1.866851	down	0.021574	0.163377	-1.731403	down	0.000652	0
Tox3	244579	TOX high mobility group bo	2.48962	up	0.001972	0.406743	4.596654	up	0.001076	0
Tprn	97031	taperin	-1.919834	down	0.001577	0.093579	-1.716729	down	0.001182	0
Trim2	80890	tripartite motif-containing 2	1.524474	up	0.030737	0.627255	-2.642147	down	0.014885	0.0168605
Trim25	217069	tripartite motif-containing 2	-1.836685	down	0.011436	0.139517	-2.156645	down	0.002959	0.000207
Trim8	93679	tripartite motif-containing 8	-1.668385	down	0.004776	0.11779	-4.658347	down	0.000715	0
Tsc1	64930	tuberous sclerosis 1	-1.826839	down	0.012157	0.139517	-1.975395	down	0.010824	0.0168605
Tsc22d3	14605	TSC22 domain family, mem	-1.576115	down	0.007772	0.1286535	-18.39346	down	0.000222	0
Tsga10	211484	testis specific 10	-2.144201	down	0.026142	0.187117	2.257944	up	0.004788	0.000207
Tspyl4	72480	TSPY-like 4	-2.982198	down	0.007733	0.125233	1.610646	up	0.005789	0.016964
Ttc28	209683	tetratricopeptide repeat do	-1.578614	down	0.016045	0.139517	-1.874957	down	0.002053	0.000207
Ttc30a1	78802	tetratricopeptide repeat do	1.88255	up	0.02585	0.627255	-1.741509	down	0.006638	0.033721
Ttll11	74410	tubulin tyrosine ligase-like 1	-1.584174	down	0.024503	0.163377	3.80086	up	0.000478	0
Ttyh3	78339	tweety family member 3	-1.628955	down	0.035642	0.215669	-4.388268	down	0.001578	0
Txndc9	98258	thioredoxin domain contain	-1.679065	down	0.027613	0.187117	-1.804877	down	0.017917	0.033721
Tyro3	22174	TYRO3 protein tyrosine kin	1.860795	up	0.042083	0.627255	1.693419	up	0.003552	0.000207
Ube2r2	67615	ubiquitin-conjugating enzy	-1.512387	down	0.010361	0.125233	-2.009696	down	0.012062	0.016964
Ubl3	24109	ubiquitin-like 3	1.503154	up	0.026258	0.627255	-22.21834	down	0.000449	0
Ubqln2	54609	ubiquilin 2	2.081837	up	0.009996	0.560498	-8.173464	down	0.002687	0.000207
Ubr2	224826	ubiquitin protein ligase E3 c	-1.834257	down	0.006058	0.11779	-4.199217	down	0.000385	0
Ubxn2b	68053	UBX domain protein 2B	1.558152	up	0.021701	0.592628	-3.871333	down	0.002038	0.000207

Uch15	56207	ubiquitin carboxyl-terminal	1.582378	up	0.004979	0.459167	-13.06738	down	0.000195	0
Ufsp1	70240	UFM1-specific peptidase 1	-2.056231	down	0.000956	0.092902	2.203062	up	0.000497	0
Ulk3	71742	unc-51-like kinase 3	-1.501305	down	0.0327	0.187117	-2.353539	down	0.000926	0
Unc13b	22249	unc-13 homolog B (C. eleg	2.085439	up	0.001761	0.406743	2.378567	up	0.001781	0.000207
Uso1	56041	USO1 vesicle docking facto	1.51226	up	0.019788	0.592628	-3.151299	down	0.002484	0.000207
Usp26	83563	ubiquitin specific peptidase	-2.524403	down	0.030903	0.187117	2.525641	up	0.02871	0.033721
Ust	338362	uronyl-2-sulfotransferase	-1.513707	down	0.015251	0.139517	-2.794997	down	0.001715	0.000207
Vapb	56491	vesicle-associated membra	-1.675358	down	0.036723	0.215669	1.664826	up	0.00895	0.033721
Vars2	68915	valyl-tRNA synthetase 2, mi	-1.579414	down	0.008055	0.125233	-1.576428	down	0.007968	0.0168605
Vma21	67048	VMA21 vacuolar H+-ATPas	-1.756421	down	0.011187	0.139517	-2.621114	down	0.002843	0.000207
Vps13b	666173	vacuolar protein sorting 13b	-1.62252	down	0.025252	0.187117	-6.487746	down	0.001312	0
Vps13c	320528	vacuolar protein sorting 13c	1.605725	up	0.013439	0.560498	2.548135	up	0.003798	0.000207
Vps13d	230895	vacuolar protein sorting 13d	-1.611919	down	0.025365	0.187117	1.798379	up	0.000999	0
Vps35	65114	VPS35 retromer complex co	1.538578	up	0.008622	0.511605	-2.084738	down	0.002817	0.000207
Vsir	74048	V-set immunoregulatory re	-1.513181	down	0.044068	0.215669	-3.513836	down	0.001707	0.000207
Wdr31	71354	WD repeat domain 31	-1.590203	down	0.024015	0.163377	-1.63331	down	0.006153	0.000207
Wdr59	319481	WD repeat domain 59	1.789001	up	0.036351	0.627255	-2.468102	down	0.001794	0.000207
Wdr86	269633	WD repeat domain 86	-2.33689	down	0.022164	0.163377	4.223933	up	0.001133	0
Wfdc2	67701	WAP four-disulfide core do	-1.621972	down	0.006078	0.11779	2.152962	up	0.001507	0
Xylb	102448	xylulokinase homolog (H. in	-1.585275	down	0.019192	0.163377	-1.815362	down	0.001709	0.0001035
Yjefn3	234365	YjeF N-terminal domain co	-1.64986	down	0.003153	0.103486	-1.676805	down	0.006322	0.033721
Zbtb7a	16969	zinc finger and BTB domain	-2.270573	down	0.007421	0.1215115	-2.208492	down	0.002023	0.000207
Zc3h6	78751	zinc finger CCCH type cont	-1.65844	down	0.01222	0.139517	2.418633	up	0.026523	0.033721
Zdhhc8	27801	zinc finger, DHHC domain c	-1.659349	down	0.003194	0.103486	3.88232	up	0.000675	0
Zfp125	22651	zinc finger protein 125	-1.767766	down	0.025802	0.187117	1.715789	up	0.023335	0.033721
Zfp212	232784	Zinc finger protein 212	-1.545288	down	0.014843	0.139517	-2.039993	down	0.001899	0.000207
Zfp39	22698	zinc finger protein 39	-1.761732	down	0.033833	0.187117	-2.062194	down	0.002784	0.000207
Zfp414	328801	zinc finger protein 414	-1.713055	down	0.000344	0.069898	-1.710629	down	0.000536	0
Zfp560	434377	zinc finger protein 560	-2.324004	down	0.002433	0.103486	-3.510425	down	0.000449	0
Zfp655	72611	zinc finger protein 655	1.597393	up	0.03334	0.627255	-2.656767	down	0.004694	0.000207
Zfp688	69234	zinc finger protein 688	-1.523936	down	0.038417	0.215669	-1.942909	down	0.000395	0
Zfp7	223669	zinc finger protein 7	-1.542365	down	0.033855	0.187117	-3.354382	down	0.000886	0
Zfp781	331188	zinc finger protein 781	2.03158	up	0.01783	0.592628	-2.152431	down	0.00508	0.000207
Zfp871	208292	zinc finger protein 871	-1.892117	down	0.021371	0.163377	-1.814381	down	0.010458	0.033721
Zfp933	242747	zinc finger protein 933	-1.844961	down	0.008815	0.125233	-2.192286	down	0.006616	0.033721
Zfp940	233057	zinc finger protein 940	-1.552596	down	0.04436	0.215669	-2.05244	down	0.001856	0.000207
Zfp952	240067	zinc finger protein 952	-2.525776	down	0.020236	0.163377	-3.172976	down	0.002328	0.000207
Zfp955a	77652	zinc finger protein 955A	1.596815	up	0.005853	0.511605	-5.887672	down	0.001826	0.000207

Zhx1	22770	zinc fingers and homeobox	-1.512609	down	0.042081	0.215669	-4.927741	down	0.001483	0
Zhx3	320799	zinc fingers and homeobox	-1.520716	down	0.022839	0.163377	1.99903	up	0.001125	0
Zic1	22771	zinc finger protein of the ce	-1.799535	down	0.005485	0.11779	38.275037	up	0.000218	0
Zik1	22775	zinc finger protein interacti	2.098132	up	0.003332	0.459167	-2.819836	down	0.002304	0.000207
Zmym6	100177	zinc finger, MYM-type 6	1.815665	up	0.025093	0.627255	1.96132	up	0.028585	0.033721
Zmynd10	114602	zinc finger, MYND domain	-1.731778	down	0.045351	0.215669	1.507772	up	0.003999	0.000207
Zpr1	22687	ZPR1 zinc finger	-1.654857	down	0.032107	0.187117	-1.793059	down	0.008531	0.033721
Zswim1	71971	zinc finger SWIM-type cont	-1.797189	down	0.011067	0.139517	-2.305435	down	0.002427	0.000207