

Transcripts Cluster Id	p (Corr)	p	Regulation	Fold Change	Log FC	Average expression B6	Average expression MRL	genesymbol	entrezgene	genesdescription
10504164	3.62E-04	2.47E-08	down	-7.25399	-2.85878	952.3529	6902.74	Ccl27a Gm20301	10	chemokine (C-C motif) ligand 27A predicted gene 13306
10504194	3.62E-04	2.51E-08	down	-7.25387	-2.85875	952.4516	6903.215	Ccl27a Gm20301	10	chemokine (C-C motif) ligand 27A predicted gene 13306
10365769	5.21E-04	1.54E-07	down	-6.80358	-2.76629	63.81808	435.2295	Hal	15109	histidine ammonia lyase
10419568	5.21E-04	8.75E-08	down	-13.6116	-3.76677	77.95621	1059.322	Ear11	93726	eosinophil-associated, ribonuclease A family, member 11
10439651	5.21E-04	1.69E-07	down	-9.17102	-3.19708	90.6681	829.2231	Cd200	17470	CD200 antigen
10448916	5.21E-04	1.32E-07	down	-12.3478	-3.62618	84.02135	1037.634	Tpsab1	17230	tryptase alpha/beta 1
10499935	5.21E-04	1.27E-07	up	4.207304	2.072896	1776.557	422.4203	Lce1i	76585	late cornified envelope 1l
10508800	5.21E-04	1.81E-07	up	8.671551	3.11629	923.8954	105.9365	LOC433762	433762	
10512315	5.21E-04	1.79E-07	down	-5.61311	-2.4888	446.4913	2499.513	Ccl27a Gm20301	10	chemokine (C-C motif) ligand 27A predicted gene 13306 RIKEN cDNA 1700008B15 gene predicted gene 2438
10573865	5.21E-04	1.80E-07	up	8.693842	3.119994	923.2285	105.5923	LOC433762	433762	
10421186	5.45E-04	2.08E-07	up	5.301896	2.406508	256.9292	48.33885	Gm10002	791405	predicted gene 10002
10510580	6.85E-04	3.04E-07	up	6.851568	2.776434	1118.219	162.3253	Tnfrsf9	21942	tumor necrosis factor receptor superfamily, member 9
10584572	6.85E-04	3.09E-07	up	3.334472	1.737458	11804.29	3540.624	Hspa8	15481	heat shock protein 8
10432897	7.78E-04	3.78E-07	down	-6.06776	-2.60116	291.5023	1763.882	Krt79	223917	keratin 79
10372648	8.03E-04	4.18E-07	down	-3.34918	-1.74381	805.7399	2696.809	Lyz2	17105	lysozyme 2
10415081	8.52E-04	5.71E-07	down	-3.86826	-1.95169	52.85723	204.3319	EG665955	665955	
10466712	8.52E-04	5.24E-07	up	10.3398	3.370137	688.0851	65.7795	Mamdc2	71738	MAM domain containing 2
10520121	8.52E-04	5.28E-07	down	-3.88186	-1.95675	53.01575	205.6533	EG665955	665955	
10578405	8.52E-04	5.91E-07	down	-3.87543	-1.95436	52.91244	204.8959	EG665955	665955	
10586076	8.52E-04	5.74E-07	down	-3.87857	-1.95552	52.89587	205.0295	EG665955	665955	
10490923	8.80E-04	6.53E-07	down	-4.4025	-2.13832	84.49819	373.2215	Car2	12349	carbonic anhydrase 2
10584435	8.80E-04	6.72E-07	down	-2.96773	-1.56936	768.2622	2278.745	Vwa5a	67776	von Willebrand factor A domain containing 5A
10469774	9.62E-04	7.68E-07	down	-2.93917	-1.55541	167.3408	492.0131	Il1f8	69677	interleukin 1 family, member 8
10407435	0.001035	8.93E-07	down	-8.57547	-3.10022	112.0744	965.7035	Akr1c18	105349	aldo-keto reductase family 1, member C18
10444780	0.001035	8.98E-07	up	7.377561	2.883144	3795.815	516.0573	H2-D1 H2-14964	14	histocompatibility 2, D region locus 1
10384458	0.001212	1.09E-06	down	-4.22495	-2.07893	191.7961	806.7989	Plek	56193	pleckstrin
10493905	0.0014	1.36E-06	up	7.394135	2.886381	547.5425	73.20709			
10541753	0.0014	1.32E-06	down	-3.43669	-1.78102	112.2873	386.5712	C5300280C	319352	RIKEN cDNA C530028021 gene
10352267	0.001448	1.51E-06	down	-2.46186	-1.29975	134.4251	330.8753	Lin9	72568	lin-9 homolog (C. elegans)
10551264	0.001448	1.51E-06	down	-10.8907	-3.44502	130.9563	1402.836	Cyp2b19	13090	cytochrome P450, family 2, subfamily b, polypeptide 19
10351504	0.001624	1.80E-06	up	3.073955	1.620096	1316.331	427.2271	EG665955	665955	
10550650	0.001624	1.80E-06	down	-2.73925	-1.45378	913.4891	2503.939	Ercc1	13870	excision repair cross-complementing rodent repair deficiency, complementation group 1
10499909	0.001709	2.05E-06	down	-2.54044	-1.34508	189.0926	480.2234	Lce6a	78382	late cornified envelope 6A
10502196	0.001709	2.04E-06	up	3.171693	1.665253	709.2014	223.7146	Rpl34	68436	ribosomal protein L34
10539135	0.001709	2.08E-06	up	2.572144	1.362971	1792.179	696.9216	Capg	12332	capping protein (actin filament), gelsolin-like
10592266	0.001743	2.18E-06	down	-2.43698	-1.2851	103.1609	251.3974	Slc37a2	56857	solute carrier family 37 (glycerol-3-phosphate transporter), member 2
10444459	0.001929	2.52E-06	down	-2.52987	-1.33906	135.6229	343.1412	Tnxb	81877	tenascin XB
10510221	0.001929	2.54E-06	up	2.786674	1.478544	196.1733	70.25885	LOC433762	433762	
10572591	0.002097	2.84E-06	down	-2.70263	-1.43437	151.3158	409.5728	Ocel1	77090	occludin/ELL domain containing 1
10598794	0.002176	3.02E-06	down	-3.6254	-1.85814	246.131	888.0271			
10528207	0.002193	3.12E-06	down	-2.43923	-1.28643	932.5074	2272.262	Cd36	12491	CD36 antigen
10425822	0.002209	3.22E-06	down	-3.886	-1.95828	148.4254	573.3731	Pnpla3	116939	patatin-like phospholipase domain containing 3
10459496	0.00254	3.88E-06	up	2.691487	1.428403	645.9241	239.4278	Ccbe1	320924	collagen and calcium binding EGF domains 1
10480275	0.00254	3.84E-06	down	-2.77114	-1.47048	208.1824	576.6094	Neb1	74103	nebulin
10580469	0.002656	4.15E-06	down	-2.27982	-1.18892	169.5831	386.9246	Cbln1	12404	cerebellin 1 precursor protein
10412394	0.002692	4.40E-06	down	-2.35465	-1.23551	237.0551	558.8286	Nnt	18115	nicotinamide nucleotide transhydrogenase
10502156	0.002692	4.48E-06	up	2.733702	1.450856	218.7733	80.15046	Ccdc109b	66815	coiled-coil domain containing 109B
10569618	0.002692	4.48E-06	down	-2.50014	-1.32201	100.0566	249.8848	Ano1	101772	anoctamin 1, calcium activated chloride channel
10489569	0.00278	4.92E-06	down	-2.05665	-1.0403	332.1082	683.0921	Pltp Ctsa	18830	19 phospholipid transfer protein cathepsin A
10493903	0.00278	4.73E-06	up	3.68495	1.881645	7004.433	1892.649	Lce3c Lce394060	54	late cornified envelope 3C late cornified envelope 3A late cornified envelope 3F late cornified envelope 3B
10568731	0.00278	4.84E-06	down	-4.49827	-2.16937	62.58948	279.1684			
10394776	0.002919	5.27E-06	up	2.179468	1.123976	739.0707	339.3437			
10565255	0.002985	5.49E-06	up	2.346432	1.230469	1256.794	535.5091	9930013L2	80982	RIKEN cDNA 9930013L23 gene
10573910	0.003034	5.68E-06	down	-2.32311	-1.21606	295.8131	687.9241	Irx5	54352	Iroquois related homeobox 5 (Drosophila)
10494271	0.00305	5.82E-06	down	-2.00353	-1.00255	376.6377	754.6416	Ctsa	13040	cathepsin S
10385325	0.003094	6.42E-06	up	3.059395	1.613246	573.4376	186.4922	Pttg1	30939	pituitary tumor-transforming gene 1
10418198	0.003094	6.44E-06	up	2.15996	1.111004	1932.175	894.1013	D14Ert444:66039	10	DNA segment, Chr 14, ERATO Doi 449, expressed predicted gene 10395

10439732	0.003094	6.29E-06	up	2.712126	1.439424	673.1559	249.063	Plcx2	433022 phosphatidylinositol-specific phospholipase C, X domain containing 2
10493900	0.003094	6.03E-06	up	3.65185	1.868627	8489.123	2323.472	Lce3c	94060 late cornified envelope 3C
10595803	0.003094	6.16E-06	up	4.226502	2.079464	456.3539	109.0878	Rnf7	19823 ring finger protein 7
10418185	0.003153	6.70E-06	up	2.145387	1.101238	1927.703	898.1673	D14Ertdd44 ⁶⁶⁰³⁹	10 DNA segment, Chr 14, ERATO Doi 449, expressed predicted gene 10395
10418210	0.003153	6.96E-06	up	2.161244	1.111862	1748.243	808.5557	D14Ertdd44 ⁶⁶⁰³⁹	10 DNA segment, Chr 14, ERATO Doi 449, expressed predicted gene 10395
10511353	0.003153	6.99E-06	down	-2.89644	-1.53428	195.1562	563.3076	Sdr16c6	242286 short chain dehydrogenase/reductase family 16C, member 6
10588043	0.003153	7.00E-06	down	-4.01007	-2.00363	415.6528	1665.519	Rbp2	19660 retinol binding protein 2, cellular
10384223	0.003258	7.36E-06	down	-1.992	-0.99422	1668.48	3323.577	Igfbp3	16009 insulin-like growth factor binding protein 3
10405566	0.003258	7.85E-06	down	-2.00196	-1.00141	168.4088	337.1515	AU042651	328258
10423049	0.003258	7.68E-06	down	-2.63398	-1.39725	76.48405	200.8523	Prlr	19116 prolactin receptor
10496438	0.003258	7.91E-06	down	-2.35386	-1.23503	177.366	418.3948	Adh1	11522 alcohol dehydrogenase 1 (class I)
10529485	0.003258	7.79E-06	down	-2.24609	-1.16742	380.2815	853.1252	Htra3	78558 HtrA serine peptidase 3
10571840	0.003258	7.56E-06	down	-2.51755	-1.33202	168.044	424.2941	Hpgd	15446 hydroxyprostaglandin dehydrogenase 15 (NAD)
10378787	0.003404	8.50E-06	down	-2.7735	-1.47171	233.7111	645.5581	Tusc5	237858 tumor suppressor candidate 5
10498584	0.003404	8.40E-06	down	-2.10584	-1.0744	73.32475	154.287	Rarres1	109222 retinoic acid receptor responder (tazarotene induced) 1
10469358	0.00344	8.71E-06	down	-2.16053	-1.11138	82.92863	179.1292	Mrc1	17533 mannose receptor, C type 1
10576152	0.003511	9.02E-06	down	-2.23522	-1.16042	849.6195	1902.431	Trappc2l	59005 trafficking protein particle complex 2-like
10375121	0.003581	9.32E-06	up	3.30874	1.726282	6145.405	1845.532	C530030PC	97730 RIKEN cDNA C530030P08 gene
10349968	0.003634	9.71E-06	down	-5.31941	-2.41127	176.8878	944.2849	Chi3l1	12654 chitinase 3-like 1
10439895	0.003634	9.67E-06	down	-1.90089	-0.92668	682.8355	1298.127	Alcam	11658 activated leukocyte cell adhesion molecule
10547807	0.003696	1.00E-05	down	-3.45797	-1.78993	284.8925	983.9302	Eno2	13807 enolase 2, gamma neuronal
10351491	0.003744	1.04E-05	down	-2.59534	-1.37593	560.5433	1449.524	Olfml2b	320078 olfactomedin-like 2B
10418193	0.003744	1.03E-05	up	1.906539	0.930956	252.574	132.4917	Plac9	211623 placenta specific 9
10350630	0.003778	1.06E-05	up	1.99464	0.996128	1079.418	540.9371	Fam129a	63913 family with sequence similarity 129, member A
10408693	0.003871	1.10E-05	down	-3.5509	-1.82819	120.1875	423.2235	F13a1	74145 coagulation factor XIII, A1 subunit
10400109	0.003873	1.21E-05	up	2.063753	1.04527	272.1617	131.9559	Zfp277	246196 zinc finger protein 277
10407467	0.003873	1.22E-05	up	2.785354	1.477861	244.422	88.16687	Akr1e1	56043 aldo-keto reductase family 1, member E1
10414262	0.003873	1.14E-05	down	-3.43632	-1.78087	66.4525	227.3367	Ear2	13587 eosinophil-associated, ribonuclease A family, member 2
10418180	0.003873	1.19E-05	up	1.884558	0.914227	261.1652	138.6005	Plac9	211623 placenta specific 9
10418205	0.003873	1.20E-05	up	1.883611	0.913501	260.5262	138.3314	Plac9	211623 placenta specific 9
10449356	0.003873	1.17E-05	down	-2.3117	-1.20895	252.8239	582.9562	Al413582	106672
10467153	0.003873	1.12E-05	down	-2.15986	-1.11094	84.22523	181.6505	Slc16a12	240638 solute carrier family 16 (monocarboxylic acid transporters), member 12
10522335	0.003873	1.22E-05	down	-2.76863	-1.46917	202.8869	563.0496	Atp10d	231287 ATPase, class V, type 10D
10587655	0.003873	1.19E-05	down	-1.92121	-0.94202	98.86994	189.9837	493042210	71640 RIKEN cDNA 4930422107 gene
10379866	0.003905	1.35E-05	down	-3.03124	-1.59991	122.1368	371.4811	Car4	12351 carbonic anhydrase 4
10395155	0.003905	1.31E-05	down	-2.08614	-1.06084	172.7677	360.331	Fam110c	104943 family with sequence similarity 110, member C
10400006	0.003905	1.34E-05	down	-2.07232	-1.05125	777.1364	1612.479	Ahr	11622 aryl-hydrocarbon receptor
10401114	0.003905	1.28E-05	down	-1.88035	-0.911	188.1519	353.7452	Rab15	104886 RAB15, member RAS oncogene family
10423030	0.003905	1.37E-05	down	-1.888	-0.91686	71.84295	135.5828	Prlr	19116 prolactin receptor
10428857	0.003905	1.25E-05	down	-2.40665	-1.26702	222.3626	534.5234	Mtss1	211401 metastasis suppressor 1
10499939	0.003905	1.36E-05	up	2.096769	1.068168	3370.577	1608.709	Gm7055	631101 predicted gene 7055
10508663	0.003905	1.35E-05	down	-2.16156	-1.11207	416.7069	899.0816	Laptm5	16792 lysosomal-associated protein transmembrane 5
10547056	0.003905	1.34E-05	up	1.828427	0.870603	1850.73	1012.228	Tmem40	94346 transmembrane protein 40
10601088	0.003905	1.29E-05	down	-2.88506	-1.5286	132.0234	382.3726	Gm9078	668271 predicted gene 9078
10375123	0.00401	1.42E-05	up	3.385641	1.759429	5371.39	1576.11	C530030PC	97730 RIKEN cDNA C530030P08 gene
10466200	0.004156	1.49E-05	down	-2.62823	-1.39409	76.86017	200.9741	Ms4a7	109225 membrane-spanning 4-domains, subfamily A, member 7
10446739	0.004195	1.51E-05	down	-2.17353	-1.12004	662.5613	1437.482	Clp4	78785 CAP-GLY domain containing linker protein family, member 4
10346448	0.004209	1.55E-05	down	-2.09627	-1.06782	74.53879	155.9661	Aox4	71872 aldehyde oxidase 4
10446713	0.004209	1.54E-05	down	-2.29215	-1.1967	323.3979	739.2461	Snord53	1E+08 small nucleolar RNA, C/D box 53
10463844	0.00432	1.60E-05	down	-3.41496	-1.77187	141.6899	485.9161	Gsto2	68214 glutathione S-transferase omega 2
10406581	0.004582	1.73E-05	up	2.25076	1.170412	252.0425	111.6388	Dhfr[Msh3 13361]	17 dihydrofolate reductase mutS homolog 3 (E. coli)
10440522	0.004582	1.75E-05	down	-1.91109	-0.9344	2058.874	3932.124	Adamts1	11504 a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1
10583112	0.004582	1.74E-05	down	-2.24447	-1.16638	93.54936	209.3619	Mmp27	234911 matrix metallopeptidase 27
10514347	0.004626	1.78E-05	down	-1.77751	-0.82986	245.5999	436.545	Cdkn2b	12579 cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
10530029	0.004674	1.82E-05	up	1.902078	0.927576	680.5145	357.6835	Lgi2	246316 leucine-rich repeat LGI family, member 2
10514956	0.004728	1.87E-05	down	-2.10903	-1.07658	147.5996	310.6384	Scp2	20280 sterol carrier protein 2, liver
10555197	0.004728	1.87E-05	down	-1.91627	-0.9383	299.1388	572.7074	Mtap6	17760 microtubule-associated protein 6
10460468	0.004758	1.90E-05	down	-2.01935	-1.01389	344.9997	697.6071	Ctsf	56464 cathepsin F
10455873	0.00482	1.98E-05	down	-2.0785	-1.05554	478.4523	992.4663	Slc12a2	20496 solute carrier family 12, member 2
10507059	0.00482	1.97E-05	down	-2.41544	-1.27228	91.35607	221.6637	Skint7	328505 selection and upkeep of intraepithelial T cells 7
10511345	0.00482	1.99E-05	down	-3.88286	-1.95712	75.00573	289.1764	Sdr16c5	242285 short chain dehydrogenase/reductase family 16C, member 5
10515220	0.00482	1.94E-05	down	-2.85054	-1.51124	184.6335	523.5322	Faah	14073 fatty acid amide hydrolase
10427035	0.004823	2.04E-05	down	-2.27373	-1.18506	3029.524	6877.129	Nr4a1	15370 nuclear receptor subfamily 4, group A, member 1
10442580	0.004823	2.02E-05	up	1.818916	0.863079	7054.224	3880.123	Rps2	16898 ribosomal protein S2
10506571	0.004823	2.04E-05	down	-1.84672	-0.88497	1855.93	3429.395	Dhcr24	74754 24-dehydrocholesterol reductase

10497451	0.004824	2.06E-05	down	-3.39437	-1.76314	128.6757	440.8759	Cpa3	12873	carboxypeptidase A3, mast cell
10400941	0.004933	2.15E-05	down	-2.23629	-1.16111	570.5282	1275.607	Dhrs7	66375	dehydrogenase/reductase (SDR family) member 7
10409579	0.004933	2.15E-05	down	-2.04766	-1.03397	616.2372	1259.19	Cxcl14	57266	chemokine (C-X-C motif) ligand 14
10498168	0.004933	2.16E-05	up	1.734574	0.794582	821.5424	473.6325	Exosc8	69639	exosome component 8
10531724	0.004933	2.17E-05	up	2.295517	1.198819	197.5746	86.03823	Plac8	231507	placenta-specific 8
10394119	0.004962	2.20E-05	down	-1.86357	-0.89807	2057.702	3836.884	Zfp750	319530	zinc finger protein 750
10399588	0.005004	2.24E-05	up	1.761741	0.817002	104.8701	59.51827	Zfp125	22651	zinc finger protein 125
10399360	0.005005	2.29E-05	down	-1.86447	-0.89877	930.5606	1734.875	Rhob	11852	ras homolog gene family, member B
10423825	0.005005	2.31E-05	down	-1.83208	-0.87349	475.2285	870.7232	Fzd6	14368	frizzled homolog 6 (Drosophila)
10573430	0.005005	2.29E-05	up	1.820369	0.864231	590.3523	324.5133	Gadd45gip	102060	1 growth arrest and DNA-damage-inducible, gamma interacting protein 1 RAD23a homolog (S. cerevisiae)
10603066	0.005005	2.31E-05	down	-1.83088	-0.87254	50.07396	91.74189	Ace2	70008	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
10578264	0.005057	2.35E-05	down	-2.01551	-1.01115	242.4615	489.5801	Msr1	20288	macrophage scavenger receptor 1
10544573	0.005061	2.39E-05	down	-1.7606	-0.81607	4177.509	7356.915	Rarres2 Lrn	71660	24 retinoic acid receptor responder (tazarotene induced) 2 leucine rich repeat containing 61
10550487	0.005061	2.38E-05	down	-3.03212	-1.60033	309.8798	932.5256	Mill1	266815	MHC I like leukocyte 1
10444824	0.005399	2.57E-05	up	5.099031	2.350223	942.3573	189.1093	H2-Q6 061	110557	6 histocompatibility 2, Q region locus 6 RIKEN cDNA O610037M15 gene
10355500	0.005415	2.59E-05	up	2.488041	1.31501	1395.901	561.3208	lgbfp5	16011	insulin-like growth factor binding protein 5
10373834	0.005548	2.68E-05	down	-1.70026	-0.76575	101.8525	173.1714	Sec14l4	103655	SEC14-like 4 (S. cerevisiae)
10446282	0.005585	2.77E-05	down	-1.8742	-0.90627	88.31159	165.3256	Emr1	13733	EGF-like module containing, mucin-like, hormone receptor-like sequence 1
10475324	0.005585	2.77E-05	down	-2.11991	-1.08401	282.5459	599.888	Ckmt1	12716	creatine kinase, mitochondrial 1, ubiquitous
10552480	0.005585	2.74E-05	down	-2.22023	-1.15071	174.6504	387.3779	Klk11	56538	kallikrein related-peptidase 11
10583071	0.005585	2.76E-05	up	1.837143	0.877464	6653.564	3618.224	Mmp3	17392	matrix metalloproteinase 3
10472155	0.005613	2.81E-05	down	-2.64584	-1.40373	64.37485	171.1537	Kcnj3	16519	potassium inwardly-rectifying channel, subfamily J, member 3
10595840	0.005613	2.82E-05	down	-1.88066	-0.91124	133.052	250.5586	Acpl2	235534	acid phosphatase-like 2
10406663	0.005615	2.86E-05	up	1.804928	0.851941	783.9442	434.4965	Arsb	11881	arylsulfatase B
10510399	0.005615	2.85E-05	down	-1.71744	-0.78026	66.01973	113.3901	Masp2 Tar	17175	23 mannan-binding lectin serine peptidase 2 TAR DNA binding protein
10442932	0.005635	2.89E-05	down	-1.87976	-0.91055	101.4668	190.6235	Tmem8	60455	transmembrane protein 8 (five membrane-spanning domains)
10512574	0.005667	2.95E-05	up	1.796661	0.845318	417.9823	232.5192	Gba2	230101	glucosidase beta 2
10583090	0.005667	2.94E-05	up	2.52622	1.33698	1379.206	547.9342	Mmp10	17384	matrix metalloproteinase 10
10571344	0.0057	2.99E-05	down	-1.98629	-0.99007	436.2532	867.9384	D8Erdt82e	244418	DNA segment, Chr 8, ERATO Doi 82, expressed
10360070	0.005812	3.09E-05	down	-1.94653	-0.96091	316.5116	615.1166	Fcer1g	14127	Fc receptor, IgE, high affinity I, gamma polypeptide
10491699	0.005812	3.07E-05	up	2.441263	1.287628	616.4712	253.6807	Fgf2 LOC11	14173	10 fibroblast growth factor 2 similar to Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin)
10516484	0.005931	3.19E-05	down	-2.04485	-1.032	976.7542	2002.525	Gjb3	14620	gap junction protein, beta 3
10588701	0.005931	3.19E-05	down	-1.71306	-0.77657	183.5216	314.2846	Hyal3	109685	hyaluronoglucosaminidase 3
10474129	0.005996	3.25E-05	down	-1.66953	-0.73944	234.1667	390.9566	Pamr1	210622	peptidase domain containing associated with muscle regeneration 1
10368638	0.006067	3.33E-05	down	-2.21098	-1.14469	264.1396	582.3003	Fam26e	103511	family with sequence similarity 26, member E
10522411	0.006067	3.32E-05	down	-2.21285	-1.14591	562.8341	1241.325	C130090K2	231293	RIKEN cDNA C130090K23 gene
10445061	0.006202	3.42E-05	up	1.887211	0.916255	5148.043	2726.96	Rnf39	386454	ring finger protein 39
10530986	0.006403	3.56E-05	down	-2.7473	-1.45801	74.10137	203.1628	9930032O2	320454	RIKEN cDNA 9930032O22 gene
10392834	0.006676	3.75E-05	down	-1.66032	-0.73146	188.6492	313.2308	OTTMUSG100043125	predicted gene, OTTMUSG00000003606	CMRF-35-like molecule 3
10398859	0.006676	3.76E-05	up	1.951176	0.964344	875.1865	447.7408	Adssl1	11565	adenylosuccinate synthetase like 1
10533720	0.006676	3.78E-05	down	-1.9574	-0.96894	279.8764	547.2818	Niacr1	80885	niacin receptor 1
10588283	0.00681	3.92E-05	up	2.042224	1.030141	189.1907	92.6085	Rab6b	270192	RAB6B, member RAS oncogene family
10590320	0.00681	3.91E-05	up	1.707149	0.771589	279.4569	163.6502	Rpl14	67115	ribosomal protein L14
10595871	0.00681	3.92E-05	up	1.848965	0.886718	696.6336	376.4556	Cln2	64085	calsyntenin 2
10345807	0.007112	4.12E-05	down	-2.15285	-1.10625	79.40665	171.6904	Il18r1	16182	interleukin 18 receptor 1
10376269	0.007201	4.22E-05	up	1.650333	0.722757	434.7251	263.4162	Galnt10	171212	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10
10575120	0.007201	4.20E-05	down	-1.64341	-0.71669	638.1719	1048.888	Sntb2	20650	syntrophin, basic 2
10550394	0.007444	4.39E-05	down	-1.62854	-0.70358	709.6094	1155.583	Ptgir	19222	prostaglandin I receptor (IP)
10494016	0.007524	4.47E-05	down	-2.00166	-1.00119	59.59626	119.0209	Them5	66198	thioesterase superfamily member 5
10440993	0.007615	4.57E-05	down	-1.79803	-0.84641	424.2643	762.1209	Rcan1	54720	regulator of calcineurin 1
10592705	0.007615	4.56E-05	down	-3.29718	-1.72123	169.2217	552.5587	Pou2f3	18988	POU domain, class 2, transcription factor 3
10566366	0.007622	4.60E-05	up	1.823359	0.866599	90.02922	49.29189	Al451617	209387	
10440344	0.007638	4.64E-05	down	-2.12113	-1.08484	243.6154	514.4726	Robo2	268902	roundabout homolog 2 (Drosophila)
10392825	0.007674	4.80E-05	down	-1.70111	-0.76648	209.4769	356.1437	OTTMUSG100043125	predicted gene, OTTMUSG00000003606	CMRF-35-like molecule 3
10404439	0.007674	4.97E-05	down	-1.66292	-0.73372	107.9551	179.5386	Serpinh9b	20706	serine (or cysteine) peptidase inhibitor, clade B, member 9b
10432661	0.007674	4.98E-05	down	-1.86076	-0.89589	98.68674	183.7936	Galnt6	207839	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6
10447594	0.007674	4.97E-05	down	-1.64085	-0.71444	4892.648	8025.948	Dynl1	21648	dynein light chain Tctex-type 1
10461721	0.007674	4.90E-05	down	-1.86509	-0.89925	130.1513	242.5767	Mpeg1	17476	macrophage expressed gene 1
10472050	0.007674	4.94E-05	down	-2.22088	-1.15113	1120.505	2479.1	Tnfrsf6	21930	tumor necrosis factor alpha induced protein 6
10472538	0.007674	4.96E-05	down	-1.67126	-0.74094	66.85464	111.6846	Dhrs9	241452	dehydrogenase/reductase (SDR family) member 9
10498972	0.007674	4.71E-05	down	-1.93738	-0.9541	74.91068	145.2884	Rbm46	633285	RNA binding motif protein 46
10502805	0.007674	4.82E-05	down	-1.64739	-0.72018	739.0151	1217.091	Ptgir	19220	prostaglandin F receptor
10520452	0.007674	4.94E-05	down	-2.04513	-1.03219	524.7877	1069.237	Il6	16193	interleukin 6
10542395	0.007674	4.80E-05	up	1.834332	0.875255	211.7689	115.5512	Atf7ip	54343	activating transcription factor 7 interacting protein
10595953	0.007674	4.73E-05	up	2.338262	1.225437	908.3716	388.2633	Esyt3	272636	extended synaptotagmin-like protein 3

10440238	0.007816	5.13E-05	up	2.105888	1.074429	588.9935	279.1187	Nsun3	106338 NOL1/NOP2/Sun domain family member 3
10601588	0.007816	5.11E-05	up	1.625408	0.700802	78.97044	48.59161	3110007F1 73061 62 RIKEN cDNA 3110007F17 gene predicted gene 6604 predicted gene 5167 predicted gene 2411	
10379535	0.007862	5.18E-05	down	-2.07378	-1.05226	112.9625	233.8982	Ccl8	20307 chemokine (C-C motif) ligand 8
10411668	0.00792	5.27E-05	down	-1.70728	-0.7717	203.838	347.8715	Ocln	18260 occludin
10499927	0.00792	5.28E-05	up	2.146014	1.101659	415.2496	193.2898	Lce1f	67828 late cornified envelope 1F
10397346	0.007953	5.41E-05	down	-2.54482	-1.34756	377.8899	966.3014	Fos	14281 FBJ osteosarcoma oncogene
10481627	0.007953	5.33E-05	up	1.62709	0.702294	6663.799	4096.515	Lcn2	16819 lipocalin 2
10512279	0.007953	5.40E-05	down	-3.31681	-1.7298	274.556	897.5313	Cntfr	12804 ciliary neurotrophic factor receptor
10593024	0.007953	5.38E-05	down	-1.96121	-0.97174	119.7479	235.5267	Cd3e	12501 CD3 antigen, epsilon polypeptide
10502881	0.0081	5.54E-05	down	-1.61657	-0.69293	87.08275	140.7935	St6galnac5	26938 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5
10437151	0.008111	5.62E-05	down	-1.84867	-0.88649	163.04	301.897	Kcnj15	16516 potassium inwardly-rectifying channel, subfamily J, member 15
10502949	0.008111	5.63E-05	down	-1.7811	-0.83277	265.714	473.3729		
10573939	0.008111	5.63E-05	down	-1.83149	-0.87302	644.7298	1178.43	Lpcat2	270084 lysophosphatidylcholine acyltransferase 2
10580160	0.008129	5.67E-05	up	1.702585	0.767727	451.3322	265.3057	Mri1	67873 methylthioribose-1-phosphate isomerase homolog (S. cerevisiae)
10500736	0.008386	5.88E-05	down	-1.65466	-0.72654	425.6407	703.9056	Vangl1	229658 vang-like 1 (van gogh, Drosophila)
10511779	0.008402	5.92E-05	down	-1.8001	-0.84808	109.5943	197.2245	Atp6v0d2	242341 ATPase, H+ transporting, lysosomal V0 subunit D2
10530615	0.008441	5.98E-05	down	-1.94246	-0.95788	119.8516	232.2446	Ociad2	433904 OCIA domain containing 2
10399555	0.008573	6.16E-05	up	2.107115	1.075269	155.285	73.32503	Kcnf1	382571 potassium voltage-gated channel, subfamily F, member 1
10462623	0.008573	6.16E-05	up	2.129386	1.090437	130.9111	61.16066	Ifit1	15957 interferon-induced protein with tetratricopeptide repeats 1
10548785	0.008573	6.11E-05	down	-1.63458	-0.70892	4904.553	8014.281	Dynl1t	21648 dynein light chain Tctex-type 1
10358476	0.008633	6.28E-05	down	-2.38377	-1.25324	71.85813	170.4056	Prg4	96875 proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone protein)
10359235	0.008633	6.25E-05	down	-1.61225	-0.68908	265.5006	428.1159	Rasal2	226525 RAS protein activator like 2
10452648	0.008633	6.34E-05	down	-1.62603	-0.70136	612.7522	996.8001	Emilin2	246707 elastin microfibril interfacer 2
10551883	0.008633	6.35E-05	down	-1.62975	-0.70465	299.0322	487.5367	Tyrobp	22177 TYRO protein tyrosine kinase binding protein
10554800	0.008633	6.33E-05	down	-1.63955	-0.7133	165.4917	271.4708	Rab38	72433 RAB38, member of RAS oncogene family
10547657	0.008646	6.39E-05	down	-2.0608	-1.0432	393.3294	810.4061	C3ar1	12267 complement component 3a receptor 1
10373702	0.008838	6.56E-05	up	1.610557	0.68756	323.4736	200.9123	Pisd-ps1 Pi 236604 6 phosphatidylserine decarboxylase, pseudogene 1 phosphatidylserine decarboxylase, pseudogene 3	
10464084	0.008905	6.64E-05	down	-1.61002	-0.68708	581.2135	935.544	Tcf7l2	21416 transcription factor 7-like 2, T-cell specific, HMG-box
10411082	0.008909	6.68E-05	down	-2.06651	-1.0472	1521.534	3157.135	Thbs4	21828 thrombospondin 4
10414065	0.008911	6.74E-05	down	-1.61337	-0.69008	2396.458	3866.108	Anxa8	11752 annexin A8
10428089	0.008911	6.73E-05	down	-3.07592	-1.62102	162.7751	493.0064	Nipal2	223473 NIPA-like domain containing 2
10584604	0.009139	6.95E-05	down	-1.58605	-0.66544	4806.309	7621.479	Trim29	72169 tripartite motif-containing 29
10347036	0.00916	6.99E-05	down	-2.08182	-1.05785	90.65149	187.8066	Mtap2	17756 microtubule-associated protein 2
10513008	0.009204	7.06E-05	down	-1.63266	-0.70722	877.5335	1433.348	Klf4	16600 Kruppel-like factor 4 (gut)
10439881	0.009292	7.22E-05	up	2.455063	1.29576	592.1352	241.8256	5330426P1	68190 RIKEN cDNA 5330426P16 gene
10458960	0.009292	7.17E-05	up	1.582537	0.66224	774.4233	489.456	Aldh7a1	110695 aldehyde dehydrogenase family 7, member A1
10591806	0.009292	7.22E-05	up	1.578221	0.658299	338.9061	214.778	rp9	55934 retinitis pigmentosa 9 (human)
10405918	0.009455	7.38E-05	up	2.162656	1.112804	233.0924	108.0428	Rsl1	380855 regulator of sex limited protein 1
10411454	0.009531	7.51E-05	down	-2.20589	-1.14136	407.3042	898.1632	Sec61b	66212 Sec61 beta subunit
10476759	0.009531	7.50E-05	up	1.567507	0.648472	1180.347	752.9248	Rin2	74030 Ras and Rab interactor 2
10406672	0.009699	7.71E-05	up	1.667782	0.737931	471.5566	282.9103	Arsb	11881 arylsulfatase B
10458709	0.009699	7.68E-05	down	-3.45627	-1.78921	219.8928	751.1387	Gm94	225443 predicted gene 94
10478066	0.009699	7.74E-05	up	1.661343	0.73235	110.935	66.72238	Shng11	319317 small nucleolar RNA host gene 11 (non-protein coding)
10523182	0.009929	7.96E-05	down	-2.42704	-1.2792	548.1796	1336.971	Areg	11839 amphiregulin
10359861	0.010007	8.47E-05	down	-1.60692	-0.6843	203.1434	326.348	Mgst3	66447 microsomal glutathione S-transferase 3
10377473	0.010007	8.14E-05	up	1.973021	0.980406	535.3527	270.5134	Aloxe3	23801 arachidonate lipoxygenase 3
10395466	0.010007	8.51E-05	up	1.654384	0.726294	937.3113	566.3429	Dock4	238130 dedicator of cytokinesis 4
10407387	0.010007	8.45E-05	up	1.773209	0.826363	418.4966	236.0228	Gm7120	633640 predicted gene 7120
10409278	0.010007	8.41E-05	down	-1.63383	-0.70825	892.934	1459.923	Nfil3	18030 nuclear factor, interleukin 3, regulated
10424370	0.010007	8.09E-05	down	-1.74742	-0.80523	392.8605	685.219	Trib1	211770 tribbles homolog 1 (Drosophila)
10449644	0.010007	8.38E-05	down	-1.7423	-0.80099	976.2949	1700.468	Glo1	109801 glyoxalase 1
10471675	0.010007	8.08E-05	down	-1.7501	-0.80744	1200.803	2101.24	Glo1	109801 glyoxalase 1
10504838	0.010007	8.32E-05	down	-2.82043	-1.49592	409.2011	1138.705	Nr4a3	18124 nuclear receptor subfamily 4, group A, member 3
10545255	0.010007	8.48E-05	down	-1.68824	-0.75552	168.0154	283.2716	Rpia	19895 ribose 5-phosphate isomerase A
10555389	0.010007	8.21E-05	down	-1.84027	-0.87992	2391.857	4388.869	Ucp2	22228 uncoupling protein 2 (mitochondrial, proton carrier)
10586614	0.010007	8.34E-05	down	-1.72041	-0.78276	240.7612	414.002	Fam148b	75697 family with sequence similarity 148, member B
10596303	0.010007	8.43E-05	down	-3.85245	-1.94578	645.6599	2422.788	Acpp	56318 acid phosphatase, prostate
10598175	0.010007	8.21E-05	down	-2.31728	-1.21243	71.31818	166.4832	Ear10 Ear2 93725 13 eosinophil-associated, ribonuclease A family, member 10 eosinophil-associated, ribonuclease A family, member 1	
10524089	0.010053	8.58E-05	up	1.971357	0.979189	520.4571	263.9837	Plcx1	403178 phosphatidylinositol-specific phospholipase C, X domain containing 1
10414433	0.010155	8.70E-05	up	1.812578	0.858043	568.398	312.8879	6720456H2	218989 RIKEN cDNA 6720456H20 gene
10383194	0.010262	8.87E-05	up	1.696075	0.7622	584.6686	345.1004		
10579987	0.010262	8.87E-05	up	1.610012	0.687071	235.0775	145.9259	Scoc	56367 short coiled-coil protein
10499924	0.010278	8.95E-05	up	2.154967	1.107666	4282.617	1995.974	Lce1e	68694 late cornified envelope 1E
10526087	0.010278	8.93E-05	up	1.63102	0.705775	486.4675	298.1942	Sumf2	67902 sulfatase modifying factor 2
10552140	0.010327	9.03E-05	down	-1.76256	-0.81767	460.6234	811.4	Cebp2	12606 CCAAT/enhancer binding protein (C/EBP), alpha

10565775	0.010383	9.12E-05	down	-1.7251	-0.78668	950.1238	1636.638	Dgat2	67800 diacylglycerol O-acyltransferase 2
10359917	0.010751	9.54E-05	up	1.751267	0.808399	1152.487	657.2196	Hsd17b7	15490 hydroxysteroid (17-beta) dehydrogenase 7
10377364	0.010751	9.48E-05	up	1.577405	0.657553	600.905	381.0722	Rnf222	320040 ring finger protein 222
10527638	0.010751	9.57E-05	down	-1.90098	-0.92674	120.3538	229.0753	Alox5ap	11690 arachidonate 5-lipoxygenase activating protein
10569870	0.010751	9.59E-05	down	-2.00214	-1.00154	134.6318	269.7759	Retn	57264 resistin
10347888	0.010788	9.70E-05	down	-1.86869	-0.90203	147.9504	275.4756	Ccl20	20297 chemokine (C-C motif) ligand 20
10526514	0.010788	9.69E-05	down	-1.7095	-0.77358	217.3209	370.8098	Cldn15	60363 claudin 15
10491300	0.010959	9.89E-05	down	-1.53134	-0.61479	565.6836	866.2016	Skil	20482 SKI-like
10521038	0.011013	9.98E-05	down	-1.59317	-0.6719	117.1989	186.5882	Slc5a1	20537 solute carrier family 5 (sodium/glucose cotransporter), member 1
10522467	0.011155	1.01E-04	up	1.537733	0.620805	212.507	138.2205	Rasl11b	68939 RAS-like, family 11, member B
10383196	0.011444	1.05E-04	up	1.716059	0.779099	317.3258	184.6677		
10391378	0.011444	1.06E-04	up	2.226624	1.154858	682.7758	307.4733	Ezh1	14055 enhancer of zeste homolog 1 (Drosophila)
10406017	0.011444	1.05E-04	down	-1.64164	-0.71514	102.3395	168.1862	Irx4	50916 Iroquois related homeobox 4 (Drosophila)
10453423	0.011444	1.05E-04	down	-1.70679	-0.77128	90.21242	153.8215	Gm10309	1E+08 predicted gene 10309
10414514	0.011446	1.06E-04	up	1.627024	0.702235	706.6363	434.2158	Pnp1	18950 purine-nucleoside phosphorylase 1
10377439	0.011452	1.07E-04	down	-1.61764	-0.69389	540.1254	874.1057	Per1	18626 period homolog 1 (Drosophila)
10566026	0.011452	1.07E-04	down	-1.54869	-0.63105	84.2837	130.566	Folr2	14276 folate receptor 2 (fetal)
10601595	0.011452	1.07E-04	up	1.560167	0.641701	66.16308	42.41514	3110007F173061	62 RIKEN cDNA 3110007F17 gene predicted gene 6604 predicted gene 5167 predicted gene 2411
10358038	0.011502	1.09E-04	up	1.689613	0.756692	421.5963	249.2067	Rnpep	215615 arginyl aminopeptidase (aminopeptidase B)
10369647	0.011502	1.08E-04	down	-1.58051	-0.66039	304.1973	481.1144	Ddx50	94213 DEAD (Asp-Glu-Ala-Asp) box polypeptide 50
10452202	0.011743	1.11E-04	down	-2.00287	-1.00207	91.06202	182.6874	Acer1	171168 alkaline ceramidase 1
10474467	0.0118	1.12E-04	down	-1.60048	-0.6785	101.3842	162.2083	Muc15	269328 mucin 15
10359266	0.011852	1.13E-04	down	-2.28199	-1.19029	110.8865	250.7852	Pappa2	23850 pappalysin 2
10539238	0.011862	1.14E-04	down	-1.54512	-0.62772	335.9209	518.9041	Fam176a	232146 family with sequence similarity 176, member A
10572449	0.011862	1.14E-04	up	1.578412	0.658474	1315.888	833.0855	Lsm4	50783 LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)
10517236	0.011934	1.15E-04	up	1.777157	0.829572	430.0887	241.9457	Zfp593	68040 zinc finger protein 593
10516266	0.012	1.16E-04	down	-1.7041	-0.76901	621.145	1058.655	Zc3h12a	230738 zinc finger CCCH type containing 12A
10575153	0.012	1.17E-04	up	1.630202	0.705051	1086.551	665.9782	Cyb5b	66427 cytochrome b5 type B
10488020	0.012006	1.17E-04	down	-1.88024	-0.91092	859.0883	1616.045	Tmx4	52837 thioredoxin-related transmembrane protein 4
10572693	0.012006	1.17E-04	down	-1.91975	-0.94092	278.8494	533.0833	Jak3 Insl3	16453 16 Janus kinase 3 insulin-like 3
10537785	0.012084	1.19E-04	down	-1.81126	-0.85699	91.37072	165.4282	Tas2r143	387514 taste receptor, type 2, member 143
10429555	0.012107	1.19E-04	up	1.685758	0.753398	118.2113	70.006	201010910I	67038 RIKEN cDNA 201010910I gene
10402554	0.012164	1.21E-04	down	-1.58215	-0.66189	406.4121	642.6362	Bcl11b	58208 B-cell leukemia/lymphoma 11B
10575926	0.012164	1.21E-04	down	-1.51669	-0.60092	211.154	320.2686	Atp2c2	69047 ATPase, Ca++ transporting, type 2C, member 2
10519717	0.012427	1.24E-04	down	-1.8432	-0.88221	227.0757	419.2572	Sema3a	20346 sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A
10350349	0.01245	1.24E-04	up	1.539546	0.622505	585.0264	380.0021	Dennd1b	329260 DENN/MADD domain containing 1B
10471474	0.012465	1.25E-04	down	-1.50251	-0.58737	1197.554	1799.457	Ak1	11636 adenylate kinase 1
10376332	0.012747	1.29E-04	up	1.738024	0.797448	193.6512	111.7292	4930438AC	73988 RIKEN cDNA 4930438A08 gene
10569280	0.012747	1.29E-04	down	-1.6033	-0.68105	456.1654	730.7486	Dusp8	18218 dual specificity phosphatase 8
10571467	0.012747	1.29E-04	down	-1.51208	-0.59653	187.8673	284.0107	Pdgfrl	68797 platelet-derived growth factor receptor-like
10361680	0.012884	1.32E-04	down	-1.60066	-0.67867	89.1483	142.5809	BC013529	215751
10445898	0.012884	1.32E-04	up	1.517847	0.602026	1975.819	1301.582	Rab5a	271457 RAB5A, member RAS oncogene family
10450982	0.012884	1.32E-04	down	-1.69427	-0.76066	96.33004	162.9144	Gpr115	78249 G protein-coupled receptor 115
10507334	0.012884	1.32E-04	up	1.502645	0.587504	164.7965	109.6577	0610037D1	68394 RIKEN cDNA 0610037D15 gene
10523547	0.012901	1.33E-04	up	1.7678	0.821955	494.8199	280.193	Agpat9	231510 1-acylglycerol-3-phosphate O-acyltransferase 9
10451953	0.012902	1.33E-04	down	-5.28283	-2.40131	147.3162	742.4647	Lrg1	76905 leucine-rich alpha-2-glycoprotein 1
10467124	0.012973	1.35E-04	up	1.563751	0.645011	4193.857	2683.751	Acta2	11475 actin, alpha 2, smooth muscle, aorta
10458555	0.013103	1.37E-04	down	-1.70884	-0.77301	514.9	882.1055	Spry4	24066 sprouty homolog 4 (Drosophila)
10465895	0.013103	1.38E-04	up	1.708007	0.772314	944.2929	551.4612	Fads2	56473 fatty acid desaturase 2
10545192	0.013103	1.37E-04	up	1.552709	0.634787	239.2007	154.1569	Rprl1	19783 ribonuclease P RNA-like 1
10550059	0.013103	1.37E-04	up	2.874112	1.523116	507.6807	178.3271	2310014L1	381845 RIKEN cDNA 2310014L17 gene
10383233	0.013335	1.42E-04	up	1.558457	0.640119	670.1839	430.1065	Rnf213	672511 ring finger protein 213
10444680	0.013335	1.42E-04	down	-1.97506	-0.9819	214.9153	424.2103	Ly6g6e	70274 lymphocyte antigen 6 complex, locus G6E
10451893	0.013335	1.42E-04	down	-1.49769	-0.58274	310.6571	465.1937	Stap2	106766 signal transducing adaptor family member 2
10473281	0.013335	1.43E-04	up	1.496452	0.581546	2876.643	1922.5	Itgav	16410 integrin alpha V
10528527	0.013335	1.43E-04	up	1.490559	0.575853	470.1662	315.4257	Fam126a	84652 family with sequence similarity 126, member A
10545409	0.013335	1.43E-04	down	-1.52234	-0.60629	954.2103	1451.982	Vamp8	22320 vesicle-associated membrane protein 8
10347767	0.013537	1.47E-04	down	-2.14595	-1.10162	377.5737	813.5566	Kcne4	57814 potassium voltage-gated channel, Isk-related subfamily, gene 4
10466604	0.013537	1.47E-04	down	-2.1371	-1.09565	189.0027	407.3364		
10546929	0.013537	1.48E-04	down	-1.53669	-0.61983	116.418	178.9909	Cidec	14311 cell death-inducing DFFA-like effector c
10571752	0.013537	1.46E-04	up	1.689887	0.756927	837.19	494.5069	Dctd	320685 dCMP deaminase
10587534	0.013537	1.47E-04	down	-1.85323	-0.89004	237.9324	441.8754	Bckdhh	12040 branched chain ketoacid dehydrogenase E1, beta polypeptide
10355974	0.013562	1.48E-04	down	-1.4875	-0.57289	196.2692	291.9444	Wdfy1	69368 WD repeat and FYVE domain containing 1
10500140	0.013682	1.50E-04	up	1.696843	0.762853	1067.027	629.8081	Anxa9	17190 annexin A9
10383214	0.013926	1.54E-04	up	1.476412	0.562096	1005.538	681.0508	Rnf213	672511 ring finger protein 213

10460257	0.013926	1.53E-04	down	-1.52637	-0.61011	137.6298	210.0112	1700055NC	73458	RIKEN cDNA 1700055N04 gene
10359280	0.013927	1.55E-04	down	-2.17007	-1.11774	105.4346	227.6805	Pappa2	23850	pappalysin 2
10595836	0.013927	1.55E-04	up	1.678515	0.747185	156.5514	93.37273	E0300110C	319859	RIKEN cDNA E030011O05 gene
10599463	0.013927	1.54E-04	down	-1.87169	-0.90835	189.0169	353.6507	Xpnp2	170745	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound
10505623	0.014362	1.60E-04	down	-1.57571	-0.656	546.2227	860.6103	D4Bwg095	52829	DNA segment, Chr 4, Brigham & Women's Genetics 0951 expressed
10426889	0.014388	1.61E-04	down	-1.51022	-0.59475	209.4771	316.2163	Sec61b	66212	Sec61 beta subunit
10431229	0.014388	1.62E-04	down	-1.48582	-0.57126	145.7628	216.5424	Celsr1	12614	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)
10398211	0.014567	1.64E-04	down	-1.72758	-0.78875	235.0722	405.6378	Hhpl1	214305	hedgehog interacting protein-like 1
10518484	0.014567	1.65E-04	up	1.716186	0.779206	157.4894	92.0389	Fbxo44	230903	F-box protein 44
10363070	0.014606	1.66E-04	down	-1.60877	-0.68589	296.0003	476.9646	Gp49a Lilr14727	14	glycoprotein 49 A leukocyte immunoglobulin-like receptor, subfamily B, member 4
10486029	0.014606	1.66E-04	down	-1.47777	-0.56342	529.9588	783.2448	Atpbd4	66632	ATP binding domain 4
10583809	0.014895	1.70E-04	up	1.524694	0.608519	137.0591	89.9265	Cnn1	12797	calponin 1
10472794	0.014963	1.72E-04	up	1.540364	0.623272	208.2023	135.1802	Metap1	66559	methionine aminopeptidase-like 1
10559818	0.014963	1.72E-04	down	-2.18289	-1.12624	46.97442	103.4412			
10347734	0.014973	1.74E-04	down	-1.66531	-0.73579	82.02299	136.7668	Sgpp2	433323	sphingosine-1-phosphate phosphatase 2
10389561	0.014973	1.73E-04	up	1.55572	0.637582	418.6221	269.3361	Dhx40	67487	DEAH (Asp-Glu-Ala-His) box polypeptide 40
10447004	0.014973	1.74E-04	up	1.528379	0.612002	1274.026	834.2123	Hdac1	433759	histone deacetylase 1
10457644	0.014973	1.75E-04	up	1.691045	0.757915	621.4303	367.4944	Cdh2	12558	cadherin 2
10565456	0.014973	1.75E-04	down	-1.65954	-0.73078	274.9119	455.4697	Prss23	76453	protease, serine, 23
10344966	0.01501	1.76E-04	up	1.473772	0.559513	1219.937	827.8963	Ly96	17087	lymphocyte antigen 96
10356764	0.015028	1.76E-04	down	-2.63737	-1.3991	215.8187	561.5343	2310007BC	71874	RIKEN cDNA 2310007B03 gene
10383152	0.015226	1.79E-04	up	1.458113	0.544102	665.4845	456.4053			
10417544	0.015252	1.80E-04	up	1.850418	0.887851	167.8805	90.26694	Acox2	93732	acyl-Coenzyme A oxidase 2, branched chain
10389990	0.015279	1.81E-04	up	1.692754	0.759372	1074.161	634.8758	Epn3	71889	epsin 3
10440186	0.015279	1.81E-04	up	1.921393	0.942153	791.1213	412.3763	Crybg3	224273	beta-gamma crystallin domain containing 3
10434815	0.015463	1.84E-04	down	-1.47191	-0.55769	1234.29	1816.413	Trp63	22061	transformation related protein 63
10357604	0.015585	1.87E-04	up	1.601984	0.67986	298.6919	186.6909	Ikbke	56489	inhibitor of kappaB kinase epsilon
10499914	0.015585	1.87E-04	up	1.629334	0.704283	2521.401	1550.282	Lce1b	68720	late cornified envelope 1B
10499930	0.01583	1.90E-04	up	2.197163	1.135642	356.3027	163.7589	Lce1g	66195	late cornified envelope 1G
10565315	0.015957	1.92E-04	down	-1.95484	-0.96705	1004.697	1955.391	Fah	14085	fumarylacetoacetate hydrolase
10359870	0.016074	1.95E-04	up	1.488532	0.57389	1276.739	857.622	Pbx1	18514	pre B-cell leukemia transcription factor 1
10513869	0.016074	1.96E-04	down	-1.49191	-0.57717	563.3354	840.041	Megf9	230316	multiple EGF-like-domains 9
10519983	0.016074	1.96E-04	down	-3.05624	-1.61176	134.9919	405.3379	Fgl2	14190	fibrinogen-like protein 2
10573198	0.016074	1.96E-04	down	-1.74534	-0.80351	600.3987	1049.676	Dnajb1	81489	Dnaj (Hsp40) homolog, subfamily B, member 1
10584470	0.016074	1.95E-04	down	-1.71194	-0.77563	52.60265	90.312	Olf2r Olf2r18324	25	olfactory receptor 26 olfactory receptor 933
10554969	0.016129	1.98E-04	down	-2.05442	-1.03873	196.0986	399.4865	Odz4	23966	odd Oz/ten-m homolog 4 (Drosophila)
10414527	0.016195	1.99E-04	up	1.754858	0.811355	1453.293	828.9237	Pnp2 Pnp1667034	1	purine-nucleoside phosphorylase 2 purine-nucleoside phosphorylase 1
10357249	0.016121	2.00E-04	down	-1.65437	-0.72628	352.2799	581.4354	Steap3 Ste68428	70	STEAP family member 3 six transmembrane epithelial antigen of the prostate 1
10518372	0.016121	2.01E-04	up	1.490321	0.575623	308.1374	206.8057	Miip	28010	migration and invasion inhibitory protein
10543253	0.016121	2.00E-04	down	-1.6107	-0.68769	88.58877	142.7165	Wnt2	22413	wingless-related MMTV integration site 2
10349295	0.016221	2.02E-04	up	1.81167	0.85732	212.49	116.974	Tcfcp2l1	81879	transcription factor CP2-like 1
10530100	0.016409	2.04E-04	down	-1.80584	-0.85267	435.3658	784.9616	Arap2	212285	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
10516605	0.016532	2.07E-04	up	1.530339	0.613852	1432.518	937.0135	Hdac1	433759	histone deacetylase 1
10393177	0.016542	2.08E-04	down	-1.49777	-0.58282	625.2366	936.8436	Acox1	11430	acyl-Coenzyme A oxidase 1, palmitoyl
10398442	0.016542	2.08E-04	up	1.658309	0.729713	98.35772	59.19991			
10357870	0.016672	2.10E-04	down	-1.85598	-0.89218	966.5512	1784.332	Prelp	116847	proline arginine-rich end leucine-rich repeat
10354588	0.016786	2.14E-04	down	-1.64629	-0.71921	640.9052	1054.058	Stk17b	98267	serine/threonine kinase 17b (apoptosis-inducing)
10417167	0.016786	2.14E-04	up	2.380081	1.251011	1096.907	457.326	Clybl	69634	citrate lyase beta like
10465059	0.016786	2.14E-04	up	1.441646	0.527717	164.4551	114.0727	Ctsw	13041	cathepsin W
10523717	0.016786	2.15E-04	up	1.495791	0.580909	6572.355	4392.64	Spp1	20750	secreted phosphoprotein 1
10545528	0.016786	2.13E-04	up	1.513344	0.59774	187.397	123.7568	Pigp	56176	phosphatidylinositol glycan anchor biosynthesis, class P
10560618	0.016786	2.15E-04	down	-2.58339	-1.36927	104.7558	266.6248	Apoc1 Gcc11812	74	apolipoprotein C-I golgi coiled coil 1
10357875	0.016789	2.16E-04	down	-2.63058	-1.39538	1084.855	2854.571	Btg2	12227	B-cell translocation gene 2, anti-proliferative
10496569	0.016789	2.16E-04	up	1.541169	0.624025	163.369	105.917	Gbp6	229900	guanylate binding protein 6
10457606	0.016954	2.19E-04	down	-1.4403	-0.52636	177.0004	254.9274	Kctd1	106931	potassium channel tetramerisation domain containing 1
10358408	0.017011	2.20E-04	down	-1.99038	-0.99304	146.2576	293.3946	Rgs1	50778	regulator of G-protein signaling 1
10417526	0.017205	2.24E-04	down	-1.79158	-0.84124	688.6957	1230.729	Dnase1B	13421	deoxyribonuclease 1-like 3
10444291	0.017205	2.24E-04	up	3.44653	1.785145	466.0234	134.4784	H2-Ab1	14961	histocompatibility 2, class II antigen A, beta 1
10499945	0.017205	2.26E-04	up	1.501936	0.586823	147.4804	98.16853	Lce1l	73730	late cornified envelope 1L
10501222	0.017205	2.26E-04	down	-1.68188	-0.75008	1364.737	2288.177	Gstm2	14863	glutathione S-transferase, mu 2
10516487	0.017205	2.25E-04	up	2.459981	1.298647	1511.535	615.8788	Gjb4	14621	gap junction protein, beta 4
10383204	0.017353	2.29E-04	up	1.467862	0.553716	495.368	337.4495			
10407211	0.017353	2.29E-04	up	1.570805	0.651504	1192.323	760.2876	Ppap2a	19012	phosphatidic acid phosphatase type 2A
10508770	0.017729	2.35E-04	up	1.550962	0.633163	143.0166	92.12809	Gm13033 100038703	predicted gene 13033 similar to prostaglandin-endoperoxide synthase 2 precursor	
10605303	0.017729	2.35E-04	down	-1.48827	-0.57363	145.9721	217.1808	Dnase11	69537	deoxyribonuclease 1-like 1

10359282	0.017743	2.38E-04	down	-2.01324	-1.00952	125.4815	254.7691	Pappa2	23850	pappalysin 2
10421524	0.017743	2.38E-04	down	-3.84962	-1.94471	66.32155	259.6028			
10582845	0.017743	2.37E-04	down	-3.8643	-1.95021	66.40021	260.9219			
10596051	0.017743	2.38E-04	up	1.915376	0.937628	138.6369	72.38685	Tmem22	245020	transmembrane protein 22
10451932	0.017764	2.39E-04	down	-2.7562	-1.46268	177.0823	478.7733	Plin4	57435	perilipin 4
10434808	0.017804	2.41E-04	down	-4.11024	-2.03922	241.6929	950.9918	Tprg	71338	transformation related protein 63 regulated
10512156	0.017804	2.41E-04	down	-2.40181	-1.26412	199.3277	483.1962	Aqp3	11828	aquaporin 3
10526363	0.017804	2.40E-04	down	-1.73415	-0.79422	854.5414	1488.047	Por	18984	P450 (cytochrome) oxidoreductase
10371271	0.017825	2.42E-04	up	1.471052	0.556848	296.9446	201.7706	Zfp781	331188	zinc finger protein 781
10417599	0.017825	2.42E-04	down	-3.85979	-1.94852	66.48767	261.1892			
10468898	0.017854	2.44E-04	down	-1.59566	-0.67415	122.8543	195.6771	Lax1	240754	lymphocyte transmembrane adaptor 1
10524234	0.017916	2.46E-04	down	-1.70281	-0.76792	93.23225	159.0175	Galnt9	231605	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9
10586079	0.017916	2.45E-04	up	2.38994	1.256974	414.8115	171.5953	Itga11	319480	integrin alpha 11
10357833	0.017922	2.49E-04	down	-1.63988	-0.71359	872.3765	1427.164	Atp2b4	381290	ATPase, Ca++ transporting, plasma membrane 4
10393379	0.017922	2.49E-04	up	1.538068	0.621119	513.698	334.2956	Mxra7	67622	matrix-remodelling associated 7
10439766	0.017922	2.48E-04	down	-1.66809	-0.7382	321.8963	537.1664	Pvrl3	58998	poliovirus receptor-related 3
10508368	0.017922	2.49E-04	down	-1.65372	-0.72572	145.3491	240.1156	A3galt2	215493	alpha 1,3-galactosyltransferase 2 (isoglobotriaosylceramide synthase)
10562223	0.017922	2.50E-04	down	-2.47711	-1.30866	1163.477	2834.29	Fxyd3 Lg14	17178 24	FXD domain-containing ion transport regulator 3 leucine-rich repeat LGI family, member 4
10579823	0.017922	2.47E-04	down	-3.85408	-1.94639	66.37213	260.289			
10593413	0.017922	2.49E-04	down	-1.42571	-0.51168	379.8103	541.5022	2310030G0	66952	RIKEN cDNA 2310030G06 gene
10436826	0.017924	2.51E-04	down	-3.84535	-1.94311	66.51553	260.3262			
10538459	0.017972	2.52E-04	up	1.941753	0.95736	413.8877	214.7412	Aqp1	11826	aquaporin 1
10596492	0.018019	2.53E-04	up	1.489764	0.575084	554.2906	372.1091	Parp3	235587	poly (ADP-ribose) polymerase family, member 3
10566574	0.018118	2.55E-04	up	1.525513	0.609295	141.0535	92.38255	Gvin1	74558	GTPase, very large interferon inducible 1
10399691	0.018142	2.58E-04	down	-1.89984	-0.92588	2069.52	3904.389	Id2	15902	inhibitor of DNA binding 2
10456296	0.018142	2.58E-04	down	-1.45351	-0.53954	239.3909	348.0863	Malt1	240354	mucosa associated lymphoid tissue lymphoma translocation gene 1
10476658	0.018142	2.56E-04	down	-3.8371	-1.94002	66.42921	259.4417			
10487405	0.018142	2.57E-04	down	-1.79675	-0.84539	306.4049	549.6527	Prom2	192212	prominin 2
10603485	0.018211	2.60E-04	down	-1.57917	-0.65917	573.4003	906.6511	Ebp	13595	phenylalkylamine Ca2+ antagonist (emopamil) binding protein
10348917	0.018365	2.63E-04	down	-1.4676	-0.55346	141.4209	207.6182	Fam174a	67698	family with sequence similarity 174, member A
10462005	0.01844	2.64E-04	up	1.435352	0.521405	539.9551	376.1284	Tmem2	83921	transmembrane protein 2
10426208	0.01845	2.66E-04	up	1.446051	0.532118	622.2524	430.4274	Adm2	223780	adrenomedullin 2
10584479	0.01845	2.65E-04	down	-1.81295	-0.85834	52.26371	95.00986	Olfir933	258433	olfactory receptor 933
10601598	0.01845	2.66E-04	up	1.51207	0.596525	64.41377	62.64936	3110007F1	73061 62	RIKEN cDNA 3110007F17 gene predicted gene 6604 predicted gene 5167 predicted gene 2411
10376326	0.018492	2.71E-04	up	1.421216	0.507125	122.9995	86.54371	Irgm2 Igtp	54396 16	immunity-related GTPase family M member 2 interferon gamma induced GTPase
10404407	0.018492	2.68E-04	down	-1.65641	-0.72806	223.938	371.8096	Foxc1	17300	forkhead box C1
10407350	0.018492	2.69E-04	down	-1.95204	-0.96498	339.6681	658.2447	Fgf10	14165	fibroblast growth factor 10
10448117	0.018492	2.71E-04	down	-1.52335	-0.60725	158.2534	241.2607	Has1	15116	hyaluronan synthase1
10530666	0.018492	2.71E-04	up	1.652407	0.724569	193.8656	117.4928	Lnx1	16924	ligand of numb-protein X 1
10593123	0.018492	2.69E-04	up	1.930008	0.948607	640.2074	329.4457	Tagln	21345	transgelin
10361882	0.018514	2.75E-04	down	-1.44919	-0.53525	312.0794	452.1549	Nhs1	215819	NHS-like 1
10421810	0.018514	2.75E-04	down	-1.55609	-0.63792	217.3984	338.6881	1190002H2	66214	RIKEN cDNA 1190002H23 gene
10463189	0.018514	2.72E-04	down	-2.1085	-1.07622	185.1865	391.6033	Ankrd2	56642	ankyrin repeat domain 2 (stretch responsive muscle)
10467319	0.018514	2.73E-04	down	-1.97029	-0.97841	850.7672	1666.445	Rbp4	19662	retinol binding protein 4, plasma
10499483	0.018514	2.74E-04	up	1.480328	0.565917	1253.837	847.6866	Fdps	110196	farnesyl diphosphate synthetase
10520288	0.018514	2.73E-04	down	-1.51559	-0.59988	255.2133	386.433	Galnt11 E1231050	7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 RIKEN cDNA E130116L18 gene
10369792	0.01896	2.82E-04	up	1.44029	0.52636	3769.655	2618.116	Arid5b	71371	AT rich interactive domain 5B (MRF1-like)
10398907	0.018961	2.83E-04	down	-1.51012	-0.59466	61.94978	93.649	Pld4	104759	phospholipase D family, member 4
10398751	0.019139	2.89E-04	up	1.523435	0.607328	321.4971	211.245	Zfyve21	68520	zinc finger, FYVE domain containing 21
10510574	0.019139	2.90E-04	down	-1.47058	-0.55639	4015.891	5901.358	Errf1	74155	ERBB receptor feedback inhibitor 1
10523563	0.019139	2.88E-04	down	-1.69119	-0.75804	179.596	304.7702	Cds1	74596	CDP-diacylglycerol synthase 1
10524034	0.019139	2.88E-04	up	1.491821	0.577074	592.4363	397.5275	Idua	15932	iduronidase, alpha-L-
10577641	0.019139	2.89E-04	down	-1.72236	-0.78439	711.4964	1227.53	1810011O1	69068	RIKEN cDNA 1810011O10 gene
10587503	0.019139	2.90E-04	down	-1.4835	-0.569	677.4791	1004.188	Sh3bgrl2	212531	SH3 domain binding glutamic acid-rich protein like 2
10598771	0.019139	2.87E-04	down	-1.4546	-0.54062	385.9025	561.0516	Maoa	17161	monoamine oxidase A
10383200	0.01916	2.93E-04	up	1.56704	0.648042	361.5819	231.0635			
10445781	0.01916	2.93E-04	down	-1.63439	-0.70875	180.8796	296.5513	Trem2	83433	triggering receptor expressed on myeloid cells 2
10467470	0.01916	2.93E-04	up	1.412710	0.498466	1549.386	1096.777	Aldh18a1	56454	aldehyde dehydrogenase 18 family, member A1
10541246	0.01916	2.93E-04	down	-1.75288	-0.80973	572.7018	999.4524	Il17ra	16172	interleukin 17 receptor A
10524621	0.019247	2.95E-04	up	1.838483	0.878515	454.3729	245.7247	Oasl2	23962	2'-5' oligoadenylate synthetase-like 2
10437210	0.019406	2.99E-04	down	-1.44489	-0.53096	151.1112	218.2403	Bace2	56175	beta-site APP-cleaving enzyme 2
10555041	0.019406	3.00E-04	up	1.679632	0.748145	745.566	442.3841	Alg8	381903	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)
10595070	0.019406	2.99E-04	down	-1.61918	-0.69526	842.5956	1363.437	Fam83b	208994	family with sequence similarity 83, member B
10437399	0.019451	3.01E-04	down	-1.52379	-0.60766	337.2942	513.3521	Coro7	78885	coronin 7
10346348	0.019476	3.03E-04	up	1.516544	0.600787	546.9212	361.0485	Spats2l	67198	spermatogenesis associated, serine-rich 2-like

10360028	0.019476	3.04E-04	down	-2.01708	-1.01227	668.0267	1334.635	Fcgr2b	14130 Fc receptor, IgG, low affinity IIb
10467739	0.019476	3.04E-04	down	-1.56569	-0.6468	738.897	1158.249	Avp1	69534 arginine vasopressin-induced 1
10476401	0.019476	3.04E-04	down	-2.12634	-1.08837	143.7568	303.226	P1cb1	18795 phospholipase C, beta 1
10431697	0.019485	3.05E-04	down	-2.13673	-1.0954	170.9184	805.1678	Abcd2	26874 ATP-binding cassette, sub-family D (ALD), member 2
10383202	0.019497	3.07E-04	up	1.470609	0.556414	1187.607	806.92		
10470248	0.019497	3.07E-04	up	1.757247	0.813317	576.9848	329.1146	Gpsm1	67839 G-protein signalling modulator 1 (AGS3-like, C. elegans)
10558295	0.019497	3.07E-04	up	1.52243	0.606376	1178.658	774.0477	Zranb1	360216 zinc finger, RAN-binding domain containing 1
10457357	0.019539	3.09E-04	down	-1.88863	-0.91734	149.1363	283.1039	Mpp7	75739 membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)
10500091	0.019546	3.09E-04	up	1.472728	0.558491	1401.724	952.6015	Scnm1	69269 sodium channel modifier 1
10456005	0.019865	3.15E-04	up	1.92599	0.9456	188.1116	98.03402	Cd74	16149 CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)
10513608	0.019917	3.18E-04	down	-1.80056	-0.84845	758.972	1358.297	Alad	17025 aminolevulinate, delta-, dehydratase
10519497	0.019917	3.18E-04	down	-2.35009	-1.23272	348.6485	806.4404	Steap4	117167 STEAP family member 4
10540897	0.019917	3.19E-04	down	-1.97117	-0.97905	390.8196	763.4261	Pparg	19016 peroxisome proliferator activated receptor gamma
10556413	0.019917	3.18E-04	down	-1.53051	-0.61401	160.3606	245.0228	Micalcl	70877 MICAL C-terminal like
10450948	0.019963	3.20E-04	up	1.622169	0.697924	128.2134	78.93756	9130008F2	71583 RIKEN cDNA 9130008F23 gene
10440050	0.020007	3.23E-04	down	-1.43197	-0.518	420.0669	601.6355	Tbc1d23	67581 TBC1 domain family, member 23
10539769	0.020007	3.22E-04	up	1.688773	0.755975	1146.223	680.0223	Nfu1	56748 NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)
10568714	0.020007	3.23E-04	up	1.424507	0.510463	404.9099	284.1924	Mki67	17345 antigen identified by monoclonal antibody Ki 67
10465701	0.020108	3.25E-04	down	-1.97602	-0.9826	116.8185	229.291	Lgals12	56072 lectin, galactose binding, soluble 12
10353272	0.020227	3.29E-04	down	-1.63522	-0.70948	336.6663	548.6608	Stau2	29819 staufen (RNA binding protein) homolog 2 (Drosophila)
10436519	0.020227	3.30E-04	down	-1.52728	-0.61097	487.3671	743.0893	Robo1	19876 roundabout homolog 1 (Drosophila)
10521566	0.020227	3.30E-04	up	1.548509	0.630879	565.8537	365.2502	Tmem128	66309 transmembrane protein 128
10529824	0.020227	3.31E-04	down	-1.49018	-0.57549	102.3753	152.6412	Prom1 Gm19126	10 prominin 1 predicted gene 16401
10537657	0.020227	3.30E-04	down	-1.81475	-0.85977	262.1135	472.7505	Ephb6	13848 Eph receptor B6
10385966	0.020264	3.32E-04	up	1.459112	0.545091	1490.316	1022.19	Anxa6	11749 annexin A6
10560481	0.020332	3.34E-04	down	-2.67885	-1.42161	218.425	573.2748	Fosb	14282 FBJ osteosarcoma oncogene B
10396402	0.020437	3.36E-04	down	-1.46218	-0.54812	399.4464	584.23	Prkch	18755 protein kinase C, eta
10509992	0.02104	3.47E-04	up	2.54293	1.346492	708.4916	277.3628	Hspb7	29818 heat shock protein family, member 7 (cardiovascular)
10383168	0.021099	3.49E-04	up	1.440806	0.526876	986.521	684.3425		
10411226	0.021159	3.51E-04	up	2.32547	1.217522	467.9925	200.732	F2r1l	14063 coagulation factor II (thrombin) receptor-like 1
10499095	0.021159	3.51E-04	down	-1.43841	-0.52448	403.2995	579.8102	Fam160a1	229488 family with sequence similarity 160, member A1
10345504	0.021354	3.56E-04	down	-1.39632	-0.48163	2657.07	3710.066	Cox5b	12859 cytochrome c oxidase, subunit Vb
10419854	0.021354	3.56E-04	down	-1.88044	-0.91107	190.055	356.8681	Sic7a8	50934 solute carrier family 7 (cationic amino acid transporter, y+ system), member 8
10460259	0.021354	3.56E-04	down	-1.51026	-0.59479	1762.858	2659.61	Aldh3b2	621603 aldehyde dehydrogenase 3 family, member B2
10360398	0.021415	3.59E-04	down	-1.95855	-0.96978	531.8843	1039.052	Irf202b	26388 interferon activated gene 202B
10383212	0.021415	3.60E-04	up	1.459971	0.545939	807.0551	552.2782		
10494060	0.021415	3.59E-04	up	1.420029	0.50592	391.1352	275.4029	Mrpl9	78523 mitochondrial ribosomal protein L9
10427336	0.021442	3.61E-04	down	-1.80944	-0.85554	199.4878	359.0552	Nckap1l	105855 NCK associated protein 1 like
10460255	0.021449	3.62E-04	down	-1.47192	-0.5577	2269.113	3336.387	1700055Nc	73458 RIKEN cDNA 1700055N04 gene
10542872	0.021637	3.66E-04	up	1.534958	0.618199	422.9452	275.3192	Rps4y2	66184 ribosomal protein S4, Y-linked 2
10371293	0.021692	3.67E-04	up	1.422293	0.508219	245.6778	172.7001	1190007I0	544717 RIKEN cDNA 1190007I07 gene
10555179	0.021757	3.69E-04	down	-1.74444	-0.80276	575.7911	1009.826	Prkrir	72981 protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)
10447634	0.021796	3.71E-04	down	-1.61272	-0.6895	555.3432	893.503	Gm9992 U667055	3 predicted gene 9992 unc-93 homolog A (C. elegans)
10503334	0.021796	3.71E-04	down	-2.03428	-1.02452	748.4942	1518.114	Gem	14579 GTP binding protein (gene overexpressed in skeletal muscle)
10409866	0.021848	3.73E-04	down	-1.39474	-0.48	56.08439	78.22588	Ctla2b	13025 cytotoxic T lymphocyte-associated protein 2 beta
10432404	0.022037	3.77E-04	up	1.629035	0.704018	3081.306	1898.409	Tuba1a	22142 tubulin, alpha 1A
10601385	0.022305	3.82E-04	down	-1.43616	-0.52222	80.07139	115.0676	Tlr13	279572 toll-like receptor 13
10521616	0.02234	3.84E-04	up	1.406386	0.491993	193.7398	137.7729	C1qtnf7	109323 C1q and tumor necrosis factor related protein 7
10350146	0.022573	3.89E-04	up	1.400607	0.486053	1866.401	1332.669	Phlda3	27280 pleckstrin homology-like domain, family A, member 3
10449631	0.022573	3.89E-04	down	-1.45538	-0.5414	417.0309	606.3485	Btb9d	224671 BTB (POZ) domain containing 9
10358928	0.022955	3.98E-04	down	-1.97549	-0.98221	126.3449	248.0598	Cacna1e	12290 calcium channel, voltage-dependent, R type, alpha 1E subunit
10490221	0.022955	3.98E-04	up	1.665776	0.736194	496.3055	298.9344	Atp5e	67126 ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
10569830	0.022955	3.97E-04	down	-1.48518	-0.57064	347.0829	515.5781	2310057J16	69697 RIKEN cDNA 2310057J16 gene
10434778	0.022961	3.99E-04	up	1.474552	0.560276	143.8638	97.59326	Rtp4	67775 receptor transporter protein 4
10399677	0.02308	4.05E-04	down	-1.55719	-0.63895	583.2452	910.0437	Cox7a2l	20463 cytochrome c oxidase subunit VIIa polypeptide 2-like
10422227	0.02308	4.05E-04	down	-1.62449	-0.69999	405.7769	656.8937	Spry2	24064 sprouty homolog 2 (Drosophila)
10430834	0.02308	4.04E-04	up	1.620267	0.696232	1011.901	623.491	Naga	17939 N-acetyl galactosaminidase, alpha
10474419	0.02308	4.04E-04	down	-1.60021	-0.67826	568.6983	907.9615	Lgr4	107515 leucine-rich repeat-containing G protein-coupled receptor 4
10552125	0.02308	4.04E-04	down	-1.49032	-0.57563	330.6283	492.8592	Pepd	18624 peptidase D
10395780	0.023144	4.07E-04	up	1.459848	0.545818	2511.114	1721.113	170004711:73385	10 RIKEN cDNA 1700047117 gene 1 signal recognition particle 54C predicted gene 9802 hypothetical protein LOC100048408
10395770	0.023217	4.09E-04	up	1.459487	0.545462	2511.307	1721.678	170004711:73385	10 RIKEN cDNA 1700047117 gene 1 signal recognition particle 54C predicted gene 9802 hypothetical protein LOC100048408
10363445	0.02323	4.10E-04	down	-1.44509	-0.53116	263.4607	381.0061	4632428Nc	74048 RIKEN cDNA 4632428N05 gene
10460085	0.023252	4.13E-04	down	-1.414	-0.49978	771.4225	1090.845	Cndp2	66054 CNDP dipeptidase 2 (metallopeptidase M20 family)
10466439	0.023252	4.13E-04	up	1.598142	0.676395	1015.216	634.9174	Pebp1	23980 phosphatidylethanolamine binding protein 1
10495285	0.023252	4.12E-04	down	-1.9031	-0.92835	315.2584	594.6643	Sort1	20661 sortilin 1

10596454	0.023361	4.16E-04	up	1.38851	0.473538	1384.292	996.9411	Alas1	11655	aminolevulinic acid synthase 1
10431017	0.023409	4.18E-04	up	1.674063	0.743353	603.8057	359.0612	Ttl1	319953	tubulin tyrosine ligase-like 1
10518428	0.023469	4.21E-04	down	-1.41201	-0.49775	297.0885	419.6316	Cln6	26372	chloride channel 6
10535938	0.023469	4.20E-04	down	-1.40854	-0.4942	82.50501	116.2287	N4bp2l1	100637	NEDD4 binding protein 2-like 1
10544089	0.023469	4.22E-04	down	-1.47603	-0.56172	544.6524	802.8247	Zc3hav1	78781	zinc finger CCCH type, antiviral 1
10547009	0.023469	4.22E-04	up	1.414912	0.500712	986.3294	696.8178	Vgll4	232334	vestigial like 4 (Drosophila)
10581266	0.023469	4.23E-04	up	1.517713	0.601899	281.7081	185.2955	Tpp3	67971	tubulin polymerization-promoting protein family member 3
10465424	0.023485	4.24E-04	down	-1.46843	-0.55428	332.1104	487.9755	Nrxn2 Gm 18190	10	neurexin II predicted gene 14964
10586174	0.023485	4.25E-04	down	-1.41726	-0.5031	386.1359	547.3037			
10427253	0.023546	4.27E-04	down	-1.58639	-0.66575	141.88	224.5375	Map3k12	26404	mitogen-activated protein kinase kinase kinase 12
10576911	0.023546	4.27E-04	down	-1.65405	-0.72601	748.6847	1232.928	Efnb2	13642	ephrin B2
10490129	0.023635	4.30E-04	down	-1.61023	-0.68727	840.5869	1349.748	Bmp7	12162	bone morphogenetic protein 7
10400293	0.023769	4.33E-04	up	1.479276	0.564891	348.1301	235.6875	6530401NC	328092	RIKEN cDNA 6530401N04 gene
10466587	0.023769	4.34E-04	down	-1.75439	-0.81097	76.12672	134.2466	Rorb	225998	RAR-related orphan receptor beta
10358389	0.023946	4.38E-04	down	-1.54829	-0.63068	1602.397	2478.486	Rgs2	19735	regulator of G-protein signaling 2
10442786	0.02418	4.43E-04	down	-1.87642	-0.90799	250.0841	470.7464	Tpsb2	17229	tryptase beta 2
10350838	0.024245	4.47E-04	up	1.375106	0.459543	406.634	295.7111	2810417H1	68026	RIKEN cDNA 2810417H13 gene
10377859	0.024245	4.49E-04	up	1.430055	0.516071	1256.147	378.082	Pld2	18806	phospholipase D2
10447619	0.024245	4.48E-04	up	1.380949	0.46566	514.9802	372.9374	Rshl2a Rsh 66832	10	radial spokehead-like 2A radial spokehead-like 2B
10466210	0.024245	4.49E-04	down	-2.06407	-1.04549	247.0278	504.3696	Ms4a6d	68774	membrane-spanning 4-domains, subfamily A, member 6D
10562251	0.024245	4.49E-04	down	-1.3948	-0.48006	415.1868	579.2168	Scn1b	20266	sodium channel, voltage-gated, type I, beta
10586491	0.024245	4.45E-04	down	-1.41816	-0.50402	201.7914	286.3428	Dapk2	13143	death-associated protein kinase 2
10451763	0.024273	4.51E-04	down	-1.57539	-0.65571	170.4143	268.6041	Satb1	20230	special AT-rich sequence binding protein 1
10454129	0.024328	4.53E-04	up	1.596112	0.674561	2091.704	1310.974	Dsg1b	225256	desmoglein 1 beta
10561498	0.024328	4.53E-04	up	1.453828	0.539856	1689.083	1161.269	C330005M	101744	RIKEN cDNA C330005M16 gene
10424363	0.024452	4.57E-04	up	1.404656	0.490217	828.6923	589.6986	Nsmce2	68501	non-SMC element 2 homolog (MMS21, S. cerevisiae)
10576854	0.024461	4.58E-04	up	1.446136	0.532203	729.03	503.6592	Ctxn1	330695	cortixin 1
10445360	0.024482	4.60E-04	up	1.428266	0.514264	496.3569	347.2412	Supt3h	109115	suppressor of Ty 3 homolog (S. cerevisiae)
10468668	0.024482	4.60E-04	down	-1.535	-0.61824	169.1676	259.5392	Afap1l2	226250	actin filament associated protein 1-like 2
10381096	0.024536	4.62E-04	down	-1.52561	-0.60938	1552.513	2364.076	Igfbp4	16010	insulin-like growth factor binding protein 4
10548905	0.024546	4.63E-04	down	-1.70013	-0.76565	309.0688	528.204	Eps8	13860	epidermal growth factor receptor pathway substrate 8
10450075	0.024555	4.64E-04	up	1.375505	0.459961	1623.926	1180.661	H2-K1	14972	histocompatibility 2, K1, K region
10345445	0.024587	4.65E-04	down	-1.41416	-0.49994	298.3877	422.1378	Arid5a	214855	AT rich interactive domain 5A (MRF1-like)
10349559	0.02485	4.71E-04	up	1.755575	0.811944	1106.541	632.1387	Yod1	226418	YOD1 OTU deubiquitinating enzyme 1 homologue (S. cerevisiae)
10401841	0.024854	4.72E-04	down	-1.4414	-0.52747	110.9831	160.0223	Dio2	13371	deiodinase, iodothyronine, type II
10404359	0.024861	4.73E-04	down	-1.49004	-0.57535	114.1246	169.7832	Mboat1	218121	membrane bound O-acyltransferase domain containing 1
10401343	0.025229	4.81E-04	up	1.442314	0.528385	204.8384	141.9172	Map3k9	338372	mitogen-activated protein kinase kinase 9
10507433	0.025355	4.84E-04	down	-1.94036	-0.95632	152.4787	294.7334	Ptch2	19207	patched homolog 2
10368409	0.025395	4.86E-04	down	-1.44151	-0.52758	269.3397	388.1821	Lama2	16773	laminin, alpha 2
10539894	0.025395	4.86E-04	down	-1.68408	-0.75196	168.0015	283.164	Mgll	23945	monoglyceride lipase
10399584	0.025519	4.91E-04	up	1.626722	0.701968	106.1109	65.09576	G730007D	1E+08	RIKEN cDNA G730007D18 gene
10425138	0.025519	4.91E-04	down	-1.3979	-0.48326	486.5359	679.9194	Sh3bp1	20401	SH3-domain binding protein 1
10480649	0.025519	4.92E-04	up	1.518687	0.602824	734.7124	484.0409	2310002J1	67859	RIKEN cDNA 2310002J15 gene
10358379	0.02585	5.00E-04	up	1.379442	0.464085	466.6094	338.3135	Trove2	20822	TROVE domain family, member 2
10427286	0.02585	5.01E-04	up	1.416961	0.5028	163.9913	115.77	Hoxc9	15427	homeo box C9
10446928	0.02585	5.00E-04	down	-1.45443	-0.54046	427.8471	621.8265	Ltbp1	268977	latent transforming growth factor beta binding protein 1
10360563	0.026016	5.05E-04	down	-1.38241	-0.46719	229.1132	316.6482	Smyd3	69726	SET and MYND domain containing 3
10604564	0.026133	5.08E-04	down	-1.55544	-0.63732	1120.077	1737.018	Gpc4	14735	glypican 4
10390748	0.026207	5.12E-04	down	-1.61006	-0.68711	1205.962	1946.394	Tns4	217169	tensin 4
10457780	0.026207	5.12E-04	down	-1.41514	-0.50094	777.5751	1100.096	Fam59a	381126	family with sequence similarity 59, member A
10537787	0.026207	5.12E-04	down	-1.59088	-0.66982	112.2343	178.9566	Tas2r135	387512	taste receptor, type 2, member 135
10352777	0.026211	5.13E-04	down	-1.59867	-0.67687	167.6858	268.5804	Slc30a1 17 22782	98	solute carrier family 30 (zinc transporter), member 1 RIKEN cDNA 1700034H15 gene
10395805	0.026237	5.15E-04	up	1.41948	0.505363	5625.045	3961.906	1700047I1	73385	RIKEN cDNA 1700047I17 gene 1
10445412	0.026237	5.15E-04	down	-1.39376	-0.47898	250.7086	349.4996	Nfkbie	18037	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon
10356520	0.026272	5.17E-04	down	-1.43993	-0.526	2716.856	3907.876	Col6a3	12835	collagen, type VI, alpha 3
10538482	0.026272	5.18E-04	up	1.375689	0.460154	134.112	97.47352	Adcyap1r1	11517	adenylate cyclase activating polypeptide 1 receptor 1
10496373	0.026361	5.21E-04	up	1.413672	0.499448	135.4929	95.82348	Ddit4l	73284	DNA-damage-inducible transcript 4-like
10347218	0.026468	5.24E-04	up	2.269724	1.182517	496.3559	215.0188			
10353871	0.026676	5.29E-04	up	1.457793	0.543786	457.4688	313.5278	Lman2l	214895	lectin, mannose-binding 2-like
10360090	0.026676	5.32E-04	up	1.376969	0.461496	575.9479	418.2347	Ppox	19044	protoporphyrinogen oxidase
10378572	0.026676	5.30E-04	down	-1.42056	-0.50646	470.8477	668.4996	Tlcd2	380712	TLC domain containing 2
10563099	0.026676	5.32E-04	down	-1.45457	-0.54059	229.4304	334.0509	Snord35b	27212	small nucleolar RNA, C/D box 35B
10586448	0.026676	5.31E-04	up	1.609608	0.686709	147.1921	91.75658	2810417H1	68026	RIKEN cDNA 2810417H13 gene
10499108	0.026719	5.34E-04	down	-1.37526	-0.45971	277.7531	382.051	Glit2d2	320302	glycosyltransferase 28 domain containing 2
10492330	0.026784	5.36E-04	down	-1.49331	-0.57851	178.2729	265.9969	P2ry1	18441	purinergic receptor P2Y, G-protein coupled 1

10437364	0.026911	5.40E-04	down	-1.39556	-0.48085	191.4777	267.0851	Adcy9	11515	adenylate cyclase 9
10442643	0.026911	5.41E-04	down	-1.40347	-0.489	237.7505	333.5227	Nme3	79059	non-metastatic cells 3, protein expressed in
10427297	0.027014	5.44E-04	up	1.362815	0.44659	148.2221	108.758	Hoxc5	15424	homeo box C5
10376899	0.027037	5.47E-04	up	1.467389	0.553248	888.3856	604.5578	Trim16 Fb:94092	21 tripartite motif-containing 16 F-box and WD-40 domain protein 10	
10383206	0.027037	5.48E-04	up	1.424268	0.510221	540.6163	379.9147			
10395457	0.027037	5.48E-04	up	1.378283	0.462872	357.1412	259.0578	Etv1	14009	ets variant gene 1
10419566	0.027037	5.47E-04	down	-1.50209	-0.58697	124.3854	187.251	Ang2	11731	angiogenin, ribonuclease A family, member 2
10393877	0.027109	5.50E-04	down	-1.58647	-0.66582	356.6097	565.3296	Mafg	17134	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)
10552245	0.027348	5.56E-04	up	1.407842	0.493485	1209.077	858.6035	Tshz3	243931	teashirt zinc finger family member 3
10398920	0.027504	5.60E-04	down	-1.76761	-0.8218	185.5408	325.6261	BC022687	217887	
10365933	0.027587	5.64E-04	down	-1.36988	-0.45405	739.8839	1013.755	Eea1	216238	early endosome antigen 1
10408044	0.027587	5.64E-04	down	-1.37425	-0.45865	2326.674	3196.609	Cox5b	12859	cytochrome c oxidase, subunit Vb
10363082	0.027603	5.65E-04	down	-1.54197	-0.62477	349.9112	539.9971	Lilrb4	14728	leukocyte immunoglobulin-like receptor, subfamily B, member 4
10438904	0.02767	5.68E-04	up	1.573706	0.654166	2026.425	1287.511	Lrrcc15	74488	leucine rich repeat containing 15
10607124	0.028406	5.84E-04	down	-1.48903	-0.57438	80.96579	120.771	Chrd11	83453	chordin-like 1
10423836	0.028432	5.85E-04	up	1.947472	0.961602	317.4012	161.6533	Cthrc1	68588	collagen triple helix repeat containing 1
10398052	0.028506	5.89E-04	down	-2.8583	-1.51516	213.7977	591.5615	Serpina3h 546546	6 serine (or cysteine) peptidase inhibitor, clade A, member 3H predicted gene 6930	
10499363	0.028506	5.90E-04	up	1.47147	0.557258	137.2575	93.13165	Bglap1	12096	bone gamma carboxylglutamate protein 1
10552064	0.028506	5.89E-04	down	-2.18239	-1.12591	2695.062	5785.752	Krtbdap	64661	keratinocyte differentiation associated protein
10422244	0.02856	5.94E-04	down	-1.41114	-0.49686	58.71344	82.78793	Slitrk6	239250	SLIT and NTRK-like family, member 6
10457359	0.02856	5.92E-04	down	-1.82679	-0.86931	379.241	694.6425	Mpp7	75739	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)
10535841	0.02856	5.95E-04	down	-1.69168	-0.75846	193.7391	325.9668	Slc46a3	17706	solute carrier family 46, member 3
10598976	0.02856	5.94E-04	up	1.533601	0.616923	4614.6	3018.193	Timp1	21857	tissue inhibitor of metalloproteinase 1
10361091	0.028703	6.00E-04	down	-1.97772	-0.98384	791.0063	1549.926	Atf3	11910	activating transcription factor 3
10376142	0.028703	6.06E-04	up	1.517059	0.601277	2157.354	1424.108	3230401D1	66680	RIKEN cDNA 3230401D17 gene
10420247	0.028703	5.99E-04	down	-2.52587	-1.33678	116.0458	298.7008	Mcpt4	17227	mast cell protease 4
10450265	0.028703	6.06E-04	up	1.394636	0.479889	270.0693	193.5889	Stk19	54402	serine/threonine kinase 19
10454077	0.028703	6.05E-04	down	-1.54582	-0.62837	187.5165	289.7641	Taf4b	72504	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor
10467508	0.028703	6.07E-04	down	-1.70876	-0.77295	100.9601	172.1518	Blink	17060	B-cell linker
10499378	0.028703	6.07E-04	down	-1.51995	-0.60403	113.9883	173.2763	Sema4a	20351	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A
10560624	0.028703	6.08E-04	down	-2.73474	-1.4514	2522.183	6691.249	Apoe	11816	apolipoprotein E
10578377	0.028703	6.01E-04	up	1.520128	0.604193	816.6905	538.1107	Frg1	14300	FSHD region gene 1
10582582	0.028703	6.06E-04	down	-1.65836	-0.72976	69.93412	116.1455			
10477022	0.028738	6.09E-04	up	2.274083	1.185285	855.3292	369.2159	Sdcbp2	228765	syndecan binding protein (syntenin) 2
10582584	0.028809	6.12E-04	down	-1.65986	-0.73107	69.94226	116.268			
10368175	0.029561	6.29E-04	up	1.353625	0.436828	928.6745	686.0425	Pde7b	29863	phosphodiesterase 7B
10570610	0.029561	6.30E-04	up	2.83808	1.504915	204.867	70.11442	Defb4	56519	defensin beta 4
10382104	0.029755	6.35E-04	down	-1.41536	-0.50117	1243.315	1761.233			
10357808	0.029784	6.37E-04	down	-1.45336	-0.53939	983.7471	1432.214	Snrpe	20643	small nuclear ribonucleoprotein E
10367775	0.029796	6.39E-04	down	-1.52596	-0.60972	821.9995	1256.002	Stxbp5	78808	syntaxin binding protein 5 (tomosyn)
10583044	0.029796	6.40E-04	up	1.445842	0.53191	5149.192	3567.076	Mmp13	17386	matrix metalloproteinase 13
10603147	0.029796	6.40E-04	down	-1.35132	-0.43437	51.95883	70.20846	Gemin8	237221	gem (nuclear organelle) associated protein 8
10539200	0.029939	6.45E-04	down	-5.45039	-2.44636	199.626	993.6894	Reg1	19692	regenerating islet-derived 1
10584595	0.029939	6.45E-04	up	1.424153	0.510105	850.3645	596.7426	2610203C2	70455	RIKEN cDNA 2610203C20 gene
10545101	0.030038	6.49E-04	down	-2.27331	-1.18479	241.6509	539.8689	Hpgds	54486	hematopoietic prostaglandin D synthase
10590438	0.030038	6.49E-04	down	-1.4958	-0.58091	74.64848	111.3972	C730027P0	245050	RIKEN cDNA C730027P07 gene
10356145	0.030056	6.52E-04	down	-1.53462	-0.61788	59.83583	92.10122	Slc19a3	80721	solute carrier family 19 (sodium/hydrogen exchanger), member 3
10431637	0.030056	6.56E-04	down	-1.77027	-0.82397	225.7432	397.2705	Cpne8	66871	copine VIII
10533751	0.030056	6.55E-04	down	-1.35864	-0.44216	258.8211	351.6121	Pitpnm2	19679	phosphatidylinositol transfer protein, membrane-associated 2
10550980	0.030056	6.54E-04	down	-1.58948	-0.66856	2512.478	3978.992	Lypd3	72434	Ly6/Plaur domain containing 3
10576639	0.030056	6.55E-04	down	-1.51447	-0.59882	448.8426	680.9053	Nrp1	18186	neuropilin 1
10584870	0.030056	6.55E-04	up	1.50762	0.592273	1518.757	1010.147	Tmprss13	214531	transmembrane protease, serine 13
10384725	0.030072	6.62E-04	down	-1.58993	-0.66896	642.2161	1022.363	Rel	19696	reticuloendotheliosis oncogene
10416199	0.030072	6.61E-04	up	1.512136	0.596588	1548.004	1020.839	Entpd4	67464	ectonucleoside triphosphate diphosphohydrolase 4
10458340	0.030072	6.59E-04	down	-1.60837	-0.6856	1006.35	1616.002	Hbegf	15200	heparin-binding EGF-like growth factor
10489434	0.030072	6.63E-04	down	-1.34417	-0.42672	55.46509	74.55403	Wfdc12	192200	WAP four-disulfide core domain 12
10518335	0.030072	6.59E-04	up	1.369345	0.453486	1080.709	789.4395	170002910:70005	43 RIKEN cDNA 1700029101 gene predicted gene 13251 predicted gene, OTTMUSG0000010657 predicted gene 13051 predicted gene 13159 predicted gene 13151 pr	
10566488	0.030072	6.60E-04	up	1.356589	0.439984	976.3176	719.7752	Trim3	55992	tripartite motif-containing 3
10461587	0.030105	6.65E-04	down	-2.02348	-1.01684	67.09906	136.8863	Ms4a4a	666907	membrane-spanning 4-domains, subfamily A, member 4A
10520622	0.030105	6.69E-04	down	-1.66215	-0.73305	213.6759	356.2715	Abhd1	57742	abhydrolase domain containing 1
10538802	0.030105	6.67E-04	down	-1.4389	-0.52497	110.1375	158.725	A930038CC	68169	RIKEN cDNA A930038C07 gene
10542470	0.030105	6.68E-04	down	-1.455	-0.54102	1250.813	1823.116	Mgst1	56615	microsomal glutathione S-transferase 1
10586616	0.030105	6.68E-04	down	-1.5222	-0.60615	346.8315	526.3874	Vps13c	320528	vacuolar protein sorting 13C (yeast)
10427816	0.030134	6.70E-04	down	-1.6541	-0.72604	211.6066	348.426	Pdzd2	68070	PDZ domain containing 2
10466888	0.03015	6.72E-04	down	-1.36207	-0.4458	1479.782	2015.989	Glis3	226075	GLIS family zinc finger 3

10565634	0.030168	6.73E-04	up	1.433407	0.519449	508.4275	354.7451	Myo7a	17921	myosin VIIA
10383192	0.030289	6.77E-04	up	1.872691	0.905113	296.2873	157.8356			
10591494	0.030481	6.82E-04	down	-1.35781	-0.44128	93.62479	127.095	S1pr5	94226	sphingosine-1-phosphate receptor 5
10425012	0.030519	6.84E-04	up	1.360013	0.44362	122.8246	90.29227	Zfp7	223669	zinc finger protein 7
10464391	0.030519	6.85E-04	up	1.396049	0.481349	181.8715	130.2435	Emx2	13797	empty spiracles homolog 2 (Drosophila)
10484371	0.030536	6.87E-04	up	1.807111	0.853685	810.5278	449.7212	Calcr1	54598	calcitonin receptor-like
10452419	0.030654	6.90E-04	down	-1.39402	-0.47925	758.4832	1057.108	EfnA5	13640	ephrin A5
10488322	0.030661	6.92E-04	down	-1.54216	-0.62495	527.3899	815.4276	A230067G;	241694	RIKEN cDNA A230067G21 gene
10606714	0.030873	6.97E-04	down	-1.42757	-0.51356	1229.886	1757.726	Gla	11605	galactosidase, alpha
10406171	0.030904	7.00E-04	down	-1.34027	-0.42253	112.3652	150.5985	Tppp	72948	tubulin polymerization promoting protein
10462140	0.030904	7.01E-04	down	-1.69735	-0.76328	121.9637	208.319	Dock8	76088	dedicator of cytokinesis 8
10545168	0.030904	7.01E-04	down	-1.36952	-0.45367	2412.76	3303.093	Tacstd2	56753	tumor-associated calcium signal transducer 2
10419154	0.030933	7.05E-04	down	-2.96576	-1.5684	75.53956	232.7624	Ear1 Ear1C	13586	93 eosinophil-associated, ribonuclease A family, member 1 eosinophil-associated, ribonuclease A family, member 2
10497817	0.030933	7.05E-04	up	1.381741	0.466487	6728.161	4870.212	Anxa5	11747	annexin A5
10556487	0.030933	7.05E-04	down	-1.41111	-0.49683	227.5813	320.8263	A630005I0	320743	RIKEN cDNA A630005I04 gene
10527475	0.031121	7.11E-04	down	-1.3408	-0.4231	792.1696	1062.125	Zfp655	72611	zinc finger protein 655
10395320	0.031147	7.14E-04	down	-1.36087	-0.44453	267.221	363.5239	Twist1	22160	twist homolog 1 (Drosophila)
10485597	0.031147	7.13E-04	down	-1.53973	-0.62268	62.78362	97.01982	Depdc7	211896	DEP domain containing 7
10493850	0.031147	7.13E-04	up	1.564604	0.645798	10192.54	6495.341	Spr2a Spr	20755	10 small proline-rich protein 2A small proline-rich protein 2A3
10399202	0.031271	7.18E-04	down	-1.42816	-0.51416	93.9086	134.0502	Maccr1	238455	metastasis associated in colon cancer 1
10590298	0.031304	7.20E-04	up	1.62437	0.69988	883.3093	541.0075	Eif1b	68969	eukaryotic translation initiation factor 1B
10384138	0.031439	7.26E-04	up	1.346528	0.429245	2014.559	1496.06	Tmed4	103694	transmembrane emp24 protein transport domain containing 4
10585286	0.031439	7.26E-04	up	1.434025	0.52007	186.6194	129.9939	Arhgap20	244867	Rho GTPase activating protein 20
10379524	0.031476	7.28E-04	down	-2.21951	-1.15024	717.8075	1577.411	Ccl11	20292	chemokine (C-C motif) ligand 11
10599927	0.031511	7.29E-04	down	-1.43488	-0.52093	160.8174	230.4303	Aff2	14266	AF4/FMR2 family, member 2
10447904	0.031623	7.33E-04	down	-1.74903	-0.80655	513.3122	890.9047	Unc93a Gr	1381058	6 unc-93 homolog A (C. elegans) predicted gene 9992
10561025	0.031773	7.38E-04	up	2.273554	1.184949	7099.521	3064.852	Cnfn	72383	cornifelin
10593713	0.031909	7.42E-04	down	-1.50042	-0.58537	311.7226	467.5897	Cib2	56506	calcium and integrin binding family member 2
10564795	0.032063	7.47E-04	down	-2.5672	-1.36019	315.085	791.4212	Plin1	103968	perilipin 1
10580577	0.032125	7.49E-04	down	-1.41606	-0.50188	272.8591	386.8571	Irx3	16373	Iroquois related homeobox 3 (Drosophila)
10396148	0.032132	7.51E-04	down	-2.27921	-1.18854	106.867	241.2362	Abhd12b	328121	abhydrolase domain containing 12B
10489092	0.032132	7.52E-04	down	-1.3712	-0.45544	180.7113	247.6463	9830001HC	320706	RIKEN cDNA 9830001H06 gene
10401428	0.032178	7.54E-04	down	-1.38791	-0.47292	412.167	572.4565	C130039O;	238317	RIKEN cDNA C130039O16 gene
10514466	0.032422	7.62E-04	down	-1.48311	-0.56863	1985.286	2951.048	Jun	16476	
10551614	0.032422	7.62E-04	down	-1.39705	-0.48238	1335.15	1865.889	Ech1	51798	enoyl coenzyme A hydratase 1, peroxisomal
10360270	0.032427	7.64E-04	up	2.102618	1.072187	540.8907	260.5472	Atp1a2	98660	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 polypeptide
10517666	0.032427	7.63E-04	up	1.400597	0.486042	197.8929	141.2218	Otdud3	73162	OTU domain containing 3
10352234	0.032663	7.77E-04	down	-1.72413	-0.78587	643.1994	1117.746	Itpkb	320404	inositol 1,4,5-trisphosphate 3-kinase B
10358027	0.032663	7.74E-04	up	1.557745	0.639459	135.4241	86.95336	Elf3	13710	E74-like factor 3
10385635	0.032663	7.74E-04	up	1.335176	0.417029	282.5248	211.6009	Zfp354c	30944	zinc finger protein 354C
10399470	0.032663	7.75E-04	up	1.356676	0.440076	357.3633	263.4926	Trib2	217410	tribbles homolog 2 (Drosophila)
10407122	0.032663	7.76E-04	down	-1.64028	-0.71394	98.48788	160.8528			
10496592	0.032663	7.78E-04	up	1.383686	0.468517	123.927	89.59595	Gbp2	14469	guanylate binding protein 2
10599008	0.032663	7.74E-04	down	-1.76796	-0.82209	134.1752	237.7695	Slc6a14	56774	solute carrier family 6 (neurotransmitter transporter), member 14
10384780	0.032679	7.79E-04	up	1.34054	0.422814	283.954	211.8121	Fancl	67030	Fanconi anemia, complementation group L
10456435	0.032726	7.82E-04	down	-1.56505	-0.64621	191.5673	298.5244			
10530633	0.032726	7.83E-04	up	1.366553	0.450541	894.9206	655.1484	Sgcb	24051	sarcoglycan, beta (dystrophin-associated glycoprotein)
10463355	0.032761	7.85E-04	up	1.80414	0.851311	3082.328	1698.375	Scd2	20250	stearoyl-Coenzyme A desaturase 2
10519012	0.032761	7.86E-04	down	-1.37843	-0.46302	108.938	150.2809	Arhgef16	230972	Rho guanine nucleotide exchange factor (GEF) 16
10556242	0.032959	7.92E-04	down	-1.42944	-0.51545	674.0832	964.6036			
10560919	0.032994	7.94E-04	down	-1.40616	-0.49176	102.5717	144.4149	Atp1a3	232975	ATPase, Na ⁺ /K ⁺ transporting, alpha 3 polypeptide
10491058	0.033065	7.96E-04	up	1.517094	0.60131	705.0345	466.2563	Rpr12	19784	ribonuclease P RNA-like 2
10360130	0.033165	8.03E-04	up	1.410167	0.495866	1292.368	917.7186	Nit1 Dedd	27045	21 nitrilase 1 death effector domain-containing
10375432	0.033165	8.00E-04	down	-1.59783	-0.67612	63.2359	101.1676	Cyfp2 C03	76884	32 cytoplasmic FMR1 interacting protein 2 RIKEN cDNA C030019I05 gene
10395978	0.033165	8.02E-04	down	-1.40816	-0.49381	115.9803	163.5382	Gm527	217648	predicted gene 527
10508986	0.033165	8.02E-04	up	1.470195	0.556008	866.8094	591.0674	Stmn1	16765	stathmin 1
10368270	0.033196	8.06E-04	down	-1.34896	-0.43184	2684.905	3622.988	Rps12 Gm	20042	67 ribosomal protein S12 predicted gene 10063
10512022	0.033196	8.06E-04	down	-1.52273	-0.60666	101.2323	153.8311	Mobkl2b	214944	MOB1, Mps One Binder kinase activator-like 2B (yeast)
10389207	0.033275	8.09E-04	up	1.467089	0.552956	190.8418	130.2532	Ccl5	20304	chemokine (C-C motif) ligand 5
10511725	0.03332	8.12E-04	up	1.529096	0.612679	819.0346	537.6313	Cyb5r4	266690	cytochrome b5 reductase 4
10345065	0.033393	8.17E-04	down	-2.4807	-1.31074	194.4364	470.1575	Gsta3	14859	glutathione S-transferase, alpha 3
10565873	0.033393	8.15E-04	up	1.333386	0.415094	1238.267	928.5959	Ppme1	72590	protein phosphatase methyltransferase 1
10569038	0.033393	8.17E-04	down	-3.0806	-1.62321	310.9556	918.8702	Ano9	71345	anoctamin 9
10572130	0.033526	8.21E-04	down	-1.78931	-0.8394	4591.733	8136.808	Lpl	16956	lipoprotein lipase
10362359	0.033552	8.23E-04	up	1.550024	0.63229	1045.222	673.9783	Pebp1	23980	phosphatidylethanolamine binding protein 1

10398814	0.033553	8.24E-04	down	-1.39158	-0.47672	186.4811	259.3858	Kif26a	668303	kinesin family member 26A
10508405	0.033561	8.26E-04	down	-1.55621	-0.63803	684.2692	1063.275	Tmem54	66260	transmembrane protein 54
10489053	0.033572	8.27E-04	up	1.655861	0.727582	110.4612	66.91368	493051811!	74704	RIKEN cDNA 4930518115 gene
10531022	0.033616	8.29E-04	down	-1.48927	-0.5746	660.0217	982.0357	Tmprss11e	243084	transmembrane protease, serine 11e
10385361	0.033628	8.31E-04	up	1.381913	0.466667	176.5501	127.7948	Ublcp1	79560	ubiquitin-like domain containing CTD phosphatase 1
10524248	0.033632	8.32E-04	down	-1.47217	-0.55794	213.5758	314.8525	Ddx51	69663	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51
10367746	0.033735	8.37E-04	down	-1.34721	-0.42997	802.419	1081.064	Sash1	70097	SAM and SH3 domain containing 1
10502791	0.033735	8.36E-04	up	1.475454	0.561159	303.435	205.1429	Ifi44	99899	interferon-induced protein 44
10531208	0.033772	8.40E-04	down	-1.37487	-0.45929	1201.393	1651.664	Cox18	231430	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)
10576235	0.033772	8.40E-04	up	2.097648	1.068772	1285.748	613.4679	Dpep1	13479	dipeptidase 1 (renal)
10360406	0.033852	8.43E-04	up	1.845637	0.884119	123.3139	66.93017	Ifi205	226695	interferon activated gene 205
10428619	0.033933	8.48E-04	down	-1.90085	-0.92665	827.4142	1577.92	Enpp2	18606	ectonucleotide pyrophosphatase/phosphodiesterase 2
10566182	0.033933	8.47E-04	up	1.405007	0.490577	132.9379	94.53005	Olfrr566	258168	olfactory receptor 566
10402268	0.034047	8.54E-04	down	-1.43603	-0.52208	1378.288	1979.429	Lgmn	19141	legumain
10431711	0.034047	8.55E-04	down	-1.35107	-0.4341	706.2956	953.8772	Slc2a13	239606	solute carrier family 2 (facilitated glucose transporter), member 13
10513818	0.034047	8.55E-04	up	1.448638	0.534697	802.6662	555.2387	Stmn1	16765	stathmin 1
10547282	0.034047	8.54E-04	up	1.36376	0.44759	314.7285	230.6511	Zfp9	22750	zinc finger protein 9
10492522	0.034206	8.61E-04	up	1.354846	0.438129	448.6768	331.0058	Schip1	30953	schwannomin interacting protein 1
10505143	0.034466	8.70E-04	down	-1.40963	-0.49532	203.4623	286.4006	Akap2 Palr11641	67 A kinase (PKA) anchor protein 2 Palr2	Akap2 readthrough transcript
10548892	0.034466	8.71E-04	up	1.473613	0.559358	3378.478	2292.222	Arhgdib	11857	Rho, GDP dissociation inhibitor (GDI) beta
10586390	0.034466	8.69E-04	up	1.33054	0.412012	185.5993	139.4762	Rasl12	70784	RAS-like, family 12
10447361	0.034689	8.79E-04	down	-1.46125	-0.5472	206.9467	301.765	Ttc7	225049	tetratricopeptide repeat domain 7
10572146	0.034689	8.79E-04	down	-1.33826	-0.42035	3113.766	4167.124	Atp6v1b2	11966	ATPase, H+ transporting, lysosomal V1 subunit B2
10541071	0.034759	8.82E-04	up	1.691788	0.758548	140.9756	82.90587	8430408G2	213393	RIKEN cDNA 8430408G22 gene
10492590	0.034905	8.87E-04	up	1.393214	0.478417	376.172	269.671	Ppm1l	242083	protein phosphatase 1 (formerly 2C)-like
10419156	0.035102	8.93E-04	down	-3.03357	-1.60102	71.94848	227.9598	Ear10 Ear293725	13 eosinophil-associated, ribonuclease A family, member 10 eosinophil-associated, ribonuclease A family, member 2 eosinophil-associated, ribonuclease A family, member 1	
10513884	0.035122	8.95E-04	down	-1.35653	-0.43992	130.8228	177.3661	Tle1	21885	transducin-like enhancer of split 1, homolog of Drosophila Elspl
10367744	0.035315	9.02E-04	down	-1.66441	-0.73501	55.12618	91.22444	LOC62944E	629446	gag protein
10462535	0.035315	9.02E-04	up	1.392172	0.477337	170.1618	122.2812	B430203M	320193	RIKEN cDNA B430203M17 gene
10479185	0.035315	9.04E-04	up	1.383949	0.468791	106.6102	77.07852			
10511446	0.035315	9.04E-04	up	1.327404	0.408607	375.7231	283.0651	Asph	65973	aspartate-beta-hydroxylase
10389222	0.035461	9.10E-04	down	-1.51101	-0.59551	520.4487	789.2339	Ccl6	20305	chemokine (C-C motif) ligand 6
10592099	0.035461	9.11E-04	down	-1.50122	-0.58614	329.2089	492.5825	Dcps	69305	decapping enzyme, scavenger
10565813	0.035619	9.16E-04	down	-1.52815	-0.61178	109.7037	168.2225	Gm5774	449630	predicted gene 5774
10357280	0.035661	9.18E-04	down	-1.40837	-0.49403	1295.101	1822.354	Insig2	72999	insulin induced gene 2
10414993	0.035732	9.23E-04	up	1.569944	0.650713	98.18549	62.2914	A630038E1	219065	RIKEN cDNA A630038E17 gene
10489364	0.035732	9.22E-04	up	1.561737	0.643151	2039.678	1305.323	3230401D1	66680	RIKEN cDNA 3230401D17 gene
10590263	0.035785	9.25E-04	down	-1.54951	-0.63181	127.6464	198.5072			
10415885	0.035884	9.30E-04	down	-2.11671	-1.08182	265.6611	570.8889	Sox7	20680	SRY-box containing gene 7
10469425	0.035884	9.30E-04	down	-1.45918	-0.54516	1368.251	2001.397	Arl5b	75869	ADP-ribosylation factor-like 5B
10404731	0.036254	9.41E-04	down	-1.46339	-0.54931	558.2325	818.2097	Tmem14c	66154	transmembrane protein 14C
10391332	0.036321	9.44E-04	down	-1.3673	-0.45133	1297.285	1773.168	Ptrf	19285	polymerase I and transcript release factor
10504775	0.03638	9.47E-04	down	-1.76237	-0.81752	292.6452	516.7364	Col15a1	12819	collagen, type XV, alpha 1
10576332	0.03638	9.48E-04	up	1.539879	0.622817	78.80217	50.9664	Tubb3	22152	tubulin, beta 3
10356475	0.03646	9.52E-04	down	-1.37735	-0.4619	110.2088	151.9157	Arl4c	320982	ADP-ribosylation factor-like 4C
10469151	0.036483	9.53E-04	down	-1.99437	-0.99593	113.355	224.6681	Itih5	209378	inter-alpha (globulin) inhibitor H5
10589889	0.036634	9.59E-04	up	1.32484	0.405818	804.3965	607.1841	Glb1	12091	galactosidase, beta 1
10357594	0.036645	9.62E-04	up	1.482093	0.567636	606.6198	408.4627	Rassf5	54354	Ras association (RalGDS/AF-6) domain family member 5
10379228	0.036645	9.64E-04	up	1.915092	0.937414	334.3857	172.2292	Nos2	18126	nitric oxide synthase 2, inducible
10481634	0.036645	9.64E-04	down	-1.46409	-0.55	271.9506	397.6848	Slc25a25 t227731	7 solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25 nuclear apoptosis inducing factor 1	
10504831	0.036645	9.63E-04	down	-1.37244	-0.45674	315.4584	433.2731	Sec61b	66212	Sec61 beta subunit
10584615	0.036646	9.65E-04	down	-1.40866	-0.49432	1037.352	1462.258	Pvr1	58235	poliovirus receptor-related 1
10589685	0.036646	9.67E-04	up	1.687522	0.754907	171.0499	100.9268	Lrrc2	74249	leucine rich repeat containing 2
10450996	0.036743	9.70E-04	down	-1.61094	-0.6879	146.3056	237.1146	Gpr111	435529	G protein-coupled receptor 111
10406419	0.036761	9.72E-04	down	-1.33096	-0.41247	518.6499	690.2587	Lysmd3	80289	LysM, putative peptidoglycan-binding, domain containing 3
10409804	0.036801	9.81E-04	down	-1.36985	-0.45402	799.3076	1095.053	Zcchc6	214290	zinc finger, CCHC domain containing 6
10436372	0.036801	9.78E-04	up	1.345247	0.427871	495.8864	368.685	Dcblid2	73379	discoidin, CUB and LCLL domain containing 2
10490248	0.036801	9.80E-04	up	1.387166	0.47214	106.8707	77.09571			
10493916	0.036801	9.81E-04	down	-1.63872	-0.71257	54.2815	89.42228	Flg2	229574	filaggrin family member 2
10533725	0.036801	9.75E-04	down	-1.61086	-0.68784	92.88226	149.9031	Gpr81	243270	G protein-coupled receptor 81
10587818	0.036801	9.77E-04	down	-1.52069	-0.60472	121.1549	184.0675	Plscr4	235527	phospholipid scramblase 4
10383198	0.036844	9.85E-04	up	1.45042	0.53647	701.2534	483.8622			
10541279	0.036844	9.84E-04	down	-1.32588	-0.40695	754.2251	1000.181	Bcl2l13	94044	BCL2-like 13 (apoptosis facilitator)
10531887	0.036904	9.87E-04	down	-1.71762	-0.78041	559.5764	952.8117	Slc10a6	75750	solute carrier family 10 (sodium/bile acid cotransporter family), member 6
10587107	0.036909	9.89E-04	down	-1.40574	-0.49133	618.4041	868.4818	Myo5a	17918	myosin VA

10564290	0.036953	9.91E-04	down	-1.33032	-0.41177	479.7871	638.4319	Klf13	50794 Kruppel-like factor 13
10399696	0.036956	9.94E-04	up	1.338002	0.42008	604.911	451.9668	Rnf144a	108089 ring finger protein 144A
10564713	0.036956	9.93E-04	up	1.33088	0.41238	2556.016	1920.27	Mfge8	17304 milk fat globule-EGF factor 8 protein
10597758	0.036956	9.95E-04	down	-1.38789	-0.4729	772.9619	1074.209	Csrnp1	215418 cysteine-serine-rich nuclear protein 1
10436623	0.036987	9.97E-04	down	-2.49487	-1.31897	90.02707	218.5936	Chodl	246048 chondrolectin
10593856	0.037197	0.001004	up	1.409089	0.494762	2405.351	1709.065	C230081A1	244895 RIKEN cDNA C230081A13 gene
10460498	0.037541	0.001016	up	1.324346	0.40528	257.1676	194.1909	Slc29a2	13340 solute carrier family 29 (nucleoside transporters), member 2
10570432	0.037541	0.001016	down	-1.34214	-0.42454	409.0677	549.0422	Snora3	1E+08 small nucleolar RNA, H/ACA box 3
10459071	0.037549	0.001019	down	-1.48929	-0.57462	650.6039	971.4286	2010002N0	106878 RIKEN cDNA 2010002N04 gene
10499937	0.037549	0.00102	up	1.727135	0.788381	4831.785	2782.048		
10515960	0.037549	0.00102	up	1.446957	0.533022	197.546	136.8288	Kcnq4	60613 potassium voltage-gated channel, subfamily Q, member 4
10393936	0.037692	0.001026	down	-1.31632	-0.39651	183.365	241.3729	Cbr2	12409 carbonyl reductase 2
10443786	0.037711	0.001027	down	-1.3354	-0.41727	75.06699	100.206	Pde9a	18585 phosphodiesterase 9A
10502772	0.037738	0.001034	down	-1.53183	-0.61526	1003.135	1529.996	Lphn2	99633 latrophilin 2
10513139	0.037738	0.001035	down	-1.31472	-0.39476	255.6038	336.0317	Ptpn3	545622 protein tyrosine phosphatase, non-receptor type 3
10521824	0.037738	0.001031	up	1.830401	0.87216	1453.454	789.7732	Sod3	20657 superoxide dismutase 3, extracellular
10593723	0.037738	0.001033	down	-1.58206	-0.6618	703.2165	1109.308	Acsbg1	94180 acyl-CoA synthetase bubblegum family member 1
10604505	0.037738	0.001032	down	-1.41318	-0.49895	491.1472	694.2476	6720401G1	103012 RIKEN cDNA 6720401G13 gene
10376803	0.037764	0.001037	down	-1.70285	-0.76795	303.6067	513.8813	Fam83g	69640 family with sequence similarity 83, member G
10402575	0.037764	0.001038	up	2.22606	1.154492	734.9857	325.665	Degs2	70059 degenerative spermatocyte homolog 2 (Drosophila), lipid desaturase
10407803	0.037792	0.001041	down	-1.31608	-0.39624	676.9969	891.0414	Gpr137b	83924 G protein-coupled receptor 137B
10587446	0.037792	0.001041	up	1.437294	0.523355	881.9406	612.4264	Myo6	17920 myosin VI
10575021	0.037946	0.001049	down	-1.32772	-0.40895	241.1119	320.1108	Zfp90	22751 zinc finger protein 90
10587226	0.037946	0.00105	down	-1.44912	-0.53517	176.3451	256.0898	Lysmd2	70082 LysM, putative peptidoglycan-binding, domain containing 2
10606654	0.037946	0.001049	down	-1.46843	-0.55427	450.4839	659.5172	Xkrx	331524 X Kell blood group precursor related X linked
10356329	0.037949	0.001051	down	-1.47815	-0.56379	206.5473	305.2262	Ncl	17975 nucleolin
10527963	0.038034	0.001055	up	1.439181	0.525248	69.61709	48.43439	Gm10484	1E+08 predicted gene 10484
10485170	0.038114	0.001058	down	-1.33181	-0.41339	369.9893	492.8622	Cry2	12953 cryptochrome 2 (photolyase-like)
10394954	0.038288	0.001064	down	-1.52719	-0.61088	527.5192	802.1388	Grlh1	195733 grainyhead-like 1 (Drosophila)
10373912	0.038344	0.001072	down	-1.3658	-0.44975	79.38937	108.3639	Osm	18413 oncostatin M
10395389	0.038344	0.001069	down	-1.5645	-0.6457	74.73895	116.3278	Sostdc1	66042 sclerostin domain containing 1
10485081	0.038344	0.001072	down	-1.41634	-0.50216	390.3834	553.5827	Dgkz	104418 diacylglycerol kinase zeta
10517250	0.038344	0.001073	down	-1.32405	-0.40496	134.9412	178.6394	Extl1	56219 exostosin (multiple)-like 1
10541614	0.038344	0.001069	down	-1.56084	-0.64233	229.9792	358.1011	Clec4d	17474 C-type lectin domain family 4, member d
10364102	0.038369	0.001076	down	-1.50186	-0.58675	1324.28	1991.443	Chchd10	103172 coiled-coil-helix-coiled-coil-helix domain containing 10
10572109	0.038369	0.001075	down	-1.40716	-0.49279	253.5458	356.424	Ints10	70885 integrator complex subunit 10
10385500	0.038371	0.001077	up	1.502815	0.587667	123.9622	82.17957	Irgm1	15944 immunity-related GTPase family M member 1
10551638	0.038436	0.00108	down	-1.72499	-0.78658	5048.294	8658.226	Lgals7	16858 lectin, galactose binding, soluble 7
10479217	0.038617	0.001087	up	1.364837	0.448728	522.9302	382.7618	Gm14420	628308 predicted gene 14420
10405587	0.038745	0.001092	down	-1.56776	-0.64871	2955.244	4624.658	Tgfb1	21810 transforming growth factor, beta induced
10514791	0.038745	0.001093	up	1.359957	0.443561	219.7911	161.6174	Pcsk9	100102 proprotein convertase subtilisin/kexin type 9
10585249	0.038745	0.001095	down	-1.37077	-0.45498	611.8993	838.9373	Ppp2r1b	73699 protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform
10428310	0.038746	0.001096	down	-1.32489	-0.40588	602.7384	798.7593	Azin1	54375 antizyme inhibitor 1
10530269	0.038759	0.001098	down	-1.43294	-0.51897	153.393	219.9088	Rbm47	245945 RNA binding motif protein 47
10603492	0.038759	0.001099	down	-1.3703	-0.4545	1563.818	2140.475	Porcn	53627 porcupine homolog (Drosophila)
10389151	0.038776	0.001101	up	1.473284	0.559035	109.6814	74.26133	Sifn10 Sifn	237887 2 schlafen 10 schlafen 8
10528484	0.038801	0.001103	down	-1.38564	-0.47055	692.995	958.8408	Srpk2	20817 serine/arginine-rich protein specific kinase 2
10352827	0.03881	0.001107	down	-1.74744	-0.80524	147.6228	258.5957	A13001011	319266 RIKEN cDNA A130010115 gene
10462618	0.03881	0.001106	up	1.378321	0.462912	75.30427	54.5653	Ifit3	15959 interferon-induced protein with tetratricopeptide repeats 3
10557585	0.03881	0.001105	up	1.328849	0.410177	120.7016	90.8115	Zfp553	233887 zinc finger protein 553
10398727	0.038926	0.001119	up	1.354868	0.438152	1676.747	1237.295	Klc1	16593 kinesin light chain 1
10407120	0.038926	0.001115	down	-1.50338	-0.58821	720.5557	1081.246	Rps3a Gm'	20091 66 ribosomal protein S3A predicted gene 9000
10416057	0.038926	0.001117	down	-1.49429	-0.57946	726.535	1081.655	Clu	12759 clusterin
10436239	0.038926	0.001114	down	-1.34319	-0.42566	728.4023	979.0187	2310061J0	66391 27 RIKEN cDNA 2310061J03 gene zinc finger and BTB domain containing 11
10530819	0.038926	0.001118	up	1.510919	0.595426	1263.015	837.1071	Hopx	74318 HOP homeobox
10586397	0.038926	0.001114	up	1.382614	0.467398	328.5432	237.8748	Mtfmt	69606 mitochondrial methionyl-tRNA formyltransferase
10556206	0.039006	0.001122	down	-1.34353	-0.42603	405.4762	545.0114	Snora3	1E+08 small nucleolar RNA, H/ACA box 3
10349404	0.039104	0.001126	down	-1.33766	-0.41971	346.5681	463.4329	Mgat5	107895 mannoside acetylglucosaminyltransferase 5
10564909	0.039341	0.001135	down	-1.31182	-0.39157	1073.685	1408.59	Man2a2	140481 mannosidase 2, alpha 2
10396608	0.039494	0.001114	down	-1.34154	-0.42389	685.0832	919.0986	Syne2	319565 synaptic nuclear envelope 2
10349752	0.039512	0.001143	down	-1.32465	-0.40561	660.5954	874.9391	Elk4 Mfsd'	13714 21 ELK4, member of ETS oncogene family major facilitator superfamily domain containing 4
10562605	0.039512	0.001145	down	-1.31981	-0.40033	92.9476	122.6994	A1987944	233168
10567086	0.039512	0.001145	up	1.370401	0.454598	68.50576	49.99722	Cyp2r1	244209 cytochrome P450, family 2, subfamily r, polypeptide 1
10579468	0.039574	0.001148	up	1.358271	0.441772	126.4414	93.18193	Haus8	76478 4HAUS augmin-like complex, subunit 8
10380699	0.039826	0.001157	up	1.549546	0.631846	1785.941	1151.379	Copz2	56358 coatomer protein complex, subunit zeta 2

10467730	0.040342	0.001173	down	-1.32156	-0.40224	236.9398	313.2033	Morn4	226123	MORN repeat containing 4
10524082	0.04053	0.00118	up	1.398157	0.483526	134.7459	96.19706	2310001H169504 10 RIKEN cDNA 2310001H12 gene hypothetical protein LOC100044193 similar to novel KRAB box and zinc finger, C2H2 type domain containing protein		
10360187	0.040611	0.001184	down	-1.37476	-0.45918	350.1148	481.674	Vangl2	93840	vang-like 2 (van gogh, Drosophila)
10432636	0.040698	0.001189	down	-1.40329	-0.48881	352.2515	493.6071	BC004728	207818	
10449266	0.040698	0.001189	down	-1.3642	-0.44805	1214.32	1657.753	Itfg3	106581	integrin alpha FG-GAP repeat containing 3
10460251	0.040765	0.001195	down	-2.2795	-1.18872	160.4064	364.4302	1700055NC	73458	RIKEN cDNA 1700055N04 gene
10585778	0.040765	0.001195	up	1.614407	0.691005	1005.687	627.2751	Sema7a	20361	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A
10589329	0.040765	0.001194	up	1.325984	0.407063	315.0906	237.6686	Pfkfb4	270198	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
10430140	0.040768	0.001197	up	2.021872	1.015691	1401.733	705.2125	Mb	17189	myoglobin
10348244	0.040786	0.001201	down	-1.3035	-0.38239	108.7942	141.8084	Inpp5d	16331	inositol polyphosphate-5-phosphatase D
10378367	0.040786	0.001201	down	-1.698	-0.76383	250.7584	424.0182	Trpv3	246788	transient receptor potential cation channel, subfamily V, member 3
10437655	0.040786	0.001203	up	1.332697	0.414349	148.3872	111.2904	Fam18a	383103	family with sequence similarity 18, member A
10572647	0.040786	0.001205	down	-1.48644	-0.57186	599.9131	894.8044	Slc27a1	26457	solute carrier family 27 (fatty acid transporter), member 1
10588201	0.040786	0.001202	down	-1.34555	-0.4282	81.56208	109.7736			
10441610	0.04082	0.001207	up	1.309126	0.388604	500.6167	382.3544	Rshl2a Rsh 66832 10 radial spokehead-like 2A radial spokehead-like 2B		
10505489	0.04082	0.001209	down	-1.46924	-0.55507	840.7814	1238.627	Pappa	18491	pregnancy-associated plasma protein A
10508012	0.04082	0.00121	down	-1.43074	-0.51676	367.4833	524.8034	Rspo1	192199	R-spondin homolog (Xenopus laevis)
10419563	0.040824	0.001211	down	-1.76978	-0.82357	364.9209	638.828	Rnase1	19752	ribonuclease, RNase A family, 1 (pancreatic)
10416302	0.040863	0.001217	down	-1.35798	-0.44146	1067.853	1450.545	Hr	15460	hairless
10430519	0.040863	0.001216	up	1.37048	0.454681	3440.8	2507.671	Csnk1e	27373	casein kinase 1, epsilon
10523260	0.040863	0.001218	down	-1.33214	-0.41375	303.9292	404.8091	Shroom3	27428	shroom family member 3
10540248	0.040863	0.001218	down	-1.43921	-0.52527	579.2437	831.897	Mitf	17342	microphthalmia-associated transcription factor
10479228	0.040871	0.00122	up	1.349622	0.432556	651.843	483.3649	Etoh1	626848	ethanol induced 1
10543031	0.041047	0.001227	down	-1.3112	-0.39089	206.8896	271.2438	Slc25a13	50799	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13
10434934	0.04119	0.001234	down	-1.55604	-0.63788	195.2574	305.4843	Bdh1	71911	3-hydroxybutyrate dehydrogenase, type 1
10518346	0.04119	0.001232	up	1.313415	0.393323	1634.688	1244.66	Gm13251 433791 7 predicted gene 13251 RIKEN cDNA 1700029I01 gene predicted gene, OTTMUSG00000010657 predicted gene 13051 predicted gene 13159 predicted gene 13235 p1		
10517421	0.041247	0.001237	up	1.318607	0.399015	2194.486	1663.925	Pncr2	52830	proline-rich nuclear receptor coactivator 2
10454353	0.041489	0.001247	down	-1.30457	-0.38357	267.3237	348.7721	Mocos	68591	molybdenum cofactor sulfuryase
10577882	0.041489	0.001246	up	1.339728	0.42194	1209.563	902.1892	Hgsnat	52120	heparan-alpha-glucosaminide N-acetyltransferase
10489429	0.041608	0.001253	down	-2.21388	-1.14658	476.2683	1032.408	Wfdc5	209232	WAP four-disulfide core domain 5
10548761	0.041608	0.001253	down	-1.54679	-0.62928	181.4084	279.1686	Hebp1	15199	heme binding protein 1
10419676	0.041927	0.001266	down	-1.33545	-0.41732	257.7936	344.5089	Rab2b	76338	RAB2B, member RAS oncogene family
10487890	0.041927	0.001265	down	-2.96761	-1.5693	235.0559	664.3408	Erv3	71995	endogenous retroviral sequence 3
10501208	0.041948	0.00127	down	-1.74648	-0.80445	56.04937	98.89374	Gstm6	14867	glutathione S-transferase, mu 6
10563178	0.041948	0.001269	down	-1.30847	-0.38788	156.0521	204.158	Cd37	12493	CD37 antigen
10571214	0.041948	0.001271	down	-1.52558	-0.60935	1425.913	2174.932	Rnf122	68867	ring finger protein 122
10364280	0.041974	0.001273	up	1.323044	0.403861	2631.215	1988.408	Pttg1ip	108705	pituitary tumor-transforming 1 interacting protein
10508917	0.042144	0.00128	up	1.405646	0.491233	601.5079	428.8096	Aim1l	230806	absent in melanoma 1-like
10543551	0.042325	0.001287	up	1.386917	0.471881	462.8152	333.6157	Rbm28	68272	RNA binding motif protein 28
10539263	0.042358	0.001289	up	1.631521	0.706217	589.1428	363.2252	Loxl3	16950	lysyl oxidase-like 3
10356461	0.042397	0.001295	up	1.516254	0.600511	631.733	414.6803	Hjurp 643 381280 7 Holliday junction recognition protein RIKEN cDNA 6430706D22 gene		
10358677	0.042397	0.001301	up	1.304847	0.38388	224.1387	171.7688	1200016B1	66875	RIKEN cDNA 1200016B10 gene
10363118	0.042397	0.001298	down	-1.32648	-0.4076	386.4546	512.4317	Dcbl1	66686	discoidin, CUB and LCCL domain containing 1
10441339	0.042397	0.0013	up	1.522597	0.606534	361.2297	237.3161	A630089N	320586	RIKEN cDNA A630089N07 gene
10444079	0.042397	0.001297	down	-1.34134	-0.42368	407.8758	547.4163	Rgl2	19732	ral guanine nucleotide dissociation stimulator-like 2
10542740	0.042397	0.001299	up	1.420069	0.505961	286.9982	201.8647	Sspn	16651	sarcospan
10593219	0.042397	0.001297	up	1.964354	0.974055	744.2852	373.8264	Nnmt	18113	nicotinamide N-methyltransferase
10381939	0.042633	0.001309	down	-1.30382	-0.38274	443.1466	577.8686	Tanc2	77097	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2
10544036	0.042801	0.001318	down	-1.41775	-0.5036	348.1702	493.4807	Atp6v0a4 140494 3 ATPase, H+ transporting, lysosomal V0 subunit A4 RIKEN cDNA D630045J12 gene		
10572755	0.042801	0.001316	down	-1.30181	-0.38052	47.01434	61.20997			
10537062	0.042855	0.001321	down	-1.57163	-0.65226	573.8581	905.6186	Mest	17294	mesoderm specific transcript
10526427	0.043034	0.001328	down	-1.42191	-0.50783	358.3933	510.0926	Dtx2	74198	deltex 2 homolog (Drosophila)
10420988	0.043292	0.001337	up	1.346274	0.428972	2236.737	1663.014	Dpysl2	12934	dihydropyrimidinase-like 2
10414612	0.043327	0.00134	down	-1.9721	-0.97973	321.6298	628.1682	Slc39a2	214922	solute carrier family 39 (zinc transporter), member 2
10561831	0.043476	0.001346	up	1.30673	0.385961	162.2444	124.1315	Zfp566 Zfp 72556 33 zinc finger protein 566 zinc finger protein 82		
10395659	0.043623	0.001355	down	-1.57922	-0.65921	134.7613	213.6419	Coch	12810	coagulation factor C homolog (Limulus polyphemus)
10478048	0.043623	0.001354	down	-3.67163	-1.87642	578.5673	1987.823	Lbp	16803	lipopolysaccharide binding protein
10502830	0.043623	0.001354	up	1.568872	0.649727	145.9852	92.5323	Nexn	68810	nexilin
10581151	0.043649	0.001357	up	1.874228	0.906297	766.8777	413.9805	Rrad	56437	Ras-related associated with diabetes
10370180	0.043856	0.001367	down	-1.3201	-0.40065	1699.534	2242.972	Col6a2	12834	collagen, type VI, alpha 2
10376912	0.043856	0.001368	up	1.470325	0.556135	114.7237	78.1875	Fbxw10	213980	F-box and WD-40 domain protein 10
10531437	0.043856	0.001368	down	-1.31663	-0.39685	896.9537	1180.888	Scarb2	12492	scavenger receptor class B, member 2
10360235	0.043878	0.001371	up	2.213199	1.146133	400.4554	181.38	Casq1	12372	calsequestrin 1
10537184	0.043878	0.001372	up	1.470596	0.556401	2287.592	1549.886	Cald1	109624	caldesmon 1
10515943	0.043991	0.001377	up	1.306533	0.385744	473.032	361.9568	Ctps	51797	cytidine 5'-triphosphate synthase

10361682	0.044038	0.001382	down	-1.34358	-0.42608	429.962	578.0845	Ppil4	67418	peptidylprolyl isomerase (cyclophilin)-like 4
10485635	0.044038	0.001381	up	1.325486	0.406521	515.2904	388.6637	Eif3m	98221	eukaryotic translation initiation factor 3, subunit M
10381260	0.044049	0.001388	up	1.36491	0.448805	338.3759	248.2366	Tubg2	103768	tubulin, gamma 2
10444268	0.044049	0.001388	down	-1.34178	-0.42415	291.5473	390.8941	Tap2	21355	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
10496425	0.044049	0.001387	down	-1.48936	-0.57469	136.9226	204.3032	Adh7	11529	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
10572637	0.044049	0.001385	up	1.342804	0.425248	1262.446	940.1877	Fam125a	73711	family with sequence similarity 125, member A
10380260	0.044114	0.001392	up	1.611321	0.688244	669.2501	418.3634	Trim25	217069	tripartite motif-containing 25
10552917	0.044124	0.001395	down	-1.33293	-0.4146	141.4959	188.6136	1700039E1 76713 67 RIKEN cDNA 1700039E15 gene ribosomal protein L14 ribosomal protein L14 pseudogene		
10555848	0.044124	0.001394	down	-1.42191	-0.50783	85.46917	121.8386	Trim6	94088	tripartite motif-containing 6
10587639	0.044164	0.001398	down	-1.34971	-0.43265	3063	4132.572	Nt5e	23959	5' nucleotidase, ecto
10441422	0.044277	0.001404	down	-1.33802	-0.4201	401.1541	536.725	Zdhhc14	224454	zinc finger, DHHC domain containing 14
10456545	0.044277	0.001404	down	-1.50655	-0.59125	96.11539	144.667	Ccdc68	381175	coiled-coil domain containing 68
10466923	0.044279	0.001406	down	-1.59498	-0.67354	2258.476	3594.958	Gm10136 672214 1 ribosomal protein L26 pseudogene		
10574384	0.044318	0.001409	up	1.325612	0.406658	241.4337	182.082	Ndr4	234593	N-myc downstream regulated gene 4
10586357	0.044705	0.001423	up	2.773478	1.471696	332.5773	114.659	Cilp	214425	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase
10370522	0.044723	0.001426	down	-1.48679	-0.5722	956.0928	1415.399	Casp14	12365	caspase 14
10487994	0.044723	0.001425	down	-1.49388	-0.57907	695.153	1038.35	Fermt1	21639	fermitin family homolog 1 (Drosophila)
10348791	0.044727	0.001428	down	-1.34192	-0.4243	63.33916	85.05816	Ano7	404545	anoctamin 7
10359948	0.044778	0.001431	down	-1.35525	-0.43856	656.0822	889.6848	Uap1	107652	UDP-N-acetylglucosamine pyrophosphorylase 1
10352867	0.044851	0.001438	down	-1.56198	-0.64338	340.3835	528.3577	Plxna2	18845	plexin A2
10509280	0.044851	0.001437	up	1.344552	0.427126	1814.437	1348.382	Hspg2	15530	perlecan (heparan sulfate proteoglycan 2)
10536658	0.044851	0.001436	down	-1.43553	-0.52158	122.1847	174.8782	Wnt16	93735	wingless-related MMTV integration site 16
10457007	0.044871	0.00144	down	-1.34885	-0.43173	227.3556	306.367	Pqlc1 Gm9 66943 79 PQ loop repeat containing 1 predicted gene 9906		
10574259	0.04508	0.001449	down	-1.31638	-0.39658	3524.188	4641.528	Gpr56	14766	G protein-coupled receptor 56
10354979	0.045101	0.001454	up	1.32731	0.408505	277.5803	208.9795	Als2	74018	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)
10396205	0.045101	0.001459	up	1.340998	0.423307	307.8103	229.7347	Arid4a	238247	AT rich interactive domain 4A (RBP1-like)
10507137	0.045101	0.001459	down	-1.45691	-0.54291	744.9989	1083.016	Pdzk1ip1	67182	PDZK1 interacting protein 1
10530998	0.045101	0.001457	down	-1.61564	-0.6921	342.2482	555.949	Tmprss11f	243083	transmembrane protease, serine 11f
10564805	0.045101	0.001455	down	-1.38967	-0.47474	322.0679	448.4311	Pex11a	18631	peroxisomal biogenesis factor 11 alpha
10586017	0.045101	0.001454	up	1.313648	0.393578	617.2942	470.1257	Uaca	72565	uveal autoantigen with coiled-coil domains and ankyrin repeats
10350039	0.04513	0.001462	up	1.297857	0.376131	813.5393	626.7254	Rabif	98710	RAB interacting factor
10584653	0.04513	0.001463	down	-1.46799	-0.55384	294.528	432.0084	C1qtnf5 M235312 2 C1q and tumor necrosis factor related protein 5 membrane-type frizzled-related protein		
10373202	0.045153	0.001465	up	1.304577	0.383582	1367.612	1048.219	Shmt2	108037	serine hydroxymethyltransferase 2 (mitochondrial)
10476299	0.045174	0.001467	up	1.329195	0.410553	354.2928	266.7582			
10366519	0.045285	0.001474	down	-1.30022	-0.37876	75.081	97.59986	5330438D1	327824	RIKEN cDNA 5330438D12 gene
10582649	0.045285	0.001474	up	1.34434	0.426898	109.7925	81.7375	Pgbd5	209966	piggyBac transposable element derived 5
10404380	0.045415	0.00148	down	-1.39412	-0.47935	1158.009	1611.117	Dusp22	105352	dual specificity phosphatase 22
10456392	0.045423	0.001482	down	-1.34129	-0.42362	516.0145	692.7062	Cidea	12683	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A
10430851	0.045465	0.001485	down	-1.41163	-0.50212	683.3184	965.5918	Cyp2d22	56448	cytochrome P450, family 2, subfamily d, polypeptide 22
10595324	0.045571	0.00149	down	-1.49438	-0.57954	228.7223	341.667	Htr1b	15551	5-hydroxytryptamine (serotonin) receptor 1B
10396511	0.045764	0.001499	down	-1.28877	-0.366	344.5494	444.0603	Syne2	319565	synaptic nuclear envelope 2
10596481	0.045764	0.001499	up	1.409416	0.495097	369.9385	262.9846	Abhd14a	68644	abhydrolase domain containing 14A
10512067	0.045795	0.001502	up	1.344487	0.427056	618.2987	459.3771	Ddx58	230073	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
10360040	0.045816	0.001505	down	-1.38488	-0.46976	143.3146	198.1149	Fcgr3	14131	Fc receptor, IgG, low affinity III
10394749	0.045816	0.001506	down	-1.44926	-0.53531	204.4429	295.9887	Nol10	217431	nucleolar protein 10
10424559	0.045988	0.001513	up	1.355347	0.438662	192.9373	142.1557	Khdrbs3	13992	KH domain containing, RNA binding, signal transduction associated 3
10401172	0.046049	0.001518	down	-1.49586	-0.58098	321.3334	482.6972	Vti1b	53612	vesicle transport through interaction with t-SNAREs 1B homolog
10573203	0.046049	0.001518	down	-1.42004	-0.50593	673.4586	957.0988	Gipc1	67903	GIPC PDZ domain containing family, member 1
10407097	0.046157	0.001523	down	-1.36274	-0.44651	1014.358	1381.205	Pde4d	238871	phosphodiesterase 4D, cAMP specific
10349147	0.046185	0.001527	down	-2.04866	-1.03468	65.95695	133.7536	Serpinh7	116872	serine (or cysteine) peptidase inhibitor, clade B, member 7
10519321	0.046185	0.001527	down	-1.51305	-0.59746	2728.317	4117.978	Gm15772 100034726 ribosomal protein L26 pseudogene		
10415784	0.046234	0.001531	down	-1.36332	-0.44713	1045.858	1425.216	Trim13	66597	tripartite motif-containing 13
10508879	0.046237	0.001534	up	1.351978	0.435072	536.4893	397.2391	Fam46b	100342	family with sequence similarity 46, member B
10544523	0.046237	0.001534	down	-1.46755	-0.5534	127.722	187.0094	Rny1	19872	RNA, Y1 small cytoplasmic, Ro-associated
10404069	0.046273	0.001541	up	1.349544	0.432472	269.8367	199.6913	Hist1h1a	80838	histone cluster 1, H1a
10433536	0.046273	0.001542	down	-1.28891	-0.36615	418.4395	539.3232	Clec16a	74374	C-type lectin domain family 16, member A
10518300	0.046273	0.001537	up	1.324003	0.404906	493.5619	372.7323	Tnfrsf1b	21938	tumor necrosis factor receptor superfamily, member 1b
10598626	0.046273	0.001542	down	-1.43802	-0.52409	1129.716	1619.18	Tspan7	21912	tetraspanin 7
10476545	0.04634	0.001545	down	-1.48917	-0.57451	112.0419	167.0464	Sptlc3	228677	serine palmitoyltransferase, long chain base subunit 3
10364262	0.04688	0.001566	down	-1.43467	-0.52072	133.1151	190.3779	Itgb2	16414	integrin beta 2
10443131	0.04688	0.001567	down	-1.30113	-0.37976	849.7315	1105.506	Itp3	16440	inositol 1,4,5-triphosphate receptor 3
10484503	0.04688	0.00157	up	1.362786	0.446558	97.21409	71.27352	Lrrc55	241528	leucine rich repeat containing 55
10489246	0.04688	0.001569	down	-1.81659	-0.86123	412.7614	740.1893	Mafb	16658	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)
10499921	0.047007	0.001576	up	1.889343	0.917884	778.0522	408.6096	Lce1d	69611	late cornified envelope 1D
10588691	0.047047	0.001579	down	-1.39722	-0.48256	1098.417	1537.97	Hyal1 Natf 15586 56 hyaluronoglucosaminidase 1 N-acetyltransferase 6		

10392063	0.047087	0.001582	up	1.296489	0.37461	957.4465	738.5748	Limd2 Sm: 67803 83 LIM domain containing 2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
10508829	0.047536	0.001599	up	1.323318	0.40416	295.1128	223.121	Map3k6 53608 mitogen-activated protein kinase kinase kinase 6
10595404	0.047571	0.001601	down	-1.35167	-0.43475	772.3046	1043.309	Fam46a 212943 family with sequence similarity 46, member A
10367717	0.047592	0.001604	down	-1.38102	-0.46574	917.9693	1267.036	BC013529 215751
10368343	0.047899	0.001617	down	-1.61603	-0.69246	401.9778	654.6815	Arg1 11846 arginase, liver
10571241	0.047899	0.001617	up	1.284846	0.361596	265.4673	206.6239	Purg 75029 purine-rich element binding protein G
10489471	0.047965	0.001625	down	-1.34802	-0.43084	92.13826	124.2413	Matn4 17183 matrilin 4
10555297	0.047965	0.001622	down	-1.80527	-0.85221	63.07825	115.2002	Kcne3 57442 potassium voltage-gated channel, Isk-related subfamily, gene 3
10600357	0.047965	0.001624	down	-1.35345	-0.43664	485.414	657.7478	Taz 66826 tafazzin
10400984	0.047997	0.001629	down	-1.3529	-0.43606	160.2889	217.0242	Tmem30b 238257 transmembrane protein 30B
10478884	0.047997	0.001631	up	1.288299	0.365468	1148.119	891.168	Snai1 20613 snail homolog 1 (Drosophila)
10567171	0.047997	0.001629	down	-1.53021	-0.61373	214.2366	329.7354	Rps13 68052 ribosomal protein S13
10380381	0.048083	0.001635	up	1.314129	0.394106	2072.299	1575.992	Tob1 22057 transducer of ErbB-2.1
10476252	0.048146	0.001641	down	-1.31595	-0.3961	167.3666	220.233	Cdc25b 12531 cell division cycle 25 homolog B (S. pombe)
10523134	0.048146	0.001642	down	-1.53826	-0.6213	441.1903	679.2973	Pf4 56744 platelet factor 4
10531931	0.048146	0.001639	down	-1.7671	-0.82138	187.1031	327.0449	Sparcl1 13602 SPARC-like 1
10586166	0.048162	0.001645	down	-1.37772	-0.46228	280.1991	386.7795	
10452613	0.048707	0.001665	up	1.2979	0.37618	219.4091	169.0682	Arhgap28 268970 Rho GTPase activating protein 28
10587880	0.048736	0.001668	up	1.469099	0.554931	131.32	89.15618	Pcolce2 76477 procollagen C-endopeptidase enhancer 2
10408557	0.04878	0.001671	down	-1.57234	-0.65291	214.3742	339.1694	Serp1nb1a 66222 serine (or cysteine) peptidase inhibitor, clade B, member 1a
10354374	0.049014	0.001686	down	-1.87666	-0.90817	334.0258	616.883	Slc40a1 53945 solute carrier family 40 (iron-regulated transporter), member 1
10394786	0.049014	0.001693	up	1.317365	0.397655	209.252	158.962	1700030C169513 23 RIKEN cDNA 1700030C10 gene hypothetical protein LOC236260
10431210	0.049014	0.001694	down	-1.40056	-0.486	117.9513	165.6336	Wnt7b 22422 wingless-related MMTV integration site 7B
10449955	0.049014	0.001692	up	1.363787	0.447619	573.0893	420.6456	Cyp4f13 170716 cytochrome P450, family 4, subfamily f, polypeptide 13
10460253	0.049014	0.001693	down	-1.62131	-0.69716	2577.315	4144.125	Aldh3b2 621603 aldehyde dehydrogenase 3 family, member B2
10462406	0.049014	0.001689	down	-1.29692	-0.37509	1563.469	2027.534	C030046E1 226089 RIKEN cDNA C030046E11 gene
10496405	0.049014	0.001682	up	1.925001	0.944859	423.62	218.3583	Gm5105 329763 predicted gene 5105
10497012	0.049014	0.001692	down	-1.40274	-0.48825	68.67232	96.53736	4922501L1 209601 RIKEN cDNA 4922501L14 gene
10524866	0.049014	0.001689	down	-1.31889	-0.39932	274.902	362.5114	BC023744 231668
10468980	0.049041	0.001697	up	1.34849	0.431345	233.2751	172.7748	Fam107b 66540 family with sequence similarity 107, member B
10601581	0.049041	0.001699	down	-1.33637	-0.41832	134.0061	178.8793	9230105E1 319236 6 RIKEN cDNA 9230105E10 gene predicted gene 8833 predicted gene 4992
10460400	0.049257	0.00171	down	-1.3933	-0.4785	390.4788	543.0163	Pcx 18563 pyruvate carboxylase
10480027	0.049257	0.001714	down	-1.34193	-0.42431	210.4795	282.2658	Zbtb2 381990 zinc finger and BTB domain containing 2
10505779	0.049257	0.001715	down	-1.48363	-0.56913	145.3938	215.8921	Acer2 230379 alkaline ceramidase 2
10509441	0.049257	0.001711	up	1.438185	0.52425	1572.849	1097.098	Ece1 230857 endothelin converting enzyme 1
10540705	0.049257	0.001713	down	-1.36257	-0.44633	684.7842	933.5144	Il17rc 171095 interleukin 17 receptor C
10481304	0.049307	0.001718	up	1.288207	0.365364	144.2653	112.0096	Gfi1b 14582 growth factor independent 1B
10447130	0.04933	0.001723	down	-1.44338	-0.52945	275.736	397.7856	Pkdcc 106522 protein kinase domain containing, cytoplasmic
10475866	0.04933	0.001724	down	-1.49696	-0.58204	357.3879	533.9146	Bcl2l11 12125 BCL2-like 11 (apoptosis facilitator)
10521759	0.04933	0.001721	up	1.31786	0.398197	1026.398	779.4603	Slit2 20563 slit homolog 2 (Drosophila)
10427628	0.049378	0.001727	down	-1.3503	-0.43328	154.3762	208.4588	Il7r 16197 interleukin 7 receptor
10403081	0.049383	0.001733	up	1.299296	0.37773	103.9721	80.01584	Wdr60 217935 WD repeat domain 60
10419370	0.049383	0.001731	down	-1.33203	-0.41363	596.3099	794.6001	Exoc5 105504 exocyst complex component 5
10425335	0.049383	0.001731	down	-1.3218	-0.40251	318.3993	420.516	Syng1 20972 synaptogyrin 1
10373569	0.049682	0.001753	down	-1.45942	-0.5454	5062.022	7372.087	Rpsa Gm9:16785 10 ribosomal protein SA ribosomal protein SA pseudogene
10550451	0.049682	0.001747	up	1.509916	0.594468	124.4947	82.27453	
10557960	0.049682	0.001752	up	1.342109	0.424501	1097.069	817.8352	Tgfb1i1 21804 transforming growth factor beta 1 induced transcript 1
10563108	0.049682	0.001755	down	-1.37192	-0.4562	344.7509	472.9459	Snord35a 27211 small nucleolar RNA, C/D box 35A
10575074	0.049682	0.001754	up	1.287196	0.364232	205.7771	159.894	Tmco7 272538 transmembrane and coiled-coil domains 7
10578324	0.049682	0.001747	down	-1.32702	-0.40819	205.7282	272.7287	Mtus1 102103 mitochondrial tumor suppressor 1
10595793	0.049682	0.001749	down	-1.31419	-0.39417	2098.771	2758.24	Atp1b3 11933 ATPase, Na+/K+ transporting, beta 3 polypeptide
10382866	0.049992	0.001768	down	-1.34789	-0.4307	119.9313	161.8962	Mgat5b 268510 mannoside acetylglucosaminyltransferase 5, isoenzyme B